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HIGH LEVEL PANEL *for*
**A SUSTAINABLE
OCEAN ECONOMY**

BLUE PAPER

The Ocean Genome:

Conservation and the Fair, Equitable and Sustainable Use of Marine Genetic Resources

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About this Paper

Established in September 2018, the High Level Panel for a Sustainable Ocean Economy (HLP) is a unique initiative of 14 serving heads of government committed to catalysing bold, pragmatic solutions for ocean health and wealth that support the Sustainable Development Goals and build a better future for people and the planet. By working with governments, experts and stakeholders from around the world, the HLP aims to develop a road map for rapidly transitioning to a sustainable ocean economy, and to trigger, amplify and accelerate responsive action worldwide.

The HLP consists of the presidents or prime ministers of Australia, Canada, Chile, Fiji, Ghana, Indonesia, Jamaica, Japan, Kenya, Mexico, Namibia, Norway, Palau and Portugal, and is supported by an Expert Group, Advisory Network and Secretariat that assist with analytical work, communications and stakeholder engagement. The Secretariat is based at World Resources Institute.

The HLP has commissioned a series of ‘Blue Papers’ to explore pressing challenges at the nexus of the ocean and the economy. These Blue Papers summarise the latest science and state-of-the-art thinking about innovative ocean solutions in the technology, policy, governance and finance realms that can help accelerate a move into a more sustainable and prosperous relationship with the ocean. This paper is part of a series of 16 papers that are being published between November 2019 and June 2020. It considers the existing and potential benefits associated with the ocean genome, the threats it is facing, and the crucial importance of conservation to maintain the ocean’s genetic diversity. The paper also explores how efforts to promote inclusive innovation and better governance can contribute to more equitable sharing of benefits derived from the use of marine genetic resources.

This Blue Paper is an independent input to the HLP process and does not represent the thinking of the HLP, Sherpas or Secretariat.

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Foreword

The High Level Panel for a Sustainable Ocean Economy (HLP) commissioned us, the co-chairs of the HLP Expert Group (a global group of over 70 content experts), to organise and edit a series of ‘Blue Papers’ to explore pressing challenges at the nexus of the ocean and the economy. The HLP identified 16 specific topics for which it sought a synthesis of knowledge and opportunities for action. In response, we convened 16 teams of global content experts. Each resulting Blue Paper was independently peer-reviewed and revised accordingly. The final Blue Papers summarise the latest science and state-of-the-art thinking on how technology, policy, governance and finance can be applied to help accelerate a more sustainable and prosperous relationship with the ocean, one that balances production with protection to achieve prosperity for all, while mitigating climate change.

Each Blue Paper offers a robust scientific basis for the work of the HLP. Together, they provide the foundation for an integrated report to be delivered to the HLP. In turn, the HLP plans to produce by mid-2020 its own set of politically endorsed statements and pledges or recommendations for action.

The ocean genome is the foundation upon which all marine ecosystems rest. As such, a sustainable ocean economy is one that prioritises the conservation and sustainable use of the ocean genome and leads to equitable outcomes for all. This paper takes a holistic approach to the issue of the ocean genome by analysing our understanding of the genetic diversity of life within the ocean, the threats posed to such diversity, the benefits it provides in the context of a changing world and the tools and approaches that can protect it. We are delighted to be able to share this paper because it provides guidelines to ensure smart conservation and sustainable and equitable use of the ocean genome.

As co-chairs of the HLP Expert Group, we wish to warmly thank the authors, the reviewers and the Secretariat at World Resources Institute for supporting this analysis. We thank the members of the HLP for their vision in commissioning this analysis. We hope they and other parties act on the opportunities identified in this paper.



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Key Messages

- A sustainable ocean economy prioritises the conservation and sustainable use of the 'ocean genome' and leads to equitable outcomes for all.
- Marine life is incredibly diverse—having existed in the ocean for three times as long as life has existed on land—and comprises a minimum of 2.2 million existing eukaryotic marine species, of which some 91 percent remain undescribed.
- The ocean genome is the genetic material present in all marine biodiversity, including both the physical genes and the information they encode. It determines the abundance and resilience of biological resources, including fisheries and aquaculture, which collectively form a pillar of global food security and human well-being. It is the foundation upon which all marine ecosystems, including their functionality and resilience, rest.
- The ocean genome is threatened by overexploitation, habitat loss and degradation, pollution, impacts from a changing climate, invasive species and other pressures, as well as their cumulative and interacting effects.
- Fully and highly protected marine protected areas (MPAs) are proven tools for safeguarding genetic diversity at the ecosystem level, along with other effective area-based conservation measures (OECMs)—if they are effectively designed and managed. Yet, only 2.5 percent of the ocean is in MPAs considered fully or highly protected. Urgent action is required to apply measures based on scientific evidence and meet internationally agreed targets along with growing calls to fully or highly protect at least 30 percent of the ocean to support ocean health, productivity and resilience.
- In parallel, significant efforts are needed to ensure that genetic diversity in areas outside of MPAs and OECMs is conserved. These include effectively managing the sustainable use of resources; preventing habitat degradation; cautiously using previously unexploited places; enforcing and complying with regulations; and protecting rare, threatened and endangered species and populations.
- Rapid advances in sequencing technologies and bioinformatics have enabled exploration of the ocean genome. These new findings are informing innovative approaches to conservation and a growing number of commercial biotechnology applications, from anticancer treatments to cosmetics and industrial enzymes.
- At the same time, the environmental, social and ethical risks arising from using existing and new biotechnologies such as CRISPR (Clustered Regularly Interspaced Short Palindromic Repeats) remain under-investigated and poorly known, especially in marine environments.
- The capacity to undertake genomic research and to access, download and analyse massive amounts of sequence data relating to marine genetic resources is inequitably distributed among countries. There is an urgent need to build capacity; increase access to affordable innovation and technologies; and ensure that research and innovation is ethically and socially acceptable, environmentally sustainable, and delivering solutions to the problems of the poorest and most marginalised communities and income groups.
- Scientific and commercial benefits arising from using the ocean genome must be fairly and equitably shared. Reforms to intellectual property rights should support this shift.
- International legal measures governing aspects of the conservation and use of the ocean genome must comprehensively, actively and persistently engage with scientists and other actors from both commercial and noncommercial sectors. This will ensure that regulations reflect up-to-date scientific knowledge and understanding, are needs based and enable a shared sense of responsibility to conserve and protect the ocean genome.
- This paper takes a holistic approach to evaluating the prospects for conservation and sustainable use of the ocean genome. It does this by analysing our understanding of the genetic diversity of life within the ocean, the threats posed to such diversity, the benefits provided by genetic diversity and the ecosystems it supports in the context of a changing world, as well as tools and approaches for ensuring fair and equitable sharing of these benefits.
- The paper concludes with opportunities for action that, if followed, would improve our understanding of the ocean genome and support its conservation as well as its sustainable and equitable use.

1. Introduction

1.1 Overview

The ‘ocean genome’ is the foundation upon which all marine ecosystems rest and is defined here as the ensemble of genetic material present in all marine biodiversity, including both the physical genes and the information they encode. The dynamics of the ocean genome enable organisms to adapt to diverse ecological niches and changing environmental conditions. The ocean genome also determines the productivity and resilience of biological resources, including fisheries and aquaculture, which collectively support global food security, human well-being and a sustainable ocean economy.

A deeper understanding of the ocean genome has contributed to an increased awareness of the pressures facing marine biodiversity, including those from habitat loss and degradation; overfishing and other extractive activities such as mining; climate change and the spread of invasive species. Rapid advances in sequencing technologies and bioinformatics have enabled exploration of the ocean genome, which is informing the designation of marine protected areas as well as innovative approaches to conservation such as the establishment and incorporation of temporal genetic monitoring datasets into conservation planning and management as well as the sustainable use of resources. Exploring the ocean genome has also enabled a growing number of commercial biotechnology applications, extending from multiple anticancer treatments to cosmetics and industrial enzymes. At the same time, the environmental, social and ethical risks arising from the use of existing and new biotechnologies such as CRISPR (Clustered Regularly Interspaced Short Palindromic Repeats) remain under-investigated and poorly known, especially in marine environments.

As awareness of the unique nature and consequent value of the ocean genome grows and the importance of ensuring its conservation and sustainable use becomes

more pressing, so too has the complexity of the national and transnational legal, institutional and ethical contexts that govern it. Within national jurisdictions, the Convention on Biological Diversity (CBD) and its Nagoya Protocol comprise key governance mechanisms for the conservation and sustainable use of marine biodiversity. For biodiversity in areas beyond national jurisdiction (BBNJ), a new United Nations (UN) agreement is under negotiation focusing on issues of crucial importance to the ocean genome, including area-based management tools, access to and intellectual property protection of marine genetic resources and their commercial exploitation, as well as capacity building.

Sharing benefits arising from the use of the ocean genome is a central issue. There is an urgent need to promote inclusive and responsible research and innovation that addresses equity differentials and fosters enhanced capacity and access to technology while facilitating the realisation of commitments to conserve and sustainably use the ocean’s genetic diversity.

1.2 Scope and Ambition

This Blue Paper takes a holistic approach to the issue of the ocean genome and addresses

- our understanding of the genetic diversity of life within the ocean;
- the threats posed to these building blocks of life;
- the many benefits this diversity provides for functional ocean ecosystems, humanity and the biosphere in the context of a changing world;
- the tools and approaches that have been demonstrated to protect and restore genetic, species and ecosystem diversity; and
- stumbling blocks and opportunities for achieving sustainable and equitable use.

After introducing the ocean genome and the ecological benefits it provides, we present an overview of the expanding range of commercial activities it enables. This is followed by a description of the challenges facing the conservation and sustainable use of the ocean genome, including the primary anthropogenic threats to marine biodiversity. We then discuss the pathways to solutions, spanning novel conservation approaches, efforts to promote inclusive and responsible research and innovation and equitable access and benefit sharing from the use of marine genetic resources.

Ultimately, individuals, communities, companies and states have all contributed to different degrees to the degraded state of marine ecosystems. Their reliance on and stewardship of these resources varies, as do the benefits they derive from the ocean genome. Equity and sustainability are therefore crosscutting themes, and attention is given not only to evidence of inequitable and unsustainable practices, but also to the institutional and informal approaches and tools available to address these challenges.

The paper concludes with a number of opportunities for action that, if adopted, would improve our understanding of the ocean genome, and contribute to ensuring its conservation as well as its sustainable and equitable use.

1.3 What Is the Ocean Genome and Why Is It Uniquely Important?

The ocean covers 70 percent of the Earth's surface and represents 99 percent of the habitable space on the planet by volume (Costanza 1999). Life has existed in the ocean for at least 3.7 billion years, over three times as long as on land (Pearce et al. 2018; Strother et al. 2011). This long evolutionary history has resulted in some 2.2 million existing eukaryotic marine species (estimates range from 0.3 to 10 million species), of which 230,000 are confirmed (Mora et al. 2011; Louca et al. 2019). Marine species have been discovered at a higher rate than terrestrial species since the 1950s (Costello et al. 2012); indeed, the ocean harbours unique biodiversity that dwarfs the biodiversity found on land. For example, of the 34 major known animal phyla, 33 are found in the ocean while only 12 are found on land (Jaume and Duarte 2006). On land, a single phylum accounts for 90

percent of all terrestrial animal species (Arthropoda—including insects and arachnids), but in the ocean 90 percent of the animal species are distributed across eight phyla (Mollusca, Arthropoda, Chordata, Annelida, Nematoda, Cnidaria, Bryozoa and Porifera), showing a remarkable range of biodiversity at higher taxonomic levels (Jaume and Duarte 2006; Sullivan et al. 2019). Depending on the taxon group, some 24–98 percent of eukaryotic marine species remain undescribed. Even less is known about prokaryotic marine life (bacteria and archaea) and viruses, which form the majority of life in the ocean by weight—some 1.2×10^{29} prokaryote cells (Bar-On et al. 2018) and 1.3×10^{30} virus particles (Cobián Güemes et al. 2016). The estimated number of microbial species (operational taxonomic units of bacteria, archaea and microscopic fungi) in the ocean ranges widely, due to extrapolation based on scaling laws, from 1.0×10^6 to 3.0×10^{27} (Locey and Lennon 2016; Louca et al. 2019; Mora et al. 2011).

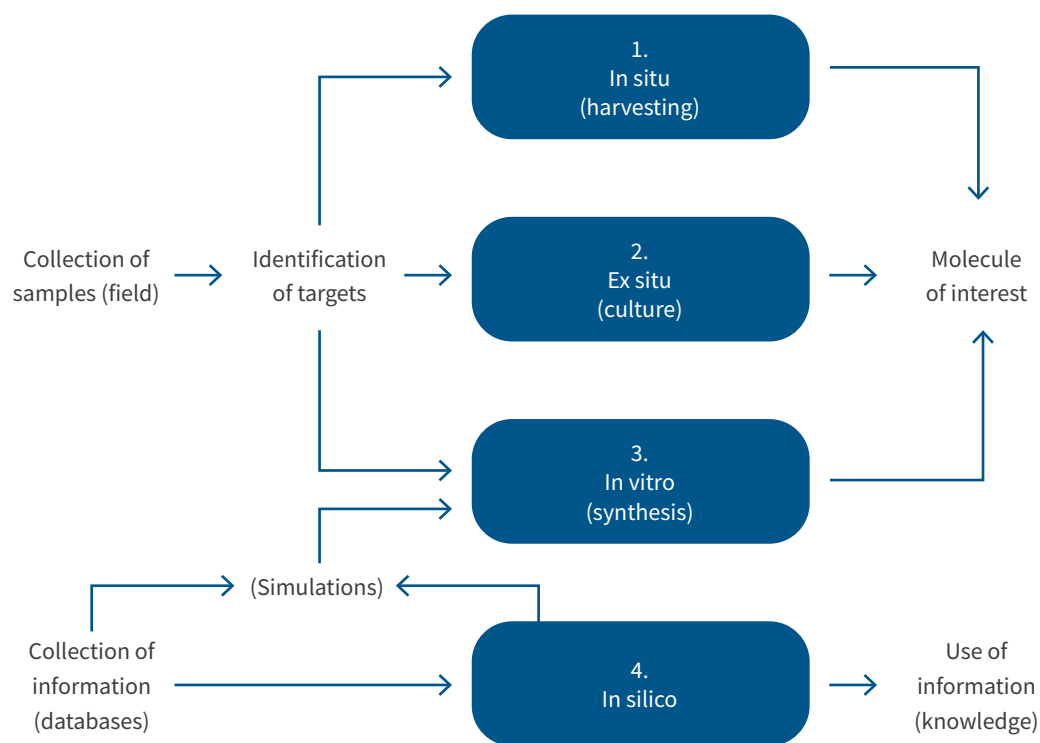
Genetic diversity—the total number of genetic characters in the genetic makeup of a species—is a foundational component of biodiversity, strongly determining the biogeography of species distribution and allowing us to indirectly retrace the history of life and its evolution on Earth. Its conservation is necessary for evolution and, through genetic variability, for greater population fitness and potential to adapt and recover (Reed and Frankham 2003). Such attributes are especially critical in the context of rapid environmental change (Hilborn et al. 2003; Ellegren and Galtier 2016). Genetically diverse fish stocks, for instance, may be able to exploit a range of environments and have a better ability to withstand anomalous conditions, and are therefore of key interest to fishery managers (Schindler et al. 2010; Ruzzante et al. 2006). Genetic diversity is also important for understanding long-term climate resilience, such as the ability of some corals to be heat resistant in the face of mass bleaching events (Norström et al. 2016; Cornwall 2019; Morikawa and Palumbi 2019).

The 'ocean genome' is defined here as the ensemble of genetic material present in all marine biodiversity, including both the physical genes and the information they encode. While discussions of genetic resources typically centre on physical resources, the informational component of genes has become increasingly important. This is due to the possibility of storing the nucleotide sequences of DNA (deoxyribonucleic acid) and RNA

(ribonucleic acid) as digital information and using this information to create proteins, molecular processes, innovation and even organisms (Gibson et al. 2010; Hutchison et al. 2016). Patent and ownership claims now often centre on using genetic sequence data in addition to the physical genetic material from which they were extracted. Patent applications require sequences to be disclosed, depending on what is being patented, and many scientific journals also require sequences to be deposited and an accession number to be supplied prior to publishing associated research (Giles 2011; Blasiak

et al. 2019). Limiting genetic resources to their material representation does not encompass the diverse ways in which these resources are used and commercially exploited; therefore, for the purposes of this paper, we conceptualise genetic material, and by extension the ocean genome, to include both physical molecules and their genetic sequence information (Elkin-Koren and Netanel 2002). Figure 1, developed by Broggiato et al. (2014), provides an illustration of the pathways that can lead to using marine genetic resources (MGR) after sampling and identifying interesting applications.

Figure 1. Pathways for Using Marine Genetic Resources



Notes:

1. Harvest of in-situ biological material.

2. Ex situ culture of biological material.

3. In vitro laboratory synthesis of interesting molecules.

4. Use of information in databases (in silico), sometimes also leading to the use of this information for in-vitro synthesis.

Source: Broggiato et al. 2014.

Box 1. A Note on Scientific Terminology and Legal Scope

Following the negotiations and signing of the Convention on Biological Diversity (CBD), one observer claimed that ‘biodiversity is dead’ on the basis that its definition was simply too inclusive and non-specific^a. Over two decades later, the term ‘genetic resources’ is causing similar disquiet due to its scope^b, and an expanding library of sometimes overlapping terminology is complicating the global task of governing the access, use and circulation of genetic resources. The following is a brief guide to the current or emerging legal terminology relevant to this paper:

Biodiversity (from CBD): The variability among living organisms from all sources including, among others, terrestrial, marine and other aquatic ecosystems and the ecological complexes of which they are part; this includes diversity within species, between species and of ecosystems.

Genetic resources (from CBD): Genetic material of actual or potential value.

Genetic material (from CBD): Any material of plant, animal, microbial or other origin containing functional units of heredity, such as individual genes or genetic sequences.

Digital sequence information (or data): Used in association with research and development, and the use of genetic resources, this is a placeholder term in international discussions under the CBD. As used, it includes various types of information including nucleic acid sequences; information on sequence assembly that may describe whole genomes, individual genes or fragments; single nucleotide polymorphisms; information on gene expression structures including morphological data and phenotype; data on macromolecules and cellular metabolites; information on ecological relationships and abiotic factors of the environment; behavioural data; information related to taxonomy; and modalities of use. The term is typically used in negotiating processes linked to international agreements such as the CBD, United Nations Convention on the Law of the Sea (UNCLOS) and the International Treaty on Plant Genetic Resources for Food and Agriculture.

Genetic sequence data: The order of nucleotides found in nucleic acid molecules—DNA (deoxyribonucleic acid) or RNA (ribonucleic acid)—which contain the genetic information that determines the biological characteristics of an organism or a virus. The term is widely used in the scientific community, and is preferred by some parties to the CBD.

Nucleotide sequence data: The arrangement of nucleotides on strands of naturally occurring DNA or RNA. Information about the genetic resources arises through analysis of these data.

Marine genetic resources: The genetic material of marine plant, marine animal, microbial or other origin containing functional units of heredity, which have an actual or potential value. The scope of this term is subject to negotiations related to biodiversity in areas beyond national jurisdiction, but, as such, it is not defined or used in UNCLOS.

In many ways, the battle over terminology is central to the effective and equitable governance of genetic resources. The terms above straddle environmental and biotechnological norms, and are therefore defined both by tangible parameters such as location and place, as well as intangible parameters such as information and function.

Notes:

^a. Lautenschlager 1997.

^b. Thambisetty 2020.

1.4 How Do We Benefit from the Ocean Genome?

The ocean genome is the foundation upon which all marine ecosystems rest and is therefore integrally linked to the existence of all life on Earth, including humanity. Throughout human history, diverse cultures, societies and knowledges have evolved that are integrally linked to marine and coastal biodiversity, leading over time to the emergence of a rich diversity of social-ecological systems and worldviews in coastal regions around the world. As the custodians of many coastal areas, and the repositories of associated traditional knowledge, local and traditional communities have played a critical role in contributing such knowledge toward our food, medicines, cosmetics and emotional connections to the ocean.

Maintaining the health of ocean ecosystems is critical; these ecosystems provide over 50 percent of the oxygen on the planet, sustain vast fisheries generating 17 percent of the animal protein we consume and shape and regulate global climate patterns (FAO 2018; IPBES 2019). The genetic diversity within the ocean genome contributes to the capacity of species and populations to adapt to a changing ocean and helps mitigate the impacts associated with realised and projected climate change (Reed and Frankham 2003).

Marine plants, animals, fungi and microorganisms have evolved to occupy a variety of niches, being able to thrive in the extremes of heat, cold, water chemistry and darkness found in the ocean. The resulting adaptations are recorded in their genetic codes, enabling them to produce a wide variety of primary and secondary metabolites with significant biological activities that have attracted growing commercial interest from a range of industries (Blasiak et al. 2018; Arnaud-Haond et al. 2011; Arrieta et al. 2010). Applications include the development of industrial enzymes, pharmaceuticals, cosmeceuticals, nutraceuticals, antifoulants, adhesives and tools for research and conservation purposes (Leary et al. 2009). Over 34,000 marine natural products—naturally occurring molecules produced by marine organisms—have been discovered (MarinLit 2020), many with remarkable levels of bioactivity, resulting in rates of drug discovery from marine organisms that are up to 2.5 times the industry average (Carroll et al. 2019; Gerwick and Moore 2012; Arrieta et al. 2010).

In addition to these commercial uses, a range of noncommercial applications based on the ocean genome has also emerged. Through the use of genetic sequence data, a substantial and growing body of work has been done in the fields of evolution and ecology to inform our knowledge on taxonomy, connectivity, demography and evolution, while new techniques, such as the sampling of environmental DNA (eDNA), are enhancing our understanding of marine taxonomy and enabling noninvasive study methods (Hansen et al. 2018). DNA barcodes have also been used to help identify mislabeled seafood and fight wildlife trafficking (Di Muri et al. 2018). Finally, the potential of gene editing tools like CRISPR (Clustered Regularly Interspaced Short Palindromic Repeats) as novel conservation techniques is now being explored (Phelps et al. 2019), although its application remains theoretical. Moreover, environmental, social and ethical risks remain under-investigated and poorly known, especially for the marine environment (CSS et al. 2019; Jasanoff et al. 2015).

1.5 How Is the Ocean Genome at Risk?

Multiple threats face the ocean genome, largely through overexploitation, habitat destruction, pollution, invasive species and, increasingly, the degradation of marine ecosystems, all of which are additionally impacted by a changing climate (Aburto-Oropeza et al. 2020). Land-based activities such as high-input industrialised agriculture are leading to pollution and eutrophication from excessive nutrient runoff and expanding low-oxygen dead zones around river deltas. Coastal aquaculture (mariculture) can also have significant environmental impacts due to high nutrient inputs, chemical pollution, the removal of large amounts of fry from the wild and the large-scale destruction of coastal habitats such as mangroves, among other issues (Hamilton 2013; Ahmed and Glaser 2016). Mariculture has also created an immediate threat to the genetic diversity of native fish populations, most prominently perhaps in the southern hemisphere where salmonids, absent from the native fauna (Arismendi et al. 2009), have been introduced as aquaculture escapees and in areas supporting wild capture salmon fisheries (McGinnity et al. 2003; 2009). Shipping activities and the flow of ballast water and waste into the ocean have contributed to the spread of invasive species and pathogens, and to the creation of

anoxic, no-oxygen zones and toxic red tide algal blooms (Pitcher and Probyn 2016).

Ocean-based activities like trawl fisheries, mining, dredging and the construction of artificial islands are drastically reducing biodiversity and completely reshaping some marine environments (Halpern et al. 2008; Du Preez et al. 2020). Overfishing has led to the collapse of major fisheries like the Newfoundland cod fishery, where a regime shift has subsequently resulted in a restructuring of regional food webs (Pedersen et al. 2017). Overfishing is also damaging the genetic diversity of fish and bycatch species, with one study suggesting that overfished species carry about 18 percent fewer unique genetic variations than their lightly fished relatives (Pinsky and Palumbi 2014). In some cases, multiple threats combine synergistically; for instance, aquaculture salmon broodstock escapes and fishing of wild populations have led to the loss of genetic diversity (Waples et al. 2012).

At a global scale, the burning of fossil fuels has generated greenhouse gas emissions and led to climate change—and the ocean absorbs 93 percent of the increased heat associated with these greenhouse gas emissions (Resplandy et al. 2018). The majority of marine species have narrower windows of thermal tolerance compared with those of terrestrial species, and local extinctions of marine species have been twice as common as those of species on land based on a global dataset of the range-edge positions of species on land and in the sea (Pinsky et al. 2019). Increased heating of the ocean remains the biggest climate impact to date, with the absorption of excess carbon also resulting in ocean acidification, which has negatively impacted marine ecosystems as it interacts synergistically with other drivers of loss such as direct exploitation and pollution (IPBES 2019).

About 20 marine species are known to have gone extinct over the past 500 years (McCauley et al. 2015), yet this is likely an underestimate given that little is known about how many species inhabit the marine environment. Some marine species have not been observed for decades and could already be extinct, while others, including 25 percent of marine mammals, sharks and rays, are at risk of extinction or are globally threatened (IUCN 2019; Dulvy et al. 2014). Although advances in working with ancient DNA may still allow species' genomes to be recovered from remains held in museums

(McCormack et al. 2017), these would be devoid of the variability present in viable existing populations.

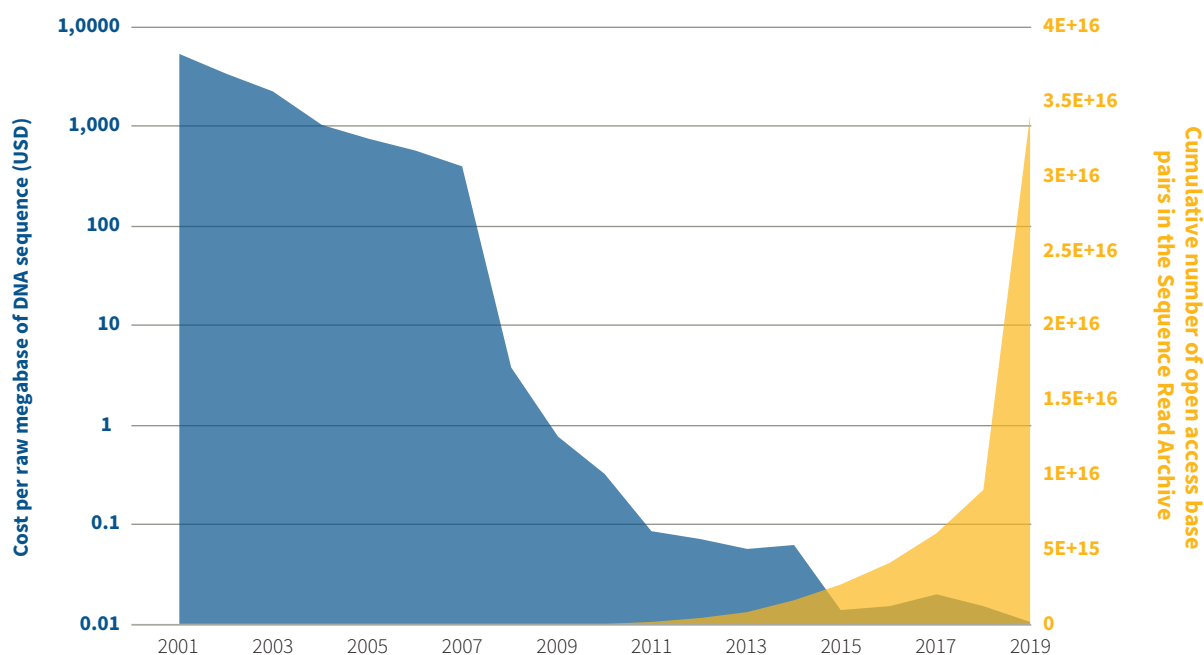
In the face of these threats to marine biodiversity and the ocean genome, adequate protection lags significantly. For most of human history the ocean was largely a de facto fully protected area that was too remote, too distant and too deep to exploit based on technological, economic and social limitations to access (Lubchenco and Gaines 2019). The creation of marine protected areas (MPAs) is in recognition of the need to reestablish places that are protected from exploitation. International targets including the Convention on Biological Diversity's Aichi Target 11 and the United Nations' Sustainable Development Goal 14 call for protecting 10 percent of the ocean by 2020 in MPAs and other effective area-based conservation measures (OECMs). Yet only 8 percent of the ocean is in any kind of designated MPA, including 5 percent in implemented MPAs, and only 2.5 percent is in fully or highly protected, implemented MPAs (Sala et al. 2018, updated via Marine Conservation Institute 2020). Further, there are growing calls from the scientific community for at least 30 percent of the ocean to be fully to highly protected to maintain a healthy, productive and resilient ocean (O'Leary et al. 2016; Gaines et al. 2010). In parallel, significant efforts are also needed to ensure that genetic diversity in areas outside MPAs and OECMs is conserved. This would include ensuring the sustainable use of resources; preventing habitat degradation; cautiously using previously unexploited places; and protecting rare, threatened and endangered species and populations.

Marine science has contributed significantly to revolutionary scientific and technological transformations in the life sciences and microbiology over the past two decades. Advances in genomic technologies, with sequencing costs declining 4,000-fold over the past decade (Green et al. 2017), mean that millions of DNA fragments can be sequenced simultaneously and inexpensively, creating an intensely data-rich field (see Figure 2) (Pevsner 2015). While such innovations have rapidly expanded the boundaries of our knowledge, vast knowledge gaps remain (Wetterstrand 2019). For instance, a large fraction of predicted genes from marine prokaryotes cannot be assigned functions (Sunagawa et al. 2015), and the functions of some 90 percent of genetic sequences collected from viruses remain unknown (Hurwitz and Sullivan 2013).

The rapidly growing field of synthetic biology now allows genes from different organisms, from different parts of the world, and from the ocean, soil and rivers to be combined into new patented organisms, including some synthesised components. Although the full contribution of MGR remains unknown, the Synthetic Biology Project reports at least 116 synthetic biology products and applications to be near to or on the market. The pace has rapidly increased over the past five years due to the introduction of fast, reliable and low-cost genome-editing techniques such as CRISPR, gene drives, TALENs (transcription activator-like effector nucleases) and oligonucleotide-directed mutagenesis techniques (Doudna and Charpentier 2014).

While such developments could yield important benefits, they also carry significant and often unknown risks. It is especially hard to predict the ecological consequences of introducing transformed organisms into marine environments. Containing introduced organisms is likely impossible and escaped transgenic fish or bacteria may establish viable populations in the wild, leading to altered natural ecosystems (Li et al. 2015). For instance, simple, commercially available kits (GeneArt® *Synechococcus* Engineering Kits) allow the photosynthetic cyanobacteria *Synechococcus*—responsible for up to 80 percent of the photosynthetic production in the oligotrophic ocean (Campbell et al. 1994)—to be genetically manipulated. Accidental release

Figure 2. Growth in GenBank Sequence Read Archive Records, and Trend in Average Cost of Sequencing



Notes: GenBank is the genetic sequence database of the United States National Institutes of Health. It maintains the Sequence Read Archive, a bioinformatics database of sequencing data, particularly the short reads of fewer than 1,000 base pairs typical of high-throughput sequencing methods. Also note that a logarithmic scale is used on the left axis. DNA stands for deoxyribonucleic acid.

Source: Data from National Center for Biotechnology Information. 2018. "Sequence Read Archive." Last updated August 2, 2018. <https://trace.ncbi.nlm.nih.gov/Traces/sra/sra.cgi>; Wetterstrand, K.A. 2019. "DNA Sequencing Costs: Data." National Human Genome Research Institute, Genome Sequencing Program. Last updated October 30, 2019. <https://www.genome.gov/about-genomics/fact-sheets/DNA-Sequencing-Costs-Data>.

of genetically modified strains in the ocean could, if viable, generate significant risks to the entire biosphere. The introduction of genome-editing techniques heightens such concerns, raising a suite of important questions about the governance and regulation of such technologies, about how problems are framed and solved, about how decisions get made about the release of modified organisms, and about the ethical considerations of international, intergenerational and interspecies justice (CSS et al. 2019).

1.6 How Is the Ocean Genome Governed and Regulated?

Governance of the ocean genome is complex. This is due, not least, to its conceptual broadness, the lack of boundaries for the spread of species in the ocean, the diversity of threats it faces and the mix of its commercial and noncommercial dimensions. The United Nations Convention on the Law of the Sea (UNCLOS), concluded in 1982, acts as a sort of ‘constitution’ for the ocean, specifying provisions for the protection of the marine environment. The convention itself does not refer to either biodiversity or genetic resources, but it does refer to the ‘conservation and utilization of living resources’ (Articles 61 and 62), including on the high seas (Articles 116 and 117). UNCLOS combines elements of different conceptions of property, with a governance approach to achieving social objectives (Allott 1992).

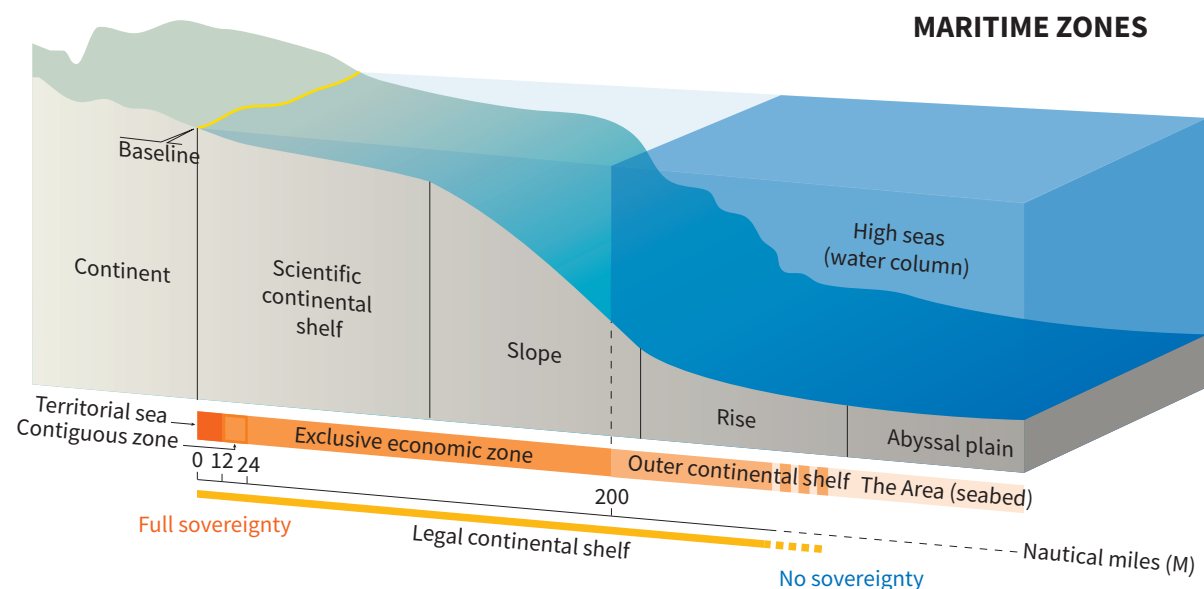
UNCLOS also defined a series of maritime zones and jurisdictional claims (Figure 3). Of particular relevance is the distinction between exclusive economic zones (EEZs) and areas beyond national jurisdiction (ABNJ), which comprise roughly 36 percent and 64 percent of the ocean’s area, respectively (Smith and Jabour 2018). According to UNCLOS, each coastal state has ‘sovereign rights [within its EEZ] for the purpose of exploring

and exploiting, conserving and managing the natural resources’. In the case of straddling and highly migratory fish stocks, many of which are found across multiple EEZs as well as ABNJ, the UN Fish Stocks Agreement applies (UN 1995). According to that agreement, states ‘shall apply the precautionary approach widely to conservation, management and exploitation [. . .] to protect the living marine resources and preserve the marine environment’.

Two international agreements under the CBD are of particular relevance: the Cartagena Protocol on Biosafety (2000), which aims to protect biological diversity from risks associated with biotechnology innovations, including genetically modified organisms; and the Nagoya Protocol on Access and Benefit-Sharing (2010), which aims to operationalise the CBD’s third objective. The 196 parties to the CBD have agreed to a wide range of obligations and relevant global targets, including safeguarding genetic diversity, operationalising the Nagoya Protocol and ensuring the integrity of ecosystems. Meeting these targets entails committing to protect 10 percent of coastal and marine areas by 2020 (Aichi Target 11) and maintaining the genetic diversity of wild animals, in addition to domesticated species, by using strategies to minimise genetic erosion (Aichi Target 13).

As mandated by UN General Assembly Resolution 72/249, an intergovernmental conference began in 2018 with the aim of negotiating a new legally binding international treaty on biodiversity in ABNJ (BBNJ). The negotiations cover four elements of a package: marine genetic resources including issues related to access and benefit sharing; measures such as area-based management tools, including MPAs; environmental impact assessments (EIAs); and capacity building and technology transfer.

Figure 3. Maritime Zones and Levels of Sovereignty



Source: Courtesy of Riccardo Pravettoni, cartographer. Pravettoni, R. 2010. "Maritime Zones." UN Environment Programme. <http://www.grida.no/resources/7923>.

These negotiations have been complicated by a focus on marine scientific research and the noncommercial aspects of research and development of MGR as well as the intersection with intellectual property issues. These controversies arise from the potential commercial exploitation of these resources, along with the desire to 'not undermine' mandates of the World Intellectual Property Organization (WIPO) and the World Trade Organization's Agreement on Trade-Related Aspects of

Intellectual Property Rights (TRIPS) (see Section 4.2). Additionally, definitions from the CBD and Nagoya Protocol have not been embraced by state parties in the negotiations. Strong views on the scopes and definitions of terms such as 'genetic resources', 'access', 'digital sequence information', 'derivatives' and even the need for, and scope of, a definition of 'utilisation' of genetic resources threaten the possibility of multilateral consensus positions (see Box 1).

2. Existing and Potential Benefits

2.1 Ecological Benefits Associated with Marine Genetic Diversity

The genomes of organisms encode the biological, morphological, behavioural and physiological attributes that define their structures and roles within ecosystems. In the ocean, functioning ecosystems supported by this genetic diversity contribute essential services, including producing and recycling organic matter, channelling energy across food webs, providing food, maintaining water quality, regulating climate, establishing cultural values and providing recreational opportunities and other ecosystem services that benefit humanity (Worm et al. 2006). The ecological benefits of the ocean genome are vast (See Section 1.2), with their scope broadly organised into two equally important and interrelated themes.

First, genetic diversity in the ocean is critical because it stabilises ecosystems, as well as the species and ecological processes they encompass and the ecosystem services they provide. Genetic variability, including single nucleotide base pair substitution, insertion-deletion and structural variability, can result in the presence of species with redundant functions (Li et al. 2015) as well as genotypes within species that encode variable responses to environmental pressures. These support ecosystem stability and ensure that ecosystems remain functional even if unpredictable changes lead to the loss of some species, or the loss of within-species genetic diversity at the population level (Webster et al. 2017). For example, genetic variability across more than 100 discrete populations of Bristol Bay salmon in Alaska entails greater heterogeneity and resilience to anomalous conditions, resulting in lower variability in fisheries production and greater stability than that of a homogeneous population. This has also led to fewer fisheries closures for the fishing community (Schindler et al. 2010). At the ecosystem level, nutrients from the salmon spread throughout the system as predators feed on the population during spawning season.

Genetic diversity can also stabilise populations during restoration efforts. Seagrass restoration experiments in North America and Indonesia showed plots with higher genetic diversity had increased survival, density and/or growth (Reynolds et al. 2014). In the Chesapeake Bay, restoration efforts were linked to ecosystem services, including increased primary production and nutrient retention (Reynolds et al. 2012).

Second, genetic diversity enables biological variability and drives genetic potential, which allow species to persist in changing environmental conditions and to evolve as environments change over time. Overexploitation of and declines in marine populations can lead to dwindling population sizes and greater potential for lost genes compared with the greater standing genetic variation in larger populations. This variation helps species persist and adapt to perturbations (Thornburg et al. 2018), including those associated with anthropogenic changes. For example, an experiment on marine phytoplankton showed that cultures with higher genetic diversity were better able to withstand low salinities. High diversity in the simulated populations corresponded to the highest primary production and greatest nitrogen uptake under salinity stress (Sjöqvist and Kremp 2016). This is particularly important alongside increasing evidence that adaptation in some species can take place faster than previously thought; adaptation has been shown to occur in only 200 generations of short-lived species such as tropical diatoms (Jin and Agustí 2018). Corals also provide context for this adaptive capacity with their ability to respond relatively quickly via symbiont and microbiome shuffling, phenotypic plasticity, acclimatisation and adaptation. Some corals may have already adapted to ocean warming since the Industrial Revolution (Webster et al. 2017).

The ecosystem stability and adaptive potential afforded by genetic diversity are already vital to species,

populations and communities as we know them. Yet their future values may go beyond these, as systems change at rates that are unprecedented and in ways that are unexpected, involving additive and synergistic effects. This underscores the benefits of conserving the ocean genome (See Section 4.1), particularly in areas that are minimally explored but may harbour high genetic diversity and isolated populations, including the fragile communities on seamounts and in the deep sea (Taylor and Roterman 2017; Zeng et al. 2017).

2.2 Commercial Benefits of Marine Genetic Resources

An intact and healthy ocean genome provides not only ecological benefits but also the foundation that has enabled and supported a growing range of commercial applications. Although the monetary benefits associated with these innovations are notoriously difficult to quantify (see, for example, Figure 4), it is important to emphasise how these innovations contribute to human well-being. For instance, bioactive compounds from marine microorganisms associated with sea sponges are considered promising candidates for the development of novel antibiotics, which are relevant in the context of increasing antimicrobial resistance (El Samak et al. 2018). Likewise, the venoms of species such as cone snails are of interest for the development of new drugs (see, for example, Table 1) that could replace opioids and consequently lower instances of misuse (Zachos 2017).

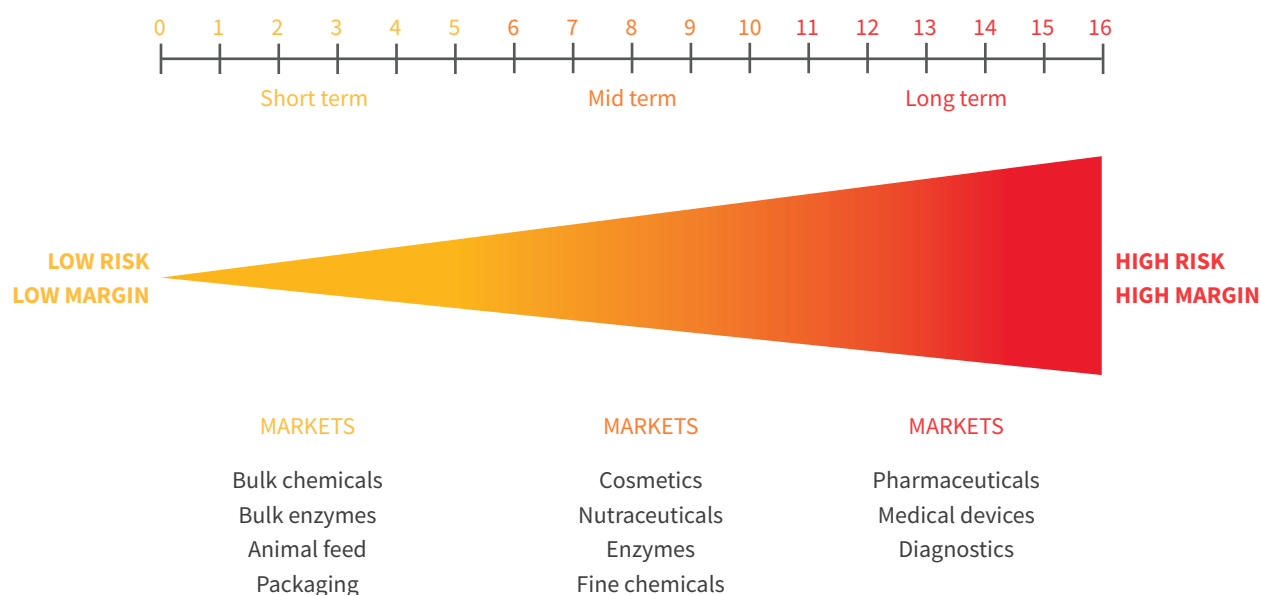
2.2.1 Marine drug discovery

The targeted search for compounds with biological activity against human diseases began in the late 1960s, but structures of compounds with high potency and selectivity were not defined until the 1980s. Extensive funding by the United States' National Cancer Institute along with its commitment to collect MGR globally meant that the focus was on the treatment of cancer, using compounds mostly collected from shallow tropical reefs and derived from marine invertebrates (Thornburg et al. 2018). As a result, five out of the eight clinically approved drugs derived from MGR are treatments for cancer; the remaining three are treatments for neuropathic pain, *Herpes simplex* virus and hypertriglyceridemia (Table 1). Out of these, seven are derived from marine invertebrates and one is derived from an oily fish. Development of and approval for all of these took many years.

As is the case for most drugs derived from MGR, the issue of a sustainable supply of the raw material/compound needs to be addressed. Attempts to solve this have involved several approaches, the most common being total chemical synthesis. Biotechnological approaches have also been employed, including hybrid synthetic/biotechnological approaches (Table 1). As an example, the case of Yondelis is described in Box 2. Two of the compounds in Table 1, Vidarabine and Cytarabine, now have second-generation analogues, Fludarabine (Fludara) and Nelarabine (Arranon), respectively (Alves et al. 2018). The European Medicines Agency has approved some over-the-counter medications based on MGR, such as Carragelose, a broadly effective antiviral drug that can be used to treat respiratory viruses such as the common cold (Alves et al. 2018). Currently, 28 marine-derived products are in clinical trials with a further 250 in preclinical investigation, all from around 33,000 reported marine natural products (MarinLit 2020). This is an astounding success rate when compared with terrestrial natural products. This success may be due in part to the vast taxonomic diversity in marine environments. For sessile marine invertebrates, the lack of an evolved immune system, combined with the pressures of preventing predation and competing for space and resources, may have led to the evolution of a chemical arsenal for survival.

Because of the supply issue associated with marine invertebrate-derived pharmaceutical candidates, the marine natural product research community has also focused on investigating marine microorganisms as sources of bioactive compounds. The long time lag between discovery and development (see Figure 4) means that most of these are still under preclinical investigation, with a smattering of microbial compounds in human clinical trials (Mayer et al. 2017) and many more at preclinical stages of development. The ability to sequence genomes quickly and cheaply coupled with bioinformatics tools—such as antiSMASH, which enables the rapid identification of secondary metabolite gene clusters in bacteria and fungi—often renders the inherent capacity for microorganisms to produce chemicals predictable even before testing begins (Medema et al. 2011). Challenges remain when genes are of completely unknown function, as is the case for many marine viruses. Advances in chemoinformatics, such as Global Natural Products Social Molecular Networking, allow

Figure 4. Risk, Profit Margins and Timelines for Commercial Activities Associated with Marine Genetic Resources



Source: Authors.

scientists to verify this latent talent, massively speeding up the biodiscovery process. Finally, advances in assay technology mean we use less material in bioassays while obtaining better quality data with higher information content (e.g. Caicedo et al. 2017). Compound isolation and structure determination, the final stages of the biodiscovery process that were previously a bottleneck, have also improved over the last decade (Chhetri et al. 2018). Much development is also focused on finding secure methods other than chemical synthesis to reliably and sustainably generate and modify bioactive compounds, using, for instance, synthetic biology (e.g. for the plant-derived natural product artemisinin, see Paddon and Keasling 2014) and enzymes in synthesis (e.g. for chemoenzymatic synthesis of cyanobactins, see Houssen et al. 2014).

Despite these developments, there is a lagging interest from major pharmaceutical companies to explore marine and terrestrial natural products as potential sources of new leads. Most large pharmaceutical companies have closed their natural product discovery sections, while small and medium-sized companies are filling this gap and leading the way in the development of innovative new treatments using MGR. Large pharmaceutical companies

will often buy small companies that have developed potential treatments to a certain stage of development, thus reducing their own risk while gaining access to the most recent innovations. The redefinition of the industrial landscape and the development of new tools and processes to investigate and develop MGR-derived bioactive compounds is thus critical for realising the overall potential of MGR for pharmaceutical discovery.

However, the benefits of marine biodiscovery extend far beyond the successful development of a product. Acknowledging the potential commercial value of biodiversity may lead to better funding for biodiversity surveys that access a broad range of marine life and assess these for bioactivity, which may lead to improved biodiversity conservation measures (Van Soest et al. 2012, see 4.1.3). A study carried out by the UN on the collaboration between Griffith University in Queensland, Australia, and the large pharmaceutical company AstraZeneca clearly articulates the regional benefits of engaging in biodiscovery research (Laird et al. 2008). These benefits include the availability of biorepositories of local species for further investigation; access to sophisticated bioassay and analytical equipment; the availability of highly skilled researchers and expertise;

Box 2. Development of the Anticancer Agent Yondelis (Trabectedin)

The discovery of the active pharmaceutical ingredient in Yondelis, Ecteinascidin-743, from the Caribbean ascidian (seasquirt) *Ecteinascidia turbinata*, was first reported by two research groups in 1990. It was shown to have antineoplastic activity in cell-based and animal models, being particularly effective against soft tissue sarcoma, for which no good treatment options existed at that time. It was shown to have a unique mechanism of action, interfering with DNA (deoxyribonucleic acid) transcription by binding to the minor groove of DNA, which together with the new structure offered a strong commercial outlook. It was licensed to the Spanish company PharmaMar, which started the development process in the early 1990s. Initially, material was produced by aquaculture (Figure B1, photo a), but this avenue was abandoned due to variability in production coupled with low yields, contamination issues and the high cost of infrastructure, among other reasons. Nevertheless, much of the clinical data were obtained using this aquaculture-derived material. To ensure a continuity of supply as well as quality of material, a semi-synthetic process was developed, modifying the fermentation product cyanosafrafrin-B to produce Yondelis economically. In 2007, the European Medicines Agency approved the use of Yondelis for advanced soft tissue sarcoma, but it took a further eight years for the U.S. Food and Drug Administration to follow suit (Figure B1, photo b). A combination treatment of Yondelis/Doxil is also being investigated as a second- and third-line treatment for ovarian cancer.

Figure B1. Successful Marine Drug Development

The product packaging for Yondelis (PharmaMar)



The Caribbean ascidian (seasquirt) *Ecteinascidia turbinata* in aquaculture.



Source: Text and photo b: used with permission from PharmaMar; photo a: S. Nash, Flickr.

Table 1. Marine-Derived Compounds Currently in Clinical Use

Plitidepsin	TRADEMARK YEAR	Aplidin® (2018)
	MARINE ORGANISM	Tunicate
	SOURCE	Mediterranean
	CHEMICAL CLASS	Depsipeptide
	MOLECULAR TARGET	eEF1A2
	DISEASE AREA	Cancer: Multiple myeloma, leukaemia, lymphoma
	COMPANY	Pharmamar
	ROUTE OF MANUFACTURE	Synthesis
Trabectedin (ET-743)	TRADEMARK YEAR	Yondelis® (2015)
	MARINE ORGANISM	Tunicate
	SOURCE	Caribbean
	CHEMICAL CLASS	Alkaloid
	MOLECULAR TARGET	Minor groove of DNA
	DISEASE AREA	Cancer: Soft tissue sarcoma, ovarian
	COMPANY	Pharmamar
	ROUTE OF MANUFACTURE	Semi-synthesis
Brentuximab vedotin (SGN-35)	TRADEMARK YEAR	Adcetris® (2011)
	MARINE ORGANISM	Mollusk/ cyanobacterium
	SOURCE	Mauritius
	CHEMICAL CLASS	ADC(MMAE)
	MOLECULAR TARGET	CD30 & microtubules
	DISEASE AREA	Cancer: Anaplastic large T-cell systemic malignant lymphoma, Hodgkin's disease
	COMPANY	Seattle Genetics
	ROUTE OF MANUFACTURE	Synthesis/biotechnology
Eribulin Mesylate (E7389)	TRADEMARK YEAR	Halaven® (2010)
	MARINE ORGANISM	Sponge
	SOURCE	Japan
	CHEMICAL CLASS	Macrolide
	MOLECULAR TARGET	Microtubules
	DISEASE AREA	Cancer: Metastatic breast cancer
	COMPANY	Eisai Inc.
	ROUTE OF MANUFACTURE	Synthesis
Omega-3-acid ethyl esters	TRADEMARK YEAR	Lovaza® (2004)
	MARINE ORGANISM	Fish
	SOURCE	Undisclosed but manufactured in the United States
	CHEMICAL CLASS	Omega-3 fatty acids
	MOLECULAR TARGET	Triglyceride-synthesising enzymes
	DISEASE AREA	Hypertriglyceridemia
	COMPANY	GlaxoSmithKline
	ROUTE OF MANUFACTURE	Refined from fish oils
Ziconotide	TRADEMARK YEAR	Prialt® (2004)
	MARINE ORGANISM	Cone snail
	SOURCE	Philippines
	CHEMICAL CLASS	Peptide
	MOLECULAR TARGET	N-Type calcium channel

Table 1. Marine-Derived Compounds Currently in Clinical Use (Cont'd)

Ziconotide	DISEASE AREA	Pain: Severe chronic pain
	COMPANY	Jazz Pharmaceuticals
	ROUTE OF MANUFACTURE	Biotechnology
Vidarabine (Ara-A)	TRADEMARK YEAR	Vira-A® (1976)
	MARINE ORGANISM	Sponge
	SOURCE	United States
	CHEMICAL CLASS	Nucleoside
	MOLECULAR TARGET	Viral DNA polymerase
	DISEASE AREA	Antiviral: Herpes simplex virus
	COMPANY	Mochida Pharmaceutical Co.
	ROUTE OF MANUFACTURE	Synthesis
Cytarabine (Ara-C)	TRADEMARK YEAR	Cytosar-U® (1969)
	MARINE ORGANISM	Sponge
	SOURCE	United States
	CHEMICAL CLASS	Nucleoside
	MOLECULAR TARGET	DNA polymerase
	DISEASE AREA	Cancer: Leukaemia
	COMPANY	Pfizer
	ROUTE OF MANUFACTURE	Synthesis

Source: Adapted from Midwestern University. n.d. "Approved Marine Drugs." <https://www.midwestern.edu/departments/marinepharmacology/clinical-pipeline.xml>).

an improved publication profile and an enhanced research reputation. All of these together can boost the capacity of a region to thrive via multiple medical and biotechnological industries while contributing to the protection and sustainable use of biodiversity itself.

2.2.2 Nutraceuticals

The original definition of nutraceuticals, or functional foods, was given as 'food, or parts of a food, that provide medical or health benefits, including the prevention and treatment of disease' (Mannion 1998). Regulation for nutraceuticals is currently changing, with stricter rules being developed in many jurisdictions to prevent unrealistic claims of possible benefits. Marine resources have a huge nutraceutical potential (Bonfanti et al. 2018; Hill and Fenical 2010; Suleria et al. 2015). Indeed, due to their genomic diversity, they comprise a very wide range of enzymes and, as a consequence, of metabolic pathways. These in turn yield an extreme diversity of bioactive compounds with possible positive effects on health and well-being. These compounds encompass specific oligo- and polysaccharides; fatty acids and more complex lipids; proteins (including enzymes);

and peptides, vitamins, minerals, phenolic substances, carotenoids, halogenated compounds and many others (Suleria et al. 2015).

Omega-3 fatty acids—EPA (eicosapentaenoic acid) and DHA (docosahexaenoic acid)—are of particular importance to the overlapping areas of nutrition and highly bioactive substances. Microalgae (as well as fish and some crustaceans, due to their consumption of microalgae) are a rich source of these polyunsaturated fatty acids (Rincón-Cervera et al. 2019; Ryckebosch et al. 2012), which are known for their positive health effects on inflammatory conditions (more importantly, EPA), cardiovascular disease (see Table 1 for examples of highly purified fish oils approved for clinical use, though the health benefits need confirmation; Manson et al. 2019) and neurocognitive development and health (DHA) (Echeverría et al. 2017). As a result, fish, crustacean and algal oils are deemed the best sources of EPA and DHA. Algal oils are a more recent development and a response to the overexploitation of fish resources. Microalgae may be produced under controlled conditions and in large quantities, and are rich in lipids (Rodolfi et al. 2009). Thraustochytrids, large-celled marine

heterokonts classified as oleaginous microorganisms, are an important example of algal sources for their lipid productivity and particular richness in EPA and DHA (Gupta et al. 2012). The technological advantages of phototrophic microalgae have fostered research that has led to a growing number of applications. While the global supply of fish oil has stabilised at around one million metric tonnes every year and is constrained by overexploitation, phototrophic microalgae can be cultivated using renewable resources such as sunlight, carbon dioxide and cheap and plentiful nutrient sources (Chauton et al. 2015).

The potential for lipid production and the ability to produce EPA and DHA differ across microalgal species (Chauton et al. 2015). Strains with a desirable fatty acid profile can be obtained by selection (Rodolfi et al. 2009). For more ambitious targets, microalgae strains can be modified by inserting genes that enhance EPA and DHA synthesis or, alternatively, by silencing gene expression in competing metabolic routes (Mühlroth et al. 2013). Provided that environmental and social risks as well as ethical and safety concerns are fully addressed, such transgenic approaches may become solutions for the production of these invaluable marine nutrients, especially if new genes and corresponding enzymes from not yet prospected resources are drawn into a rigorous research and development effort.

2.2.3 Cosmetics

Cosmetics are big business—worth US\$532 billion worldwide in 2017, growing at around 7.14 percent annually and expected to reach above \$800 billion by 2023 (Orbis 2018). There is growing interest in naturally sourced products, including those derived from marine biodiversity. Additionally, products that show verifiable effects such as reducing wrinkles and protecting skin from the damaging effects of ultraviolet or infrared radiation attract a price premium and are placed at the high end of the market; these are often referred to as cosmeceuticals. The first true marine cosmeceutical, formulated in Estée Lauder’s Resilience line, is a mixture of pseudopterosins derived from the Caribbean gorgonian (seawhip) *Pseudopterogorgia elisabethae*. These compounds were originally discovered as potent anti-inflammatory agents, but their physical properties meant they were unsuitable for systemic administration

and they were therefore used topically. The material for the Resilience products is derived from environmentally managed seawhip farms, with population-level effects of the harvest studied in detail (Lasker 2013).

Two cosmeceuticals derived from vent bacteria have been commercialised, Abyssine 657 (Meyer/L’Oreal) and Venuceane (Sederma/Croda). The active product in Abyssine, Deepthane, is an anti-inflammatory polysaccharide obtained from a deep-sea bacterium *Alteromonas macleodi*, which is isolated from an annelid worm collected from a hydrothermal vent in the East Pacific Rise at 2,625 metres (m) depth (in ABNJ) (Rogers et al. 2015). Venuceane, a product marketed as anti-ageing, detoxifying and moisturising, screens damaging infrared radiation and is derived from another hyperthermophile bacterium, *Thermus thermophilus*, obtained at 2,000 m depth in the Guaymas Basin in the Gulf of California (Martinson et al. 1999). It has also been shown to screen ultraviolet radiation to prevent radical damage of DNA, thus protecting skin.

2.2.4 Aquaculture and new food products

Whereas marine aquaculture, developed originally in Egypt, spans 4,000 years (Duarte et al. 2007), industrial aquaculture was initiated 40 years ago with the development of mussel raft aquaculture and fish aquaculture, along with the closing of the life cycle of salmon in captivity. Controlled food production from land organisms predates aquaculture by about 10,000 years, yet the number of marine species that have already been domesticated (about 270) matches that on land (about 294) (Duarte et al. 2007). Moreover, the domestication of new land species for food has remained nearly stagnant for the past two centuries, while about one-third of new marine species were domesticated in the past decade. The number of domesticated marine species continues to grow at a pace of about 10 new species introduced to marine aquaculture every year (Duarte et al. 2007). The spider crab (*Maja brachydactyla*) (Pazos et al. 2018) and the common octopus (*Octopus vulgaris*) (Cerezo Valverde et al. 2019) are examples of two species domesticated in the past two years. Indeed, there is significant potential to domesticate all 3,000 species harvested from the ocean as human food (Duarte et al. 2007).

Land species typically require a long selection process to achieve suitability for farming. On the other hand, the existing genetic diversity of marine species means that many mariculture-suitable species already exist (though selection often occurs when those growing these marine species select for specific traits—e.g. faster growth or better color). While natural and cultured populations of South African abalone (*Haliotis midae*) register similar levels of genetic diversity, cultured populations are genetically distinct from wild abalone, potentially as a result of selective pressures particular to each mariculture facility (Rhode et al. 2012). These findings highlight the need to maintain genetically diverse natural populations to support the mariculture industry, and to make provisions to ensure that commercially grown abalone are not released, accidentally or otherwise, into natural systems, as the latter poses a serious risk to the genetic integrity of an already vulnerable stock (Rhode et al. 2012; Bester-van der Merwe et al. 2011). Moreover, ongoing genetic monitoring is required for these species to maintain the genetic integrity of wild populations and to prevent genetic erosion, especially with the ongoing and largely uncontrolled release of cultivated organisms to the wild (da Silva and van Vuuren 2019). Thus far, only one aquaculture species, salmon, has been genetically modified for production (Waltz 2017), while on land genetically modified crops that are commercialised include maize, soya, cotton and canola, among others (Abberton et al. 2016).

Aquaculture now supplies almost half of the fish consumed worldwide (Troell et al. 2014), releasing some pressure on wild stocks. Yet sustainability within the sector and issues of genetic diversity within the industry will need to be addressed more comprehensively given projected expansions, linked to increased demand (Oyinlola et al. 2018).

The advantages of MGR also extend to new food products. Indeed, poorly known resources may yet be evaluated for their nutritional value and become subject to exploitation, which may then lead to cultivation. Some MGR may also provide novel functional food ingredients (Shahidi and Ambigaipalan 2015). These may encompass chitosans, specific carbohydrates, enzymes and protein hydrolysates given their ability to confer new properties to foods (e.g. altering their texture) or extend their shelf life (e.g. protein hydrolysates) (Shahidi and Ambigaipalan 2015). Recent developments in nanotechnology also

bring new possible applications, such as the preparation of biogenic nanoparticles of marine algae for antioxidant and stabilisation effects on food matrices through active packaging (Gu et al. 2018; He et al. 2019). In addition, marine microbial enzymes encompassing agarases, cellulases, collagenases, lipases and proteases display valuable properties and offer various applications. The biochemical diversity of marine microorganisms makes these enzymes possible tools for food processing (Beygmoradi and Homaei 2017).

Considerable research is still needed to explore the use of MGR for engineering new foods. Indeed, only a little more than 40 fish species and even fewer in other marine taxonomic groups have had their genomes fully sequenced (Zhu and Ge 2018). These sequenced genomes and all genetic engineering tools, including recently available gene editing techniques such as CRISPR, may pave the way for a new generation of cultured seafood products (Zhu and Ge 2018), although questions of consumer acceptability, environmental risk and social desirability remain paramount. At present, genetic transformation of fish is mainly directed toward individual growth enhancement to increase the economic advantages of aquaculture. Atlantic salmon (*Salmo salar*) is the species that has been most targeted by genetic engineering efforts (Hafsa et al. 2016). For example, a transgenic Atlantic salmon (AquAdvantage)—recently approved by the U.S. Food and Drug Administration (Ledford 2015) after a 20-year review process—has a gene construct consisting of growth hormone cDNA (complementary DNA) from Chinook salmon (*Oncorhynchus tshawytscha*) that is regulated with anti-freeze protein gene sequences obtained from an ocean pout (*Zoarces americanus*), leading to growth rates that are much higher than those of non-transgenic salmon, with fish reaching market size in 16–18 months instead of three years (Smith et al. 2010; Waltz 2016). Questions remain, however, about the overall impacts of such enterprises, given that carnivorous fish such as salmonids and Asian bass still require significant quantities of fishmeal and fish oil in their pelleted diets. Limited attention has been given in aquaculture to seaweeds and lower-trophic-level organisms such as bivalves, which might offer more sustainable targets for aquaculture and might also bring additional benefits such as removing nutrients that cause eutrophication or particulates in seawater (Aburto-Oropeza et al. 2020).

2.2.5 Bulk chemicals

MGR-derived products and processes could make a big impact in the bulk market, which includes bulk chemicals, enzymes for industrial processes and laundry detergents, probiotics in animal feed and packaging and further applications being researched to replace plasticisers in plastics with renewable resources. One of the largest markets is in alginates obtained from brown algae by wild harvest and aquaculture, which are used extensively as stabilisers and emulsifiers in food production as well as in specialty bandages for burns. Alginates are now being used to generate biodegradable drinks and food packaging, such as the Oohos produced by the Skipping Rocks Lab (Ooho Water n.d.). Its model is based around the product (e.g. ketchup) being put in the packaging at the retail outlet and being produced for that day's needs, as the material degrades in less than six weeks. Seaweed polymers are gaining attention as a source of sustainable bioplastics (Guedes et al. 2019) across a range of commercial applications, ranging from seaweed-based straws (Beygmoradi and Homaei 2017) to flip-flops (Algenesis Materials n.d.). The use of seaweed products as probiotics extends beyond human consumption, and with the 2006 banning of in-feed antibiotics given to animals in the European Union, using probiotics to prevent bacterial infections in livestock has been proposed as a sustainable solution. Sulfated polysaccharides prevent bacterial infections in pigs and other animals, thus reducing animal suffering and economic damage. Recent evidence also shows that the addition of ~1 percent red seaweed to the feed of ruminants reduces methane emissions by over 50 percent (Roque et al. 2019), thereby offering an opportunity to mitigate this significant component of global greenhouse gas emissions. However, concerns exist about the ozone-depleting properties of bromoform, a secondary metabolite produced by these seaweeds, if industrial-scale production for animal feed is pursued (Carpenter and Liss 2000).

The marine environment offers important opportunities for cold- and heat-adapted enzymes. The former is of utility in low temperature laundry detergents to reduce electrical costs during washing. One example of using heat-adapted enzymes in the bulk market is a thermostable enzyme from a hydrothermal vent organism that can be used in the production of bioethanol. Dubbed 'Fuelzyme' and licensed to the German chemical company BASF by Verenum, it is a

genetically modified version of the original enzyme that is able to function over a wide temperature and pH range, thus improving the efficiency and economics of bioethanol production (Synthetic Biology Project n.d.).

2.2.6 Other applications

Additional commercial applications of MGR relate to the capacity of certain marine microorganisms to produce extracellular polymeric substances (EPSs), which are naturally occurring polymers. EPSs can be used as vehicles of bioremediation due to their capacity to detoxify heavy metals and other pollutants (Pal and Paul 2008). ArcticZymes, a developer and marketer of enzymes for highly specialised research applications, has developed a family of isothermal polymerases—enzymes of marine origin that can be used to synthesise DNA and RNA molecules under high salinity conditions and across a flexible temperature range (Ward 2018).

Fouling of ship hulls by marine plants and animals slows vessels and increases costs, while fouling of nuclear power plant cooling water intake by mussels and other species can compromise operations (Rittschof 2017). Antifoulants such as organotin have been banned by the International Maritime Organization due to their broad toxicity and environmental impacts. There is therefore considerable interest in understanding the complexity of active and passive biological fouling processes and developing nontoxic, environmentally benign marine antifoulants. Research has focused on marine bacteria and antifoulant biomolecules, including at least 198 marine invertebrates such as gorgonians and soft corals, and over a dozen synthetic analogues with the capacity to adhere to a variety of substrates (Wang et al. 2017; Leary et al. 2009; Qi and Ma 2017).

The bioluminescence in a jellyfish discovered in the North Atlantic (*Aequorea victoria*) was found to be due to interactions between two proteins, namely aequorin and green fluorescent protein (GFP). A broad range of applications of GFP have emerged over the years, including as a reporter of gene expression, in the tagging (and subsequent photomicrography) of proteins and as a biosensor indicating levels of environmental toxicity. The scientists responsible for discovering GFP and developing its initial applications were recognised with the 2008 Nobel Prize in Chemistry, one of more than 20 Nobel Prizes linked to the ocean and ocean biology (Rogers 2019).

3. Challenges

3.1 Threats to Conserving the Ocean Genome

Human activities have been intensifying globally, threatening marine species' survival, contributing to the rapid loss of genetic diversity and weakening species' adaptive capacities (Laikre and Ryman 1996; Law 2007; Allendorf et al. 2008; Palkovacs et al. 2011; Jouffray et al. 2020). Fishing has significant negative impacts on marine ecosystems and biodiversity, which has implications for species extinction (Dulvy et al. 2014; de Mitcheson et al. 2013) and the reduction of genetic diversity or selection at specific *loci* (Pinsky and Palumbi 2014; Czorlich et al. 2018; Madduppa et al. 2018). Unsustainable coastal development, land- and sea-based pollution and growing interest in deep-sea exploration and mining constitute additional significant threats to biodiversity that often compound those from overharvesting (Devine et al. 2006; Prouty et al. 2011; Nielsen et al. 2016).

Climate change is leading to a warmer, more acidic and less oxygenated ocean, directly affecting all stages of marine life (Pörtner and Peck 2010) across all latitudes (Doney et al. 2012; Barton et al. 2016; Scheffers et al. 2016; Pratchett et al. 2018). Specific responses have included geographic distribution shifts to higher latitudes and deeper water, advances in spring phenology and increases in the abundance of warm-water species (Poloczanska et al. 2016). Climate change affects biodiversity through changes in the distribution of genetic variants in space and time, changes to the degree of phenotypic plasticity (the individual characteristics of organisms that result from interacting with the environment) as well as changes in the ability of organisms to adapt over time to changing environmental conditions (Hoffmann and Sgrò 2011). Realised climate change has already had substantial deleterious impacts across a range of biological processes and taxa, including critical habitat-forming species such as corals (Carpenter et al. 2008; Davidson et al. 2012; Spalding and Brown 2015; Ainsworth et al. 2016). Arguably, one of the most

documented impacts of climate change has been a redistribution of species as they track their preferred environmental niches (Perry et al. 2005; Pinsky et al. 2013; Pecl et al. 2017; Morley et al. 2018). Such shifts are likely to be associated with differences in genetic variability between the historical and range extension zones as well as within the extended ranges themselves (Ramos et al. 2018). Critically, patterns in genetic diversity, connectivity and population size associated with species shifts are important determinants of whether species will be able to continue shifting, adapting, establishing and persisting in their new ranges (Ramos et al. 2018). Knowledge of how genetic variation is distributed across a species' range is of particular significance, as historic refuges often harbour a large proportion of total diversity (Hampe and Petit 2005), yet are also often threatened by climate change (Provan and Maggs 2012).

While the loss of certain marine species due to human impacts has been documented (see below), this is likely an underestimate as humans have been responsible for ecological, commercial and local extinctions (McCauley et al. 2015), and the substantial decline of genetic diversity within species and across populations (Chapin III et al. 2000; Pinsky and Palumbi 2014). Loss of both types of variation in genetic diversity has pervasive impacts on ecosystem processes as well as on species' capacities to respond and adapt to change (McNaughton 1977; Allendorf et al. 2008; Grorud-Colvert et al. 2014). Continued loss of genetic diversity contributes to reduced population viability and ultimately can lead to extinction (Dawson et al. 2011).

Our activities have altered life in the ocean substantially, impacting the ability of ocean systems to provide ecological, socioeconomic and cultural benefits (Worm et al. 2006; Halpern et al. 2008). Such impacts have eroded the genetic base of biological diversity, and may make it more difficult to sustainably harvest and manage marine species (Walsh et al. 2006).

3.1.1 Species extinctions

While extinction rates in the ocean currently appear far lower than species loss in the terrestrial realm (McCauley et al. 2015), species extirpations due to climate change are likely to be twice as common in the ocean as on land due to the narrow thermal range tolerated by marine species (Pinsky et al. 2019). Estimates of marine extinctions are likely to be conservative—little is known about how many species inhabit the marine environment and there is a lack of monitoring or specific assessments of extinction risk under the IUCN Red List. Heavy use of the maritime space by humans has led to dramatic declines in the abundance of the baiji river dolphin (*Lipotes vexillifer*) and the vaquita (*Phocoena sinuata*), leading the former to be declared functionally extinct (Smith and Jabour 2018) and the latter to become the most endangered cetacean in the world as declared by the International Union for Conservation of Nature (IUCN) (Roche et al. 2016). IUCN has recorded 15 marine species extinctions, including the Caribbean monk seal (*Monachus tropicalis*), the Japanese sea lion (*Zalophus japonicus*) and the sea mink (*Neovison macrodon*) (IUCN 2019). Some species have not been observed for several decades and may be extinct. Based on available data, IUCN considers 25 percent of marine mammals at risk of extinction (Davidson et al. 2012). Eight percent of marine bony fishes from the Arabian/Persian Gulf are also considered regionally threatened due to fishing and loss of habitat—an estimate twice that of other regions where such assessments have been undertaken (Buchanan et al. 2019). In addition, 25 percent of sharks, rays and chimaeras are globally threatened (Dulvy et al. 2014). Smaller-size organisms may have a similar risk of extinction due to habitat destruction, introduction of invasive species, exploitation and the effects of climate change (Cowie et al. 2017). Yet census and extinction inventories are largely lacking for smaller marine species.

Many parts of the ocean remain unexplored (Van Dover 2014). For instance, scientific expeditions to the deep sea regularly encounter new species—a three-week expedition off the coast of Costa Rica in early 2019 led to the discovery of at least four new species of deep-sea corals and six other animals (Schmidt Ocean Institute 2019). Commercial deep-sea mining activities may result in the loss of habitat, leading to potentially irreversible

negative impacts on the biodiversity of vulnerable deep-sea communities (Van Dover et al. 2017). In June 2019, the scaly-foot snail (*Chrysomallon squamiferum*) became the first species at risk of extinction in the event of future deep-sea mining (two of the three hydrothermal vent systems where it is found are within areas under exploratory mining licenses), and it is expected to soon be joined by at least a dozen more hydrothermal vent species on the IUCN Red List (Sigwart et al. 2019).

3.1.2 Loss of populations

Population extirpations and declines in abundance due to unsustainable fishing practices, habitat destruction and pollution have led to contractions in the ranges of many fish species—including large pelagics—and invertebrates (Musick et al. 2000; Hutchings and Reynolds 2004; Worm and Tittensor 2011). Salmon have suffered significant declines in numbers and now occur over a much smaller range than historically documented (Levin and Schiewe 2001). Several sockeye salmon (*Oncorhynchus nerka*) subpopulations are classified as extinct as a result of the construction of impassable dams throughout the Columbia River basin. Columbia River chinook salmon (*Oncorhynchus tshawytscha*) have been documented to have lost up to two-thirds of their genetic diversity (Johnson et al. 2018). Declines in population diversity have been shown to increase the variability in salmon returns (Hilborn et al. 2003; Schindler et al. 2010). Declines in the size or density of individual populations also result in greater fluctuations in the frequency of certain genotypes due to the loss of certain genes over time. This process, known as genetic drift, is magnified in smaller populations (Palstra and Ruzzante 2008)—or in larger populations with a reduced number of adults who can reproduce (Hauser et al. 2002; Hare et al. 2011).

In addition, as ecosystem connectivity decreases among marine populations due to habitat fragmentation as well as lower dispersal via ocean currents, which are projected to shift with climate change, a potential loss of populations is predicted, which could result in decreased genetic connectivity (i.e. through genetic drift leading to increased isolation by distance) (Hastings and Botsford 2006; Hellberg 2009; Gerber et al. 2014; Carr et al. 2017). Genetic drift and subpopulation losses both lead to declines in genetic diversity, in turn undermining a species' ability to recover, adapt and survive in changing conditions (Walsh et al. 2006; Hare et al. 2011). This is

particularly critical as species face increasingly variable environmental conditions as a result of climate change; climate change itself is projected to have impacts on populations' and species' genetic diversities, further lowering their stress resistance and adaptive potentials (Frankham 2005).

3.1.3 Invasive species

Aquaculture and shipping are two important means by which species are being translocated around the world, leading to a rise in invasive species. While the introduced species often do not survive, when they do, they may outcompete native species or prey on them, leading to cascading changes in native communities (Sorte et al. 2010; Green et al. 2012). While aquaculture is rapidly becoming a critical component to ensuring food security (Béné et al. 2016; Thilsted et al. 2016), the sector presents important concerns with regard to genetic diversity (Weir and Grant 2005). Aquaculture often breeds species (which are often introduced) by favouring certain traits that give them an advantage over native species in the wild (Fleming et al. 2002). While the environment in which cultured species are grown tends to be carefully contained and monitored, escape events do happen. Such events can lead to farmed species interbreeding with native species (genetic introgression) and rapid genetic homogenisation (Fleming et al. 2000), resulting in the irreversible reduction in genetic diversity and fitness of wild fish (McGinnity et al. 2003; Weir and Grant 2005; Waples et al. 2012; Glover et al. 2017)—and hence lowering their capacities to adapt to environmental change. Farming can also facilitate the spread of pathogens (Naylor et al. 2005), placing further pressure on stocks and posing a serious challenge to the management of farmed and wild populations (Karlsson et al. 2016).

3.1.4 Cumulative effects

It is important to recognise that many marine species and communities are now under pressure from more than one direct or indirect human impact (Jouffray et al. 2020; Halpern et al. 2019). While species can be resilient to a single impact or even several, the additive or synergistic effects of multiple pressures or interactions between them can drive decreases in populations; affect spatial genetic structures and gene flow, including impacts on connectivity; and drive

large-scale regime changes at the community level. Fishing, for instance, has led to rapid changes in growth and reproduction schedules (e.g. earlier maturation at a smaller size, smaller adult body size). And climate change—particularly changes in temperature and dissolved oxygen—is expected to have evolutionary consequences that are qualitatively similar to those observed from exploitation (Hutchings and Fraser 2008; Waples and Audzijonyte 2016; Czorlich et al. 2018; Duncan et al. 2019). One example of synergistic effects is the interactions between eutrophication, overfishing and invasive species in the Black Sea (Oguz and Velikova 2010). Another is between aquaculture—through the release of fingerlings and escapes of broodstock—and fishing of salmon, where both activities have reduced genetic variability of wild populations (Waples et al. 2012). Such effects can prove difficult to reverse (an ecological state called hysteresis) and can lead to the occurrence of new/alternative stable states in marine ecosystems (Fauchald 2010; Fung et al. 2011).

3.2 Impediments to the Equitable Use of the Ocean Genome

3.2.1 Impediments to innovation, equity and benefit sharing

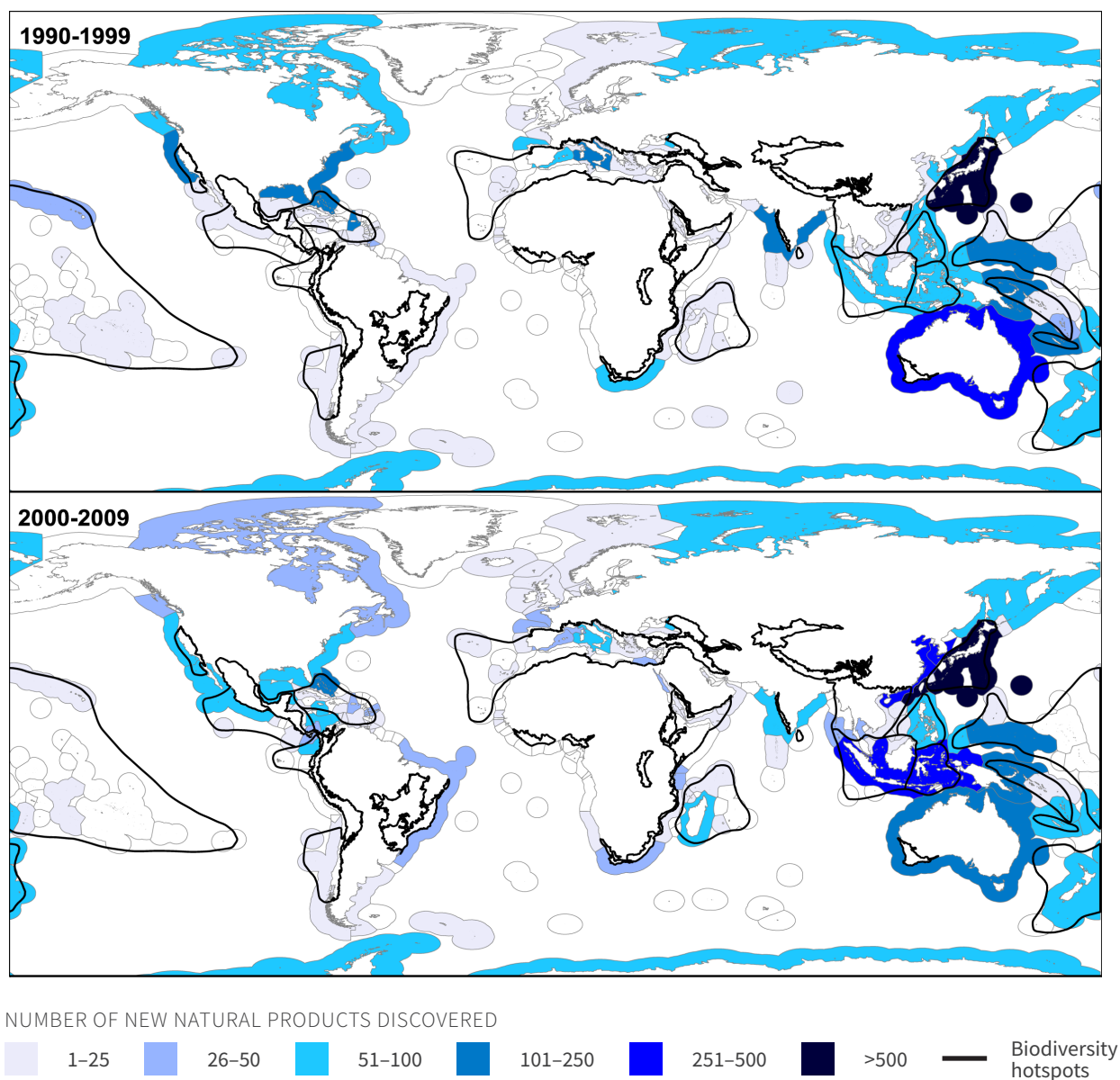
Investments in marine biodiscovery are typically costly and risky due in part to the extreme expense of sampling in areas like the deep sea, the low chances of success and the significant regulatory hurdles for product approval (Broggiato et al. 2014; Morgera 2018). Moreover, each stage of the research, development and commercialisation process requires high levels of technical, financial and scientific investment, with costs depending on the form and ease of access, the type of technology required to collect the material and undertake the research, and the sector or envisaged product involved (Laird and Wynberg 2012). Equipment costs remain high, although the costs of molecular technologies have decreased considerably in recent decades, alongside an increase in speed, efficiency and capacity. Marine biotechnology remains a rapidly developing and fast-moving sector (Leary et al. 2009; Broggiato et al. 2014). The nature of the research enterprise is also changing, as research shifts toward bioinformatics—the collection, classification, storage and analysis of complex biological data—and the mining and

exploration of these vast and growing datasets of genetic information, which requires advanced computational resources that are not broadly available (Muir et al. 2016).

The considerable costs involved in marine bioprospecting research, alongside the advanced technologies and expertise required, have meant that

most exploration has been undertaken by high-income countries. Notably, these are the United States, United Kingdom, Australia, Canada, Japan, Germany and Russia—but, as Figure 5 indicates, with the sampling often conducted in low- or middle-income tropical countries, and Australasia in particular (Greiber 2012; Leal et al. 2012; Oldham et al. 2013).

Figure 5. Sources of Natural Products from Marine Invertebrates



Note: This figure shows the number of new natural products from marine invertebrates found in exclusive economic zones during the 1990s and 2000s, as well as boundaries of biodiversity hotspots.

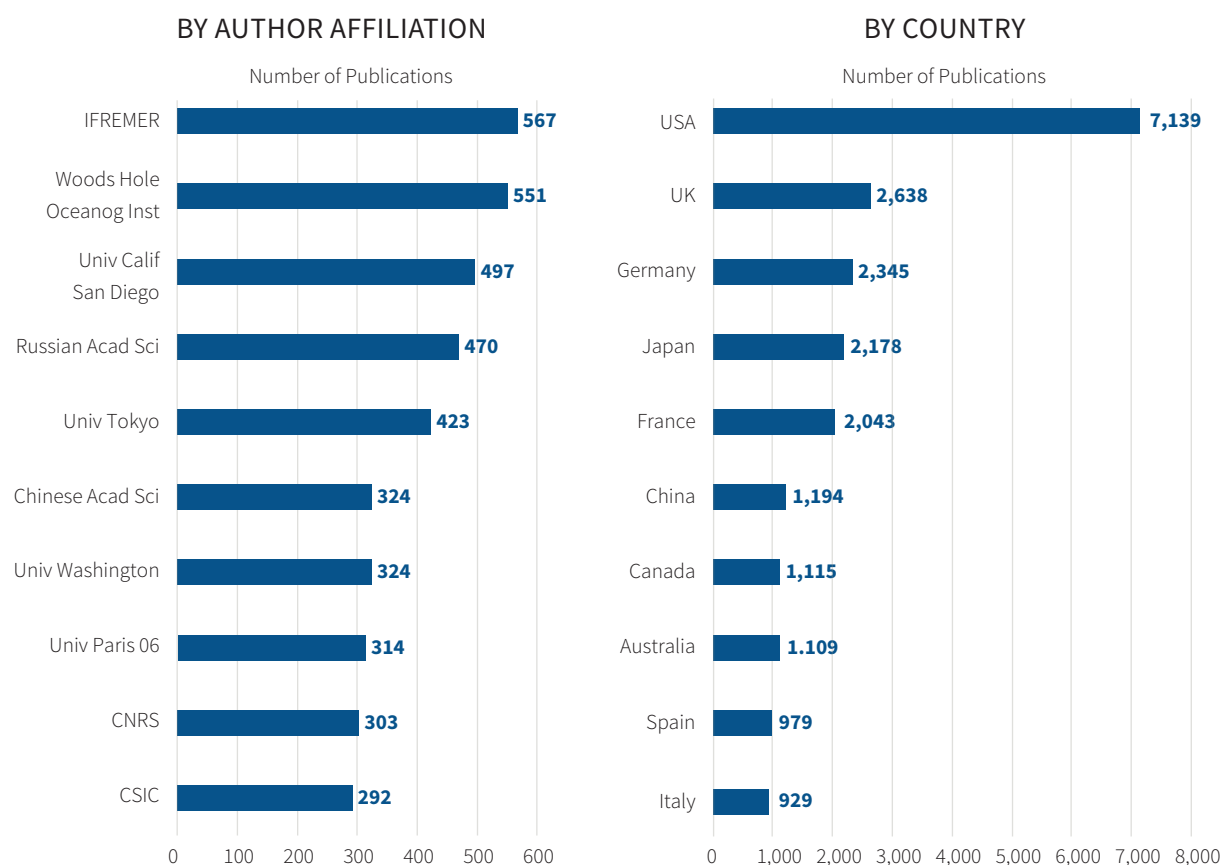
Source: Leal et al. 2012.

As an indicator, Figure 6 illustrates the global distribution of research efforts focused on marine genetic resources, using scientific publications as a proxy. Similarly, studies of patents associated with marine genes demonstrate disparities in capacity to engage in commercial activities associated with these resources, although such studies do not distinguish whether the genes are for reference or are claimed in the filings. Arnaud-Haond et al. (2011) found that patents citing marine genes originated from only 31 of the 194 countries in the world, with 10 countries responsible for 90 percent of them. By 2017, this imbalance had grown, with the share of the top 10 countries increasing to 98 percent, and 70 percent filed by researchers or companies in the United States, Germany and Japan (Blasiak et al. 2018). Approximately 1,600 patent sequences were derived from species

associated with the deep sea and hydrothermal vent systems, commonly found in ABNJ, and are of particular relevance in the context of the ongoing BBNJ negotiations. Greater specification is hampered by the lack of a legal obligation to disclose sample origin or source in patent filings, and the tendency for applicants to not volunteer such information (Blasiak et al. 2019).

Other researchers emphasise that studies of patent filings actually highlight how limited commercial interest in MGR has been (Leary 2018). Blasiak et al. (2018), for instance, analysed 7.3 million sequences and identified only 12,998 of marine origin from 862 species. A text-mining analysis employing more liberal definitions of what constitutes a ‘marine’ species identified only 1,464 marine species in the patent system

Figure 6. Author and Country Affiliations for Scientific Literature Focused on Marine Genetic Resources



Notes: The full names and locations of the authors' affiliate institutions include, from top to bottom, French Research Institute for Exploitation of the Sea, France; Woods Hole Oceanographic Institution, United States; University of California, San Diego, United States; Russian Academy of Sciences, Russia; University of Tokyo, Japan; Chinese Academy of Sciences, China; University of Washington, United States; University of Paris 06, France; French National Center for Scientific Research, France; Spanish National Research Council, Spain.

Source: Oldham et al. 2014.

(Oldham et al. 2013). However, while patents are an indication, they should not be taken as a proxy for the full scale of mature commercial interest, or research and innovation that might be pre-competitive. Not all inventions are patentable, many that are patented will never be commercialised and there are strategies other than intellectual property to protect competitive or commercial advantages, including publication (Merges 2004; Thambisetty 2007; Herrera and Schroth 2000; Quah 2002).

Disparities in research capacity, technology and finances represent major constraints that prevent the inclusion of low- and middle-income countries in marine biotechnology efforts. Biodiversity and molecular expertise is unevenly spread (Hendriks and Duarte 2008); research vessels or submersibles are typically owned by only a few high-income nations and entail substantial operational costs (Stokstad 2018); and while there are growing numbers of collaborations between high-income and lower-income countries (Kyeremeh et al. 2020), the model of international collaboration is still characterised by a pharmaceutical or biotech company working with established centres of excellence located in high-income countries. As an example, despite active marine biodiscovery programmes in the Western Indian Ocean, with the exception of South Africa and, to a lesser extent, Kenya, few African countries have engaged actively as research collaborators in international endeavours (Wynberg 2016). A particular concern across countries is the gender imbalance in marine biotechnology (and science in general) and the attrition of women in this male-dominated field (Ceci and Williams 2011; Kitada et al. 2015).

3.2.2 Regulating fair and equitable access and benefit sharing

The CBD, Nagoya Protocol and International Treaty on Plant Genetic Resources for Food and Agriculture together provide an important platform around which new models of equitable research partnerships can evolve, on the basis of the presence or absence of national sovereign rights over biological resources. As described earlier, marine biodiscovery depends in

part upon access to marine organisms, which in turn is governed by multiple legal regimes and national and international laws (Figure 3). Under UNCLOS, coastal states have the exclusive right to regulate, authorise and conduct marine scientific research in their territorial sea (Article 245). MGR found within the EEZ are subject to domestic measures implemented under the Nagoya Protocol or directly under the CBD. This means that coastal states that choose to regulate marine bioprospecting in their EEZ can specify conditions of access to this material, including mutually agreed terms on access and benefit sharing (ABS). As noted by Oldham et al. (2013), natural product research has historically concentrated on marine invertebrates *inside* national jurisdictions, with most marketed products derived from organisms found there—with limited exceptions for enzymes from extremophiles and Antarctic krill (*Euphausia superba*) as a source of nutraceuticals.

In practice, the CBD has spawned a number of approaches to regulating genetic resources, but a common element across these approaches is the requirement that researchers abide by local conditions of access to and use of genetic resources. The evolving nature of ABS governance—and negotiated compliance in different contexts and gaps in workable policies in many countries—makes this difficult terrain to navigate (Morgera 2018). From a legal perspective, perhaps the greatest current challenge is determining the full scope of the term ‘genetic resources’ and discussing whether this includes digital sequence information/genetic sequence data. For some countries, not incorporating genetic sequence data within the scope of ABS approaches undermines sovereign control over genetic resources. Other countries insist that the publication of sequence information in open-access databases can be seen as a globalised and important form of benefit sharing (Laird and Wynberg 2018).

Monitoring is an important concern given that informational resources are highly mobile and malleable and are more difficult to track than physical genetic resources, with most data held in databases typically lacking identification and origin information (Garrity et al. 2009). Several groups are working to improve

monitoring by attaching information on origin to sequences, and by including stronger links between physical samples and sequences. But monitoring has grown increasingly difficult over time as sequences pass through multiple hands, are modified or have their identities eroded (Garrity et al. 2009; Slobodian et al. 2015). The technological gap described above is exacerbated by a failure to capture traceability in legal frameworks to support appropriate law and policy.

Specialised ABS rules for MGR from ABNJ have not yet been developed and it is one of the four main issues within the BBNJ negotiations, which are ongoing under the parent treaty, UNCLOS (Leary 2018; Thambisetty 2019; 2020). The negotiations should clarify the status of MGR found beyond national jurisdiction, including whether they are to be regarded as the common heritage of humankind and what implications that would have for the private appropriation of the ocean genome in tangible and informational forms.

Such discussions also extend to the scope of regulation of marine scientific research in ABNJ. Due to the open nature of the ocean, biogeographical ranges of marine species are typically large (including those of prokaryotes, which contribute the bulk of marine genes) with connectivity driven by very large population sizes and ocean transport systems resulting in large distributions (Villarino et al. 2018). Therefore, MGR are often shared among the EEZs of multiple nations and ABNJ, which renders delineation over different ownership and governance regimes cumbersome. Central questions include whether the benefits arising from the commercial use of these resources should be shared by the entire international community; the scope of the obligation on states and corporations with the technological capacities to exploit these resources to share benefits; and whether those who first locate and describe MGR should be given certain rights of priority.

A central issue—and one that is not confined to MGR—is the blurring between noncommercial and commercial research as the academic community and governments increasingly partner with industry, and patent laws change patterns of appropriability. Most sequences move fluidly between commercial and noncommercial

institutions, and if uploaded to public databases might be available for all to use without the original providers aware of or involved in this process. Most benefit sharing under the Nagoya Protocol occurs through bilateral arrangements between users and providers who are obligated by local and international laws to enter into mutually agreed terms on benefit sharing, often when research moves from an academic to a commercial phase. The performance of contracts cannot easily be monitored by provider countries (Young and Tvedt 2017). Additionally, if scientific data and information were treated solely in a bilateral, benefit-sharing manner, countries would not benefit from information generated from non-endemic species, or from *ex situ* collections. Environmental management in particular benefits from increasing the quantity of available data.

Bilateralism presents other problems in the marine context given the challenges of delineating ownership. A multilateral mechanism such as that found in Article 10 of the Nagoya Protocol may become salient in the context of the BBNJ negotiations. The complexity of the regulatory environment demands fresh approaches that can help shape and negotiate ethical and responsible conduct on the part of marine scientists. Initiatives such as voluntary codes of conduct, good practices, training for younger scientists, funding incentives by research councils and grantmaking bodies, mentoring and other initiatives can speed up the process to internalise new behaviours and norms of research.

An important concern stems from the overregulation or poorly implemented application of ABS laws, especially given the blur between commercial and noncommercial use. Although the CBD and Nagoya Protocol explicitly support research for biodiversity conservation and enhanced scientific knowledge, national ABS legislation has often had unintended negative impacts on basic biodiversity research (Bockmann et al. 2018; Prathapan et al. 2018). It is important that new laws to regulate the use of MGR learn from these experiences to ensure that basic biodiversity research to support conservation efforts, the advancement of knowledge and equitable benefit sharing is promoted, rather than hindered.

4. Pursuing Solutions

4.1 Conservation

4.1.1 Managing competing interests in the ocean to conserve biodiversity

Despite recognition by the CBD, genetic diversity is still largely neglected in policies and management and conservation plans (Laikre 2010). Much greater attention is needed to embed genetic diversity in policies, plans and programmes and to ensure that holistic strategies are developed to use the ocean sustainably and maintain the genetic diversity that underpins biodiversity and the benefits it provides (Karlsson et al. 2016). The distribution of those uses and benefits is of particular importance when considering how to manage the many interests and stakeholders at the table. In marine systems, there are opportunities for change via key tools, among them ecosystem-based approaches to fisheries management, spatial planning, effective quotas, MPAs, protecting and managing key marine biodiversity areas, reducing runoff pollution into the ocean and working closely with producers and consumers (IPBES 2019). The conservation of genetic diversity is embedded in all of the above.

The goal of ‘conserving’ genetic diversity can differ depending on the perspective of each stakeholder. What is more, what constitutes high biodiversity in an area may mean different things to different people, especially as baselines shift and successive generations consider increasingly degraded systems to be the norm. Different stakeholders will also have inherently different interests, yet may benefit from using the same approach to conservation. A representative from a biotech firm may be primarily interested in protecting the highest diversity of marine genes possible to discover and develop new products. An ocean manager may desire the same outcome, with an interest in conserving a diversity of species in the ecosystem to provide resilience and adaptive capacity to environmental change. Many conservation goals exist, encompassing

different species with distinct distributions of genetic diversity and patterns of connectivity, yet there are also multiple management strategies that balance trade-offs with positive outcomes (Ingeman et al. 2019). If these strategies move forward from an agreed upon set of minimum conservation imperatives, multiple interests can be supported as long as incentives are in place to support participation (Lubchenco et al. 2016).

For example, North Atlantic right whales (*Eubalaena glacialis*) were historically decimated by whaling and have consistently declined after a brief increase in population size that peaked in 2010 (Corkeron et al. 2018). Anthropogenic impacts including historical whaling have reduced their abundance and the genetic variability within the small breeding population (Kraus et al. 2005). The current primary causes of mortality are ship strikes and entanglement in fishing gear—every individual North Atlantic right whale shows evidence of entanglement in fishing gear at some point in their life (Corkeron et al. 2018). If the minimum conservation imperative is to recover this species to a viable population level that prevents a further genetic bottleneck, emerging management strategies—such as real-time whale position data to prevent ship strikes and ropeless fishing gear that remains free of vertical lines until the time of retrieval—can still support multiple activities (Ingeman et al. 2019). Using real-time data also allows flexibility as management needs evolve.

This management flexibility can be critical as ecosystems change, due to both natural cycles and increasing anthropogenic impacts. At its core, adaptive management assumes that activities and regulations need to be recalibrated as changes in the system occur. Yet tighter feedback loops will be required to keep pace with the changing ocean and to acknowledge the impacts if genetic diversity is diminished (Ingeman et al. 2019). As opposed to predict-and-prescribe approaches—which require a thorough scientific understanding of the dynamics within a system to

predict how that system will change—scenario planning can help identify a number of alternative strategies that could potentially arise within a system (Schindler and Hilborn 2015). Management appropriate to one scenario may shift to another, making it necessary to combine the range of conditions encompassed by these alternate scenarios with decision-making structures that are streamlined for faster responses (Ingeman et al. 2019). Governance structures must match the flexibility required for this approach with the use of impact assessments that account for biodiversity and at the appropriate scales needed to conserve genetic diversity, whether at the scale of ecosystems, species, populations or individual genes. As technologies such as eDNA evolve, and the understanding of genomics increases, it will become increasingly feasible to implement such requirements for genetic diversity.

Prioritising interventions to conserve biodiversity, and the underlying genetic diversity, requires taking a robust approach based on sound science and available data. Yet ocean genome data over space and time are largely lacking, even though this scientific information is critical for evaluating the status and future outlook for genetic diversity, such as for fisheries encompassing multiple populations or when protecting areas of particularly high biodiversity. In the absence of data, reasonable surrogates may serve as a proxy for genetic diversity (e.g. guild-level diversity or representation of species within given taxonomic families), yet these should be coupled with the incorporation of genetic monitoring into preexisting programmes, and the creation of targeted genetic monitoring programmes for species and areas of particular interest. Such activities must go beyond simply documenting what genetic material is where, and how it is being extracted and used, to also encompass the changes in this genetic diversity and the trends in those changes over time. This requires having a baseline understanding of the genetic variability of each species. Coupled modelling and empirical approaches will also be increasingly important.

However, waiting until comprehensive datasets are available before making interventions also runs the risk of losing rapidly deteriorating storehouses of genetic information due to the overharvesting of species and habitat degradation. Interventions are already proceeding and a precautionary approach is needed to stem the loss of marine genetic resources,

including those that are not well protected by area-based management, such as pelagic species with large home ranges. Ecosystem-based fisheries management; reduction of gear impacts and bycatch; and consideration of species' life histories, population genetics and historical exploitation are all important aspects of sustainable fisheries management. As technological advancements enable the exploration and exploitation of new areas in the ocean, including the deep sea, permitting and extraction limits will need to ensure both sustainability of the resource as well as conservation of its ecosystem. Caution is needed when approving new or expanded uses of managed areas for extractive activities such as mining, particularly in areas where biodiversity is not well characterised or is potentially vulnerable. The potential loss of rare, threatened and endangered species and populations poses a serious risk of contributing to an overall loss in genetic diversity, and such populations require continual monitoring and conservation efforts to ensure their persistence. In addition, safeguarding areas of high biodiversity or those of particular importance to exploited species in fully or highly protected areas is a key strategy for protecting genetic diversity, both in the short and long terms, while scientific monitoring and evaluation keep pace with the rapidly changing ocean.

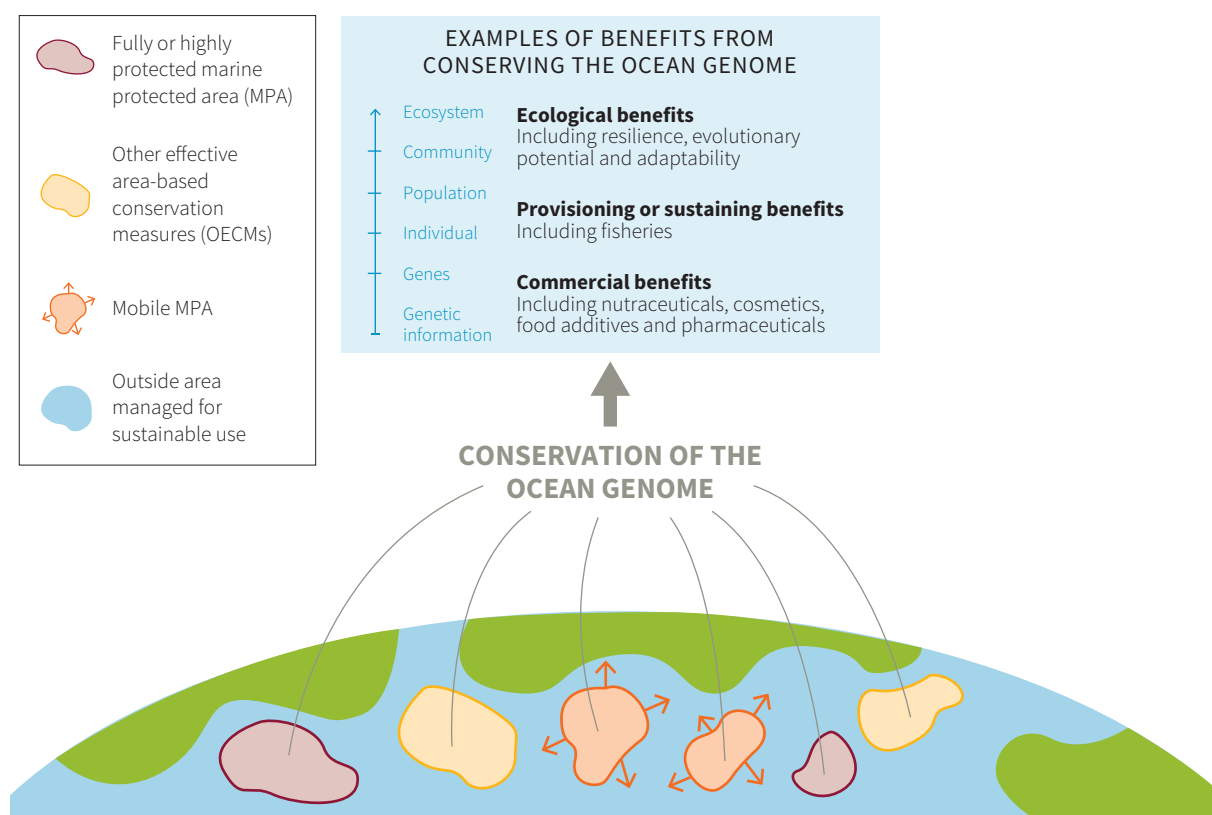
To meet the needs and uses of multiple actors, protected areas should be balanced with those set aside to support sustainable use for key services such as harvesting genes for product development by industry, or wilderness areas to protect pristine habitat that provides key ecosystem services for those actors (Schleicher et al. 2019; see also Österblom et al. 2020). Although conflicting uses can be balanced across ocean spaces in particular contexts, this is not always possible. Commercial activities are being carried out across the majority of the ocean, yet only 8 percent is set aside for biodiversity conservation, of which only 2.5 percent is fully or highly protected and implemented (Sala et al. 2018, updated via Marine Conservation Institute 2020). This falls significantly short of the targets to effectively protect 10 percent of the ocean by 2020 (see Box 3) while also leaving open the conversation around sustainability and conservation of marine genetic resources in the other 90 percent of the ocean, of which two-thirds is in ABNJ. This points to the urgent need to prioritise decisions toward biodiversity conservation, given the foundational role this plays both

for ecosystem health and for the well-being of human and nonhuman species.

Many countries fail to explicitly address the genetic level of biodiversity in fisheries policy and legislation (Dulvy and Reynolds 2009). Therefore, in enacting strategies for conservation and sustainable use, genetic biodiversity should be integrated or mainstreamed into the planning and decision-making of multiple sectors that may impact and benefit from the ocean genome, including from species that are new to science (Manuel et al. 2016). This includes fisheries, mariculture, mining, shipping and marine biodiscovery. New approaches should help integrate genetic biodiversity into ocean use planning; environmental authorisations such as licenses, permits

and registrations; and environmental management. Maintenance of genetic diversity needs more explicit consideration and planning in food systems policies and management, including for wild capture fisheries and mariculture. In addition to legal and policy instruments, industry collaboration is also needed to prevent genetic erosion, prevent and manage marine invasive species and increase the benefits from genetic diversity through inclusive and responsible research and innovation. Mainstreaming may also include strategies through which activities in production sectors may actually benefit biodiversity. For example, mariculture could relieve pressure on commonly harvested wild species if undertaken in a sustainable and responsible manner (FAO 2016).

Figure 7. How Area-Based Conservation Measures and Sustainable Use Help Conserve the Ocean Genome and Its Associated Benefits



Note: This figure depicts a portfolio approach for conserving the ocean genome and its associated benefits. Effective conservation hinges on using multiple tools, including area-based conservation measures such as fully and highly protected MPAs, that provide the greatest protection from the impacts of extractive and destructive activities. Coupling these with effective management of sustainable use can ensure wide-ranging benefits that are ecological, sustaining, provisioning and commercial.

Source: Developed by the authors. Designed by J. Lokrantz/Azote.

4.1.2 Protecting storehouses of genetic diversity

Genetic diversity in the ocean is important and needs to be conserved and managed to protect the resources it provides and the people it sustains. Many have embraced this imperative at the local, national, regional and international levels, as reflected in various commitments, goals and targets for biodiversity conservation (Grorud-Colvert et al. 2019). For example, the CBD's Aichi Target 11 and the United Nations' Sustainable Development Goal 14 call to conserve ocean areas 'through effectively and equitably managed, ecologically representative and well-connected systems of protected areas and other effective area-based conservation measures.' These protected areas—MPAs and OECMs—are central tools for protecting marine genetic diversity (Figure 7). They have been rapidly growing in number and extent over the last few decades (Lubchenco and Grorud-Colvert 2015; Sala et al. 2018), but many are poorly enforced and the total area remains below global targets, far below what scientists have recommended, and is not representative of the full range of habitats and ecosystems.

Decades of data from scientific research conducted in hundreds of fully and highly protected MPAs around the globe show clear ecological trends (Sala and Giakoumi 2018). MPAs tend to lead to positive ecological outcomes and often result in social and cultural benefits if they are properly designed, managed and sustained to ensure that full protection is real and lasting (Gill et al. 2017; Giakoumi et al. 2018). Key to achieving these benefits is an open and transparent planning process that engages stakeholders representing diverse perspectives and that integrates science-based solutions (Ruiz-Frau et al. 2015; Twichell et al. 2018). When users are involved in MPA planning, compliance with regulations tends to be higher, boosting the ecological and social benefits (e.g. Viteri and Chávez 2007; Weeks and Jupiter 2013; Giakoumi et al. 2018).

When ecosystems, habitats and species are fully protected from all extractive and destructive activities within their borders, ecological communities tend to be more diverse, and formerly targeted individual species tend to be more numerous and larger in size, and have greater reproductive capacities and higher potential to move outside the MPA borders into areas beyond (Claudet et al. 2008; Halpern et al. 2009; Lester

et al. 2009; PISCO and UNS 2016). When well-designed and managed, fully and highly protected MPAs result in greater abundance and size of previously exploited species, restoration of ecological interactions, habitat recovery, enhanced reproductive output due to larger body size of previously exploited species, greater resilience inside the MPA and higher potential for adaptation to climate and other environmental changes (e.g. Roberts et al. 2017; Hastings et al. 2017; Magris et al. 2018; Sala and Giakoumi 2018; Cheng et al. 2019). These ecological outcomes are also integrally tied to outcomes for human well-being. These can include income generated from tourism to fully and highly protected areas that preserve higher biodiversity and spectacular seascapes (e.g. Sala et al. 2013) as well as spillover from the MPA to augment catches in fished areas outside (e.g. Vandeperre et al. 2011). Fully protected areas tend to have more positive human well-being outcomes than MPAs with lower protection levels (Ban et al. 2019), provided key enabling conditions are met to ensure good governance, sound ecological and social design, and ongoing management. Fully and highly protected areas also provide reference areas for evaluating the impacts of extraction outside them, a buffer against accidental mismanagement or environmental changes, and often some enhancement of fisheries outside the MPA (e.g. Allison et al. 2003; McCook et al. 2009; De Leo and Micheli 2015; Di Lorenzo et al. 2016). Although the impacts of MPA networks on genetic diversity are implied and theoretically supported (e.g. Costello 2014; National Academies of Sciences, Engineering, and Medicine 2019; see also McInerney et al. 2012), there is an urgent need for research to test the potential outcomes of protecting genetic diversity in multiple, connected MPAs.

To effectively protect the ocean genome, fully and highly protected MPAs must be sufficiently large to encompass the relevant ecosystem and the full distribution of genetic diversity within it. Yet, in many contexts this is not possible, such as in the Mediterranean Sea, where use is high, coastal populations are dense and many countries share the sea's waters (Giakoumi et al. 2017). To support effective conservation while working within these realities, networks of MPAs are frequently used to protect multiple sites that are connected through the movement of adult or young marine organisms (Allison et al. 2003; Roberts et al. 2003). MPAs in a network can collectively encompass a large area and

Box 3. Marine Protected Areas

One of the most effective tools to protect marine genetic diversity at an ecosystem scale is through implemented and fully or highly protected marine protected areas (MPAs). Because MPAs provide place-based protection, they can conserve not only target species and genetic material, but also all associated biodiversity within that habitat. International targets such as the Convention on Biological Diversity's Aichi Target 11 and the United Nations' Sustainable Development Goal 14.5 recognise the importance of using MPAs and other effective area-based conservation measures (OECMs) to protect biodiversity in 10 percent of the ocean by 2020. However, there are growing calls from the scientific community to fully or highly protect at least 30 percent of the ocean to achieve conservation goals, and for a corresponding post-2020 target to be formulated (see Section 1.3). But what exactly is an MPA or OECM? And which types are most effective for protection?

An MPA is a clearly defined geographical space, recognised, dedicated and managed through legal or other effective means to achieve the long-term conservation of nature with associated ecosystem services and cultural values.^a

OECMs also provide conservation benefits, but biodiversity conservation is not their primary goal.^b They are sites that are not by definition protected areas but are governed and managed in ways that achieve positive and sustained long-term outcomes for the in situ conservation of biodiversity, with associated ecosystem functions and services and, where applicable, cultural, spiritual, socioeconomic and other locally relevant values.^c

MPA and OECM are broad terms that encompass many types of areas. MPAs are a focal tool for protecting genetic diversity because by definition these areas have biodiversity conservation as their primary goal. Yet MPAs can have different levels of protection and may be at different stages of establishment. *The MPA Guide*^d provides a common language for describing the types of MPAs and the outcomes arising from areas with different protection levels.

Based on these definitions, 'fully and highly protected areas' are the only protection levels that are expected to deliver sufficient biodiversity conservation to protect genetic diversity.

In fully protected areas, no extractive or destructive activities are allowed, and all impacts are minimised.^e In highly protected areas, only light extractive activities are allowed, and other impacts are minimised to the extent possible.^f These may be stand-alone MPAs or fully and/or highly protected zones within multi-use MPAs.

Lightly or minimally protected areas allow for multiple uses and activities that have moderate to high impacts on species and habitats. Thus, these are not recommended for the goal of preserving genetic diversity within a system.

Further, for biodiversity conservation to occur, an MPA cannot be merely proposed or committed through an informal announcement; an MPA must be more than designated by law or other authoritative rule on paper. An MPA must be implemented—with regulations in force on the water such that users know to comply.^g It is critical for public consultations and appropriate notification and transparency measures, as well as up-to-date scientific information, to become part of the designation and management of MPAs. Ideally, such areas should be actively managed with monitoring, enforcement and frequent review of management goals and outcomes.

Notes:

^a IUCN and WCPA 2018.

^b CBD 2018.

^c CBD 2018.

^d Oregon State University et al. 2019; Grorud-Colvert et al. 2019.

^e Oregon State University et al. 2019.

^f Oregon State University et al. 2019.

^g Oregon State University et al. 2019.

protect genetic diversity represented by different species while still allowing for sustainable use outside. A network also provides redundancy in the event that one MPA is impacted by a disturbance that reduces its ability to sufficiently protect the genetic diversity of the species inside. Networks of MPAs can have synergistic effects that lead to even greater ecological benefits than separate, unconnected MPAs that are not networked (Grorud-Colvert et al. 2014). When fully and highly protected, MPA networks provide a unique opportunity to protect storehouses of genetic diversity in a changing ocean. As organisms adapt to these changing conditions (see Section 2.1), adaptation networks can be established to identify and protect areas where genetic diversity and/or the potential for adaptation is high (Webster et al. 2017). For example, in coral reef systems, adaptation networks may be particularly useful as corals are increasingly threatened by rising temperatures, ocean acidification, pollution and overfishing (Hughes et al. 2018) while simultaneously showing quantifiably high rates of adaptation (Munday et al. 2013). A single species of coral can have a wide geographic range and inhabit different reef environments where genetic diversity is high across scales as small as less than 100 metres (Barshis et al. 2013; Webster et al. 2017). These species may benefit from networks of protected areas that span different depths and allow for redistribution across latitudes. Future research should test the rate and limit of different adaptive responses for coral species across latitudes to better understand the ranges these adaptation networks need to encompass (Logan et al. 2014).

By networking fully and highly protected areas of high diversity and ensuring connectivity among sites as well as sufficient spatial scale and ecosystem representation, it is possible to mitigate the risk of species moving outside the protected areas as their ranges shift in response to changing environmental conditions. Adaptation networks can also provide an insurance policy against ecosystem and species loss if they are sufficiently replicated within the system (Allison et al. 2003). MPAs in any effective network, including an adaptation network, should encompass a range of environmental conditions and habitat types—including both disturbed and pristine areas—that are sufficiently

replicated. Networking can also accommodate different species distributions, as well as their underlying genetic diversity, by supporting species ranges and patterns of connectivity with multiple MPAs of varying sizes and distances from each other (Pujolar et al. 2013; Jonsson et al. 2016). Connectivity is particularly vital for ensuring adaptation pathways in a network (Almany et al. 2009; Blowes and Connolly 2012). Sites should be at appropriate sizes and distances from each other to promote the exchange of genes as young organisms disperse in the plankton or adults migrate out of the protected areas. Connected areas also provide sources of population replenishment within the network if one or more sites are compromised by local disturbances or become insufficient for protection due to shifting species ranges.

The existing coverage of MPAs should be continuously evaluated, especially in the case of MPAs functioning as a network, to identify areas where urgent protection of genetic diversity is needed. MPA planning processes should identify gaps, including areas of high genetic diversity that are currently unprotected and areas where highly variable systems have led to higher adaptation rates and possibly greater capacity for adaptation in the future.

The BBNJ process is now debating the declaration and functioning of MPAs in ABNJ as a tool for area-based management. There are divergent views on whether MPAs could be used to achieve long-term biodiversity conservation and sustainable use, and whether decision-making related to MPAs should be informed by strategic environmental assessments (SEAs) (High Seas Alliance 2019). This would include broader factors relating to social and economic considerations, traditional knowledge and cultural values. The management of ABNJ is not currently designed to protect genetic diversity, and MPAs could provide a mechanism to do so (Protected Planet 2020). These should be coupled with other facets of ecosystem-based management such as sustainable fisheries, habitat restoration efforts, pollution reduction and climate mitigation. Agreements on area-based management tools would in turn need to align with EIA and SEA processes under existing national, regional and international regimes.

4.1.3 Leveraging biotechnology for conservation and biodiversity management

Starting in the late 1970s, Sanger sequencing became the primary genetic technology employed to generate organisms' genetic information. Though it produces only a single DNA sequence for a given gene region (Sanger et al. 1977), it is still considered a highly valuable tool and is often used in wildlife biology, conservation and management. For example, it remains the gold standard in seafood surveillance and for identifying biological invasion pathways and sources of introductions (e.g. Roman and Darling 2007; Dlugosch and Parker 2008; Barbuto et al. 2010; Cawthorn et al. 2012; Di Pinto et al. 2013; Xiong et al. 2016; Tinacci et al. 2018). However, over the past two decades, key advances in molecular markers, new sequencing technologies and new statistical methods have enabled researchers to tackle a wider range of questions and issues to better inform species conservation and management.

Next-generation sequencing (NGS) offers improved resolution relative to early molecular markers and Sanger sequencing, provides high throughput and better enables large-scale spatial and temporal syntheses for single species as well as entire community assemblages through DNA metabarcoding (e.g. Taberlet et al. 2012; Lindeque et al. 2013; Aylagas et al. 2016; Pitz et al. 2017; Djurhuus et al. 2018). Moreover, because multiple regions across the genome can be sequenced using NGS, fewer samples are needed to acquire a wide breadth of the genetic diversity available within populations or species—a key benefit for studying marine taxa, which often occur in small numbers or are difficult to access (Xiong et al. 2016; Arulandhu et al. 2017).

With respect to seafood surveillance, NGS has proven effective at identifying multispecies seafood products (Giusti et al. 2017), and may even prove instrumental in identifying whether certified stocks have been swapped with uncertified stocks of the same species (Barendse et al. 2019). For marine invasions, using NGS with transcriptomic and epigenetic markers provides an unprecedented opportunity for identifying adaptive

variation within and among native and nonindigenous populations, uncovering candidate genes responsible for certain adaptive traits and understanding the mechanism of epigenetic variation in plastic responses to novel environments (Sherman et al. 2016; Chan et al. 2017). Moreover, NGS coupled with environmental DNA can be used for early detection and monitoring of marine invasive species (e.g. Ardura et al. 2015; Carugati et al. 2015; Simmons et al. 2015; Zaiko et al. 2018), as well as the monitoring of rare, threatened and difficult-to-study or detect species (e.g. Bakker et al. 2017; Weltz et al. 2017; Boussarie et al. 2018; Pikitch 2018; Parsons et al. 2019).

Environmental DNA is a molecular approach that uses a passive sampling technique to acquire DNA from specific species or entire community assemblages. As species interact with their environments, their DNA is continuously being shed into their surroundings—be it soil, sediment or water—via their faeces, saliva, urine and skin cells (Baird and Hajibabaei 2012; Rees et al. 2014; Thomsen and Willerslev 2015; Deiner et al. 2016). As such, it is not necessary to have visual signs of the species under investigation, a requirement of more traditional sampling methods. The primary focus of eDNA has been to acquire species' presence and absence data to quantify their distributions, extents and connectivities (e.g. Weltz et al. 2017; Jeunen et al. 2019). Furthermore, given that several tens of species (from microbes to vertebrates) can be identified in a single sample, this technique can help identify areas of high species richness, which could prove instrumental in informing MPA design and ecosystem-level monitoring (e.g. Andruszkiewicz et al. 2017; Deiner et al. 2017; Pitz et al. 2017; Djurhuus et al. 2018; Stefanni et al. 2018). Moreover, eDNA has a very short life-span of hours or days in seawater, so analysis provides near real-time insight into the presence of species. The ability of eDNA to detect multiple species also holds great promise for rapid biodiscovery (Heidelberg et al. 2010; Chang and Brady 2012). However, the effectiveness of eDNA is fundamentally dependent on the availability of reference collections (e.g. in museums and aquaria) and a genetic reference library, which may not exist and may be

difficult to create for elusive marine species. Recently, the focus of eDNA studies has evolved beyond simple presence/absence to studies quantifying the abundance of species (Stewart 2019), which holds great value for threatened and invasive species monitoring and response planning. Moreover, there is a growing body of research focused on quantifying population genetic structures from eDNA in marine species (e.g. Jeunen et al. 2019; Parsons et al. 2019).

The latest molecular technology with a potential conservation application is CRISPR. Considering the discovery of CRISPR as a genome-editing technology was only first reported in 2012 (Jinek et al. 2012), it is still very much in its infancy and its application in threatened species conservation has yet to be tested (Johnson et al. 2016; Piaggio et al. 2017; Phelps et al. 2019). Moreover, beyond unease about the manipulation of human germline cells, significant ethical and governance concerns remain about the use of the technology. Gaps in knowledge with regard to the environmental, social and economic impacts heighten such concerns, alongside fears about the stability of modified genomes (Caplan et al. 2015; Jasanoff et al. 2015; CSS et al. 2019). The interconnectivity of marine environments in particular underpins the importance of having full and adequate knowledge before moving forward with any applications.

Despite coral reefs being among the oldest ecosystems on Earth (Roark et al. 2009), many have suffered unprecedented losses. Although their decline is partly attributed to human-mediated disturbances such as land-based pollution, introductions of invasive species and overexploitation of coral reef ecosystems (e.g. Johannes 1975; Grigg and Dollar 1990; Wilkinson and Buddemeier 1994; Roberts 1995), the rapid decline is also likely linked to the rapid changes in the Earth's climate over the past century (National Academies of Sciences, Engineering, and Medicine 2019). Many coral populations may not have the capacity to adapt to these altered conditions. The plethora of benefits that coral populations provide (see Moberg and Folke 1999)—including as sources of medicine to treat various infections and diseases (e.g. Bruckner

2002)—underscores the importance of supporting their persistence and resilience. Gene editing could theoretically provide an opportunity to increase genetic diversity within populations to allow them to adapt to a changing environment, or permit selection of traits that may improve the resilience of coral populations and species (van Oppen et al. 2015; National Academies of Sciences, Engineering, and Medicine 2019).

The jury is still out as to the costs and benefits of CRISPR, and discussions of its usage are highly controversial. For instance, one proposition by Phelps et al. (2019) is to apply genome-editing in a manner that mirrors the threat level classifications of the IUCN, whereby CRISPR is used primarily as a means of slowing the rate of decline without altering the underlying genetic diversity of species with 'near threatened' or 'vulnerable' statuses (e.g. via genetic barcoding for enhanced monitoring of populations). For more threatened species where genetic erosion is evident (e.g. those that are categorised as 'critically endangered'), this would imply a focus on enhancing the adaptive capabilities of the species within its environment. In such cases, Phelps et al. (2019) propose making genetic modifications in the form of targeted beneficial mutations and gene replacements as potential tools for species survival. However, understanding the genetic underpinnings of these adaptations (e.g. via transcriptomics and epigenetics) is critical before any such steps are explored. For example, while CRISPR may be technically feasible to apply to corals, little knowledge exists regarding candidate genes on which it could operate to increase resilience, and whether it may translate to phenotypic changes (National Academies of Sciences, Engineering, and Medicine 2019). For corals, such work has already begun with differences in genome expression found between corals that were sensitive or resilient to thermal stress (Barshis et al. 2013; Palumbi 2014). From a broader perspective, arguments have also been made about addressing the root cause of the problem rather than relying on technological 'fixes' that might well go awry (CSS et al. 2019).

Box 4. South Africa Case Study: A Lack of Knowledge and Techniques Limits Our Ability to Assess the Risks to the Genetic Component of Marine Biodiversity

South Africa has an established community of biodiversity assessment and planning practitioners whose collective experience led them to establish spatial plans for ecological sustainability. A series of spatial biodiversity layers have been used to support the Marine Protected Area Expansion program, and the National Biodiversity Assessment (NBA), which is used to inform policies and management decisions. This allowed for systematic assessments of the state of biodiversity in 2004 and 2011. In addition to the statuses and trends of ecosystems and species, the 2018 NBA reports on the state of genetic diversity.^a

From a genetics perspective, the general outcome was a clear lack of temporal genetic diversity datasets and indicators—a finding mirrored throughout the globe. Although genetic studies have been conducted on several species, these data typically represent a snapshot of a species' genetic diversity and are applicable to only a limited portion of the species' range. Although still highly informative, the lack of a temporal component prevents the tracking of genetic changes and limits the assessment of genetic risks to marine biodiversity; however, efforts are underway to rectify this.

Within the past two decades, a strong baseline understanding of the spatial genetic patterns in various coastal species and offshore commercially exploited fish stocks has been established.^b This work is primarily based on mitochondrial DNA and, to a lesser extent, microsatellite markers.^c More recently, with the advent of NGS, research is being directed toward epigenetics^d and genome-wide scanning of various coastal species to identify intraspecific variability and structure. Given the heterogeneous marine environment of South Africa, which spans a variety of ecological gradients (e.g. temperature, primary productivity, oxygen, salinity), such work is likely to provide insights into signals of local adaptation and population connectivity. In doing so, areas of evolutionary importance, persistence and resilience may be identified, which could inform marine spatial planning. Moreover, environmental DNA coupled with metabarcoding is assisting with large-scale foundational surveys to quantify the vast and mostly unexplored portions of the marine environment. These data can act as a baseline for more

targeted monitoring and assist in amassing phylogenies on specific taxonomic groups for national-level monitoring.

Although single species are typically the focus of genetic monitoring studies, the ability to track genetic diversity across species for a given taxonomic group at a seascape or ecosystem level could greatly inform biodiversity planning at a national scale. South Africa is developing a Critical Biodiversity Area (CBA) map as a spatial plan for ecological sustainability, including identification of CBAs and Ecological Support Areas (ESAs), which together with protected areas are important for landscape and seascape functioning. To bring in the genetic diversity component to this planning process, work has already begun on intertidal chitons using phylogenetic diversity to help prioritise areas of high genetic diversity for marine spatial planning.^e However, additional metrics should also be considered, such as phylogenetic endemism, evolutionary distinctiveness, and evolutionarily distinct and globally endangered. Each of these metrics can be useful for evaluating biodiversity under different scenarios, and the choice of metric depends on the conservation objectives. A recent study used all four metrics to examine patterns of genetic diversity across South Africa for terrestrial reptiles.^f Similar studies focusing on marine taxa would be of great value.

To help guide genetic monitoring research, South Africa is developing a National Genetic Diversity Monitoring Framework to ensure that comparable long-term datasets can be established and used to better inform biodiversity management. This framework will outline how to strategically prioritise taxa; identify the most appropriate genetic markers and metrics to use for national-, ecosystem- and species-level monitoring; and provide advice on the frequency of monitoring. It will also inform the spatial plan currently in revision to refine the boundaries of existing CBAs, ESAs and MPAs.

Notes:

^a da Silva and van Vuuren 2019; Skowno et al. 2019.

^b e.g. von der Heyden et al. 2007; 2010; Henriques et al. 2017.

^c von der Heyden 2009; Teske et al. 2011; Wright et al. 2015.

^d Baldanzi et al. 2017.

^e Volkmann et al. 2014.

^f Tolley and Šmíd 2019.

4.2 Toward Responsible and Inclusive Research and Innovation

Important conceptual approaches to take forward these ideas are responsible research and innovation (RRI) and inclusive innovation. RRI envisages a transparent, interactive process by which societal actors and innovators become mutually responsive to each other with a view to the ethical acceptability, sustainability and societal desirability of the innovation process and its marketable products (Von Schomberg 2013). As observed by Laird and Wynberg (2018), the CBD and ABS provisions of the Nagoya Protocol already encapsulate the principled basis of RRI, although by default rather than by design. Inclusive innovation is an alternative, and perhaps a more contextually appropriate, framing of RRI. It explicitly includes those who have been excluded from the development mainstream (Foster and Heeks 2013), and refers to the production and delivery of innovative solutions to the problems of the poorest and most marginalised communities (Heeks et al. 2013).

For example, the extent to which MGR are used to treat neglected diseases has not been as prominent as the search for treatments for cancer where the direction of research has been influenced by major funders such as the U.S. National Cancer Institute (Mayer et al. 2017). However, the funding landscape seems to be changing due to, among other things, the growing prominence of philanthropic organisations. The potential for philanthropy to help fill gaps left by a lack of focus from national science programmes or demand from the market is one of several positive contributions to ocean science: A growing fleet of research vessels are operated with philanthropic support, and some are offering access to scientists from developing countries. Yet a lack of coordination as well as a tendency for philanthropies to have narrow missions suggests the potential for more added value if efforts were aligned with global agendas such as the UN Decade of Ocean Science or the Sustainable Development Goals (SDGs). Where appropriate, these efforts could also be aligned with national initiatives such as the United Kingdom's Global Challenges Research Fund, which aims at a more inclusive approach to meeting the needs of developing countries in a range of areas, including through efforts to discover novel pharmaceuticals for neglected diseases.

There is a clear need to forge more equitable research partnerships between industrialised and developing countries—and between users and providers of MGR—centred on scientific capacity, technology transfer and adequate finance. But it is also important to look at new models of partnerships driven by scientific advances that are changing the way researchers work. These are enabling the creation of dynamic knowledge hubs, and diffuse scientific collaborations, with increasing reliance on data and information (Broggiato et al. 2014). As marine genomics increasingly enters the big data realm, the challenges in equitable access are increasingly loaded toward computational and bioinformatics capacity, a trend that will continue in the future. This trend also underscores the need to resolve what some have termed the 'definitional mistake' of the CBD and Nagoya Protocol, which is the challenge of moving beyond the physical dimension of genetic resources (Ruiz Muller 2015).

The use of genetic sequence data presents both opportunities and challenges for benefit sharing, and is an increasingly central issue within several multilateral fora and organisations, including UNCLOS, the CBD, the World Health Organization and the Food and Agriculture Organization of the United Nations (Blasiak 2019; Laird et al. 2020). Dramatic changes in science and technology have also shifted the nature of benefits (Wynberg and Laird 2018). An important benefit has emerged in the form of publicly available databases, but it has also raised questions about the monetary and nonmonetary benefits that accrue to hosting countries (typically those that can provide funds, expertise and technological capacity) and the lack of access to such databases by countries that lack sufficient molecular research capacity or biotechnology infrastructure (Rabone et al. 2019). Concerns have also been expressed about the loss of control and benefits over national patrimony when DNA is sent overseas for more affordable sequencing and loaded onto public or open-access databases (Elbe and Buckland-Merrett 2017). Progress toward creating standards for the publication of genomic data and making scientific data open access, which is now mandatory for projects funded by public funds in many places (e.g. European Union, United States, Australia), has led to massive growth in publicly available data on the ocean genome. This has become big data (Stephens et al. 2015), with several petabytes of sequence data

available, including hundreds of millions of predicted genes (e.g. Sunagawa et al. 2015; Carradec et al. 2018; Gregory et al. 2019). This development is leading toward the consideration of the global ocean genome sequence catalogue as a universal resource, although this risks exacerbating inequity due to widely differing technological capacities to benefit from such shared access. At the same time, it may well be that enabling virtual access to data and the ability to use it might prove an easier task than equalising physical access to marine genetic resources.

Industry sequencing efforts are generally excluded from benefit-sharing obligations unless supported with public funds and/or published in peer-reviewed scientific literature. This provides industry with the advantage of accessing publicly funded sequence data for the global ocean genome without any corresponding obligations to share the data they generate. This raises serious questions about equitable use and distributional justice. In addition, this development is also redefining the challenge of access—from advanced ocean sampling and sequencing technologies, to advanced computational resources and enhanced predictive modelling capacities. These modelling capacities require bandwidth to access and download massive amounts of sequence data, which in turn requires high-speed broadband connections, supercomputers to mine and analyse the sequence data and scientists with advanced bioinformatics skills to query the datasets (Quince et al. 2017).

4.3 Equitable Governance and Benefit Sharing

Capacity building, access to and the transfer of marine technology, and information exchange are critical components of responsible and inclusive research and innovation and benefit sharing (Broggiato et al. 2018; Morgera 2018; Collins et al. 2019). The low chance of commercial success from biodiscovery, combined with the long time frame for potential financial returns, means that some of the most significant benefits are nonmonetary, emerging from the research process itself rather than from commercial products. These might include scientific training; access to research infrastructure; and increased collaboration and cooperation in marine science through data collection,

technical exchange and the development of joint scientific research projects and programmes. The complexities of MGR governance mean that in addition to the scientific, institutional and legal capacities necessary to develop and administer international and national regulatory frameworks, capacity is also needed to negotiate equitable agreements, resolve disputes and untangle the knotty problems of ownership and access. A deepened social and ethical understanding (Morgera 2018), focused on the role of marine scientists, is also required to manage the use of commonly shared MGR in a sustainable and equitable manner.

Independent of the legal status of MGR, a more principled approach toward benefit sharing should be adopted, in turn fostering ‘deeper and cosmopolitan cooperation’ via existing UNCLOS obligations on scientific research, capacity building, technology transfer and environmental protection. Such a principled approach would see equitable benefit sharing as an emerging principle of international law of which the human right to science is a part (Morgera 2018).

Current frameworks, including the intersection between environment and intellectual property norms, are extrapolated from constructs that apply on land, where boundaries are more tangible and organisms tend to have restricted ranges. These frameworks neglect the open nature of the ocean, where flows transport organisms across vast distances, including microbes aerosolised from the sea surface to be deposited back in the ocean thousands of kilometres away (Mayol et al. 2017; Ramesh et al. 2019). The 200-nautical-mile legal boundary that separates most national exclusive economic zones from areas beyond national jurisdiction lacks a biological rationale or scientific basis, and a successful mechanism regulating access and benefit sharing with regard to marine genetic resources will need to address this, possibly through collaborative mechanisms between the CBD and UNCLOS.

It is important that the BBNJ process does not replicate the implementation challenges that follow from the wide disparities in domestic measures under the Nagoya Protocol. One way to avoid the pitfalls of disparate implementation would be to agree on what equitable benefit sharing means as a principle of international

law, rather than as a mere modality that has polarised the ABS debate. With benefit sharing as a freestanding principle of international law, the links between other global mandates would become clearer, including as an aspect of the human right to science (Article 15 of the International Covenant on Economic, Social and Cultural Rights), contribution to other human rights such as those to food and health, and therefore significant for the realisation of SDGs 2 (hunger) and 3 (health and well-being). It could also be linked to UNCLOS's preambular language—'just and equitable international economic order which takes into account the interests and needs of [hu]mankind as a whole'—as this was the basis for UNCLOS benefit-sharing provisions in relation to outer continental shelf resources and deep-seabed mineral resources. These are issues that require international political will (Morgera 2018), and are subject to negotiations in the upcoming intergovernmental conference.

A key question that threatens swift progress in these negotiations is the issue of intellectual property rights over marine genetic resources and their commercialisation, as well as in relation to capacity building and technology transfer. It is important to note that given existing disparities in technical capabilities to engage in marine scientific research in ABNJ, leaving intellectual property regimes unchanged would likely lead to an exacerbation of technology gaps and inequity due to differential access to MGR and technologies arising from marine scientific research. It is in this context that negotiations related to intellectual property rights and marine genetic resources in the BBNJ process are particularly significant (Thambisetty 2020) for progress toward conservation and sustainable use goals.

One of the main pillars of disagreement and a significant challenge for research on MGR is the inability of the CBD and other international processes to agree on the use of disclosure requirements in the international patent system. The patent specification is a technical and legal document that contains clear and specific information about the invention seeking to be patented. Often these specifications will include information about the source or origin of biological material. As a mandatory measure, such disclosure could facilitate bilateral, global and

multilateral benefit sharing. It could also help resolve the artificial distinction between physical and informational genetic resources, inhibit the possibility of public domain or open-access information ending up in private patents, improve trust and ease the global compliance burden of marine scientists.

In the context of the BBNJ negotiations, a global multilateral benefit-sharing mechanism would go some way toward ensuring that the commercial exploitation and use of MGR from ABNJ, whether in physical or intangible form, are subject to benefit-sharing obligations. A multilateral mechanism is particularly important as some countries are advocating for MGR of unknown provenance to be deemed to be from ABNJ. Unless benefit-sharing obligations in the new instrument match or go beyond those in the CBD, this assumption is likely to lead to a race to the bottom of lax benefit-sharing regimes. Some scientists are also urging a rethink of existing rules on disclosing the origin of genetic resources (Blasiak et al. 2019; Chiarolla 2019) while ensuring that intellectual property rights including patents, copyright trade secrets and database rights do not impede capacity building around valuable information.

One of the lessons of the CBD and Nagoya Protocol is the inadequacy of international legal measures to actively engage with scientists and researchers. This in turn negatively impacts confidence in domestic regulatory authorities and the ability to develop laws based on up-to-date scientific understanding. Such concerns highlight the need for scientists to take a more active role in self-regulation, and to instigate training, particularly for younger researchers. Global engagement by scientists and other researchers across jurisdictional boundaries is potentially a powerful dynamic that can, with the right kinds of support and incentives, catalyse effective and equitable governance, and strengthen a shared sense of responsibility to conserve and protect the ocean genome.

5. Conclusion and Opportunities for Action

The ocean genome is the genetic material present in all marine biodiversity, determining the abundance and resilience of biological resources—such as fisheries and aquaculture—that collectively form a pillar of global food security and human well-being. It is the foundation upon which all marine ecosystems, including their functionality and their resilience, rest. Thus, protecting and conserving the ocean genome is crucially important not only for the functioning, stability and integrity of ocean ecosystems and the life within these systems, but for the biosphere and humanity. Yet the ocean genome is also being degraded and eroded through overexploitation, habitat loss and degradation, pollution, impacts from a changing climate such as ocean acidification, invasive species and other pressures, as well as their cumulative and interacting effects.

Simultaneously, exploration of the ocean at a genetic level has resulted in new insights into taxonomy and adaptive capacity that can help optimise conservation efforts, while also spawning a growing number of marine biotechnology applications of commercial importance, from anticancer treatments to cosmetics and industrial enzymes. Initiatives to commercialise the ocean genome should be coupled with considerations regarding conservation, with attention given to both monetary and nonmonetary benefits, and associated environmental, social and ethical risks.

Ensuring that the ocean genome is both conserved and used in a sustainable, fair and equitable manner is urgently important, particularly through the implementation of fully and highly protected areas in the ocean. The sustainable ocean economy is underpinned by the conservation and sustainable use of the ocean genome and a focus on equitable outcomes for all. Yet effective conservation, sustainable use and economic benefits from the ocean genome are challenged by a fragmented ocean governance landscape, gaps in scientific understanding and a world in which the capacity to access and share in the benefits of utilisation of marine genetic resources and associated information varies widely across states. Addressing these issues requires the adoption of effective national and transnational legal measures that ensure both incentives for research and development as well as equitable technology diffusion. Better coordination is needed to ensure that the resources available for promoting conservation, capacity development and other activities associated with the ocean genome are effectively used and equitably shared.

Following from these conclusions, we have identified the following eight opportunities for action to address these issues:

Opportunities for Action

1) Protect Marine Genetic Diversity as Part of Conservation Measures and Monitor Outcomes

- **Protect at least 30 percent of the ocean in implemented, fully or highly protected MPAs** to effectively conserve genetic diversity and ensure ocean health, productivity and resilience. Support this progress by connecting with existing international commitments in the post-2020 framework such as those in the CBD and UN SDGs, and through new voluntary commitments, as well as with support from philanthropies.
- **Ensure the conservation of genetic diversity beyond the boundaries of MPAs and other area-based management** by supporting the sustainable use of resources; avoiding habitat and ecosystem degradation; affording special protections for rare, vulnerable, threatened or endangered genotypes and species; and using precautionary approaches when initiating exploitation of species or places.
- **Incorporate considerations for marine genetic diversity directly into the management plans of industry/production sectors and conservation**, and support monitoring under existing and new international mechanisms. **Form a joint working group of scientists, legal experts and practitioners** with expertise spanning geography, ecoregions and sectoral international institutions (CBD, UNCLOS, World Trade Organization, WIPO) to advise on best practices in genetic monitoring, planning and management.
- **Use strategic environmental assessments** to manage conflicting uses, address the cumulative effects of multiple human activities and guide marine spatial planning and EIAs.
- **Report on the conservation and use of marine genetic diversity in national and local biodiversity strategies and action plans (NBSAPs/LBSAPs).**

2) Support Greater Equity in Genomics Research and Commercialisation

- **Ensure that marine science capacity building, information exchange, collaboration and appropriate technology transfer are given adequate attention**, including through their integration into access and benefit sharing (ABS) approaches, research agreements and funder policies. Ensure that new and additional funding streams are employed beyond repackaging existing funds.
- **Facilitate the implementation of domestic legal measures** to ensure that intellectual property norms support an equitable ocean economy. Mechanisms include limitations to the exercise of intellectual property rights through fair, nonexclusive licensing terms, and in ways that do not hinder capacity building, technology transfer or affordable access to technologies.
- **Build the above components into national research policies, plans and programmes and innovation strategies. Increase efforts to ensure that biodiscovery programmes are aware of capacity-building priorities**, and that users and providers of marine genetic resources and associated information are brought into discussions about how best to implement these actions. Make analytical platforms freely available to anyone able to access an internet connection.

3) Promote Inclusive and Responsible Research and Innovation in Marine Genomics Research

- **Support a transparent, interactive process by which societal actors, innovators and scientists become mutually responsive** to each other with a view to the ethical acceptability, environmental sustainability and societal desirability of the innovation process and its marketable products.

- **Provide incentives for research that are targeted toward important, underfunded objectives**, for example, diseases afflicting the global South. Ensure a focus on lower-income countries, the most marginalised and vulnerable communities, women and environmental concerns.
- **Support scientists to enable their engagement in socially responsive processes, including through the development of new communication tools**, to determine key needs and priorities and feed these into national research agendas.

4) Embed Conservation of the Ocean Genome within Research and Commercialisation, Including Benefit-Sharing Approaches and Agreements

- **Develop a global, multilateral benefit-sharing mechanism** for the fair and equitable use of marine genetic resources beyond national jurisdiction. This could include a review of international voluntary codes of conduct, and the cataloguing of examples where conservation outcomes have been achieved through such efforts.
- **Enhance the legal capacity of developing countries** to domestically address issues emerging from multilateral processes, including those related to intellectual property, benefit sharing, capacity building and technology transfer.
- Parties to the Convention on Biological Diversity should **develop benefit-sharing agreements with mutually agreed terms** focused on conservation and sustainable and equitable use outcomes when granting access to marine genetic resources within national jurisdictions, and support countries in monitoring the performance of such contracts.

- **Funders of research related to the ocean genome should require applicants to explain the potential conservation, sustainability and equity applications and benefits of their research.**

5) Disclose the Biological and Geographical Origins of Genetic Material as a Norm across All Associated Commercial and Noncommercial Activities

- **Modify procedural aspects of international patent law to require disclosure of the origin of genetic material in patent filings.**
- **Encourage and incentivise the disclosure of the origin of genetic material among marine scientists and private institutions as an aspect of responsible research and innovation.**
- Regardless of legal obligations, funding bodies, genetic sequence database administrators and journal editors should **require disclosure of the origin of genetic material.**

6) Increase Financial and Political Support to Improve Knowledge of the Ocean Genome

- **Build support for integrative taxonomic research** aimed at understanding the ocean genome by making this a key element of the UN Decade of Ocean Science for Sustainable Development.
- **Support the research needed for genetic monitoring as part of existing environmental assessments.** Research and share results on the links between genetic diversity and adaptive capacity in the context of global change.

- **Support research on the functional biology of the ocean**, including the systematic unveiling of gene function, gene networks and species interactions.
- **Prioritise the allocation of resources to build scientific capacity** using approaches such as environmental DNA, DNA metabarcoding and other emerging genetic monitoring techniques, as well as to develop more cost-efficient methods.

7) Comprehensively Assess the Risks and Benefits of Transgenic Marine Organisms as well as the Use of New Molecular Engineering Technologies—Such as CRISPR-Cas (Gene Editing) and Gene Drives—in the Marine Environment

- **Initiate a deliberative process, beginning with a working group**, to gather scientists, ethicists, environmentalists, policymakers and other actors to develop principles and debate approaches for whether and how genetic technologies should be used in the marine environment. Address the limits and directions of current research and development activities, assess risks and wider impacts and engage in dialogue about associated ethical considerations.

8) Strengthen the Role of Philanthropy in Providing Infrastructure and Funding for Marine Science

- **Establish a network to better coordinate privately funded initiatives, align their priorities with those of states** that are acquiring knowledge for societal needs and improve the transparency of philanthropic funding.
- **Encourage financial supporters of ocean science, including philanthropies, to publish and comply with an ethical code of conduct, and sign a ‘Declaration for Coordinated Ocean Action’** based on the principles set forth in the Paris Declaration on Aid Effectiveness and the Accra Agenda for Action to ensure that support is aligned and coordinated with the objectives of the UN Decade of Ocean Science for Sustainable Development, the SDGs and priorities identified by developing countries.

Appendix

Table A1. Opportunities for Action to Conserve and Use Marine Genetic Resources Fairly, Equitably and Sustainably

To support success, we include in this table potential barriers to implementation and strategies to overcome them.

THEME	OPPORTUNITIES FOR ACTION	BARRIERS TO IMPLEMENTATION	OVERCOMING BARRIERS
1. Protect marine genetic diversity as part of conservation measures and monitor their outcomes.	<p>International level</p> <p>Post-2020 Convention on Biological Diversity (CBD) targets on marine protected areas (MPAs) should follow the scientific evidence showing that protecting at least 30% of the ocean in fully to highly protected, implemented MPAs is needed to conserve biodiversity and genetic diversity and to sustain ocean health, productivity and resilience.</p> <p>Form a joint working group of scientists, legal experts and practitioners with expertise spanning geography, ecoregions, and sectoral international institutions (CBD, United Nations Convention on the Law of the Sea [UNCLOS], World Trade Organization, World Intellectual Property Organization) to mainstream genetic monitoring into existing international mechanisms (e.g. International Seabed Authority [ISA] mining code for prospecting and exploration) and new international mechanisms (e.g. Biodiversity in Areas Beyond National Jurisdiction treaty, ISA mining code for exploitation).</p> <p>With respect to identifying priorities for conservation in areas beyond national jurisdiction, strategic environmental assessments, comprehensively understood, can help avoid conflicting uses, address cumulative effects of multiple human activities, and guide environmental impact assessments for specific current and proposed activities.</p> <p>The CBD should issue guidance on how to incorporate aspects of genetic diversity into National Biodiversity Strategies and Action Plans.</p> <p>National, regional and local levels</p> <p>Marine genetic diversity should be explicitly incorporated into the design and management of conservation measures, including by establishing fully and highly protected MPAs, as well as subsequently monitoring their outcomes.</p>	<p>Securing funding to establishing a joint working group.</p> <p>Lack of capacity at national, regional and local levels to engage in genetic monitoring activities.</p> <p>Gaps in taxonomic knowledge and datasets to enable genetic monitoring activities.</p>	<p>Connect with existing commitments (e.g. under UNCLOS and within the Sustainable Development Goals [SDGs]), voluntary commitments (e.g. from UN Ocean Conference) and philanthropy (see Opportunity for Action 8).</p> <p>On lack of capacity, see Opportunity for Action 4; on gaps in taxonomic knowledge, see Opportunity for Action 1.</p>

Table A1. Opportunities for Action to Conserve and Use Marine Genetic Resources Fairly, Equitably and Sustainably (Cont'd)

THEME	OPPORTUNITIES FOR ACTION	BARRIERS TO IMPLEMENTATION	OVERCOMING BARRIERS
2. Support greater equity in genomics research and commercialisation.	<p>International level</p> <p>Ensure that marine science capacity building, information exchange, collaboration and appropriate technology transfer are given adequate attention in international research programmes, and that priorities are well articulated in CBD and UNCLOS decisions.</p> <p>Articulate and facilitate internationally the implementation of hard-edged domestic legal measures such as limitations to the exercise of intellectual property rights through fair, nonexclusive licensing terms; market authorisations that take note of compliance with benefit-sharing mechanisms; and the application of international legal norms that facilitate technology transfer and affordable access to technologies.</p> <p>National level</p> <p>Build these components into national research policies, plans and programmes and innovation strategies. Ensure that biodiscovery programmes are aware of capacity-building priorities, and that users and providers of marine genetic resources and associated information are brought into discussions about how best to implement these actions. Make analytical platforms available to anyone able to access an internet connection.</p> <p>Explore the full range of limitations and exceptions to intellectual property rights so that capacity building and technology transfer are not precluded by exclusive intellectual property rights.</p>	<p>Ensure that prioritisation of allocating resources for researching the ocean genome results in new funding streams rather than a simple repackaging of existing funds.</p>	<p>See Opportunity for Action 8 on developing a 'Declaration for Coordinated Ocean Action'.</p>

Table A1. Opportunities for Action to Conserve and Use Marine Genetic Resources Fairly, Equitably and Sustainably (Cont'd)

THEME	OPPORTUNITIES FOR ACTION	BARRIERS TO IMPLEMENTATION	OVERCOMING BARRIERS
3.	<p>Promote inclusive innovation in marine genomics research.</p> <p>International level</p> <p>Support a transparent, interactive process by which societal actors and innovators become mutually responsive to each other with a view to the ethical acceptability, sustainability and societal desirability of the innovation process and its marketable products.</p> <p>Provide incentives for research that are targeted toward societally important yet underfunded objectives. Ensure a focus on lower-income countries, the most marginalised and vulnerable communities, women and environmental concerns.</p> <p>National level</p> <p>Support scientists to enable their engagement in socially responsive processes that determine key needs and priorities and feed these into national research agendas. Ensure a focus on the most marginalised and vulnerable communities, women and on key environmental concerns. Develop communication tools to improve linkages between societal actors.</p>	<p>Funding for research and development programmes is often driven by commercial entities, with products geared toward affluent markets rather than to either broader societal needs or diseases afflicting the global South.</p>	<p>See Opportunity for Action 8 on developing a 'Declaration for Coordinated Ocean Action'.</p>
4.	<p>Embed conservation of the ocean genome within research and commercialisation, including through benefit-sharing approaches and agreements.</p> <p>International level</p> <p>Facilitate a fair, equitable, global, multilateral benefit-sharing mechanism for the use and exploitation of marine genetic resources beyond national jurisdiction.</p> <p>Enhance the legal capacity of developing countries to address domestically issues emerging from multilateral processes including those related to intellectual property, benefit sharing, capacity building and technology transfer.</p> <p>National level</p> <p>Parties to the Convention on Biological Diversity should include benefit-sharing agreements with mutually agreed terms focused on conservation and sustainable and equitable use outcomes when granting access to marine genetic resources.</p> <p>When allocating funding for research associated with marine genetic resources, grant-making bodies and research councils should require applicants to explain the potential conservation, sustainability and equity applications and benefits of their research.</p>	<p>No legal obligation exists to undertake such actions, so states and funding bodies would be acting in a voluntary manner. Resistance to depart from the status quo.</p>	<p>Develop international voluntary codes of conduct, and catalogue case studies and best practices when conservation outcomes are achieved through such efforts.</p> <p>Develop opportunities for legal pluralism for specific problems through training and the exchange of legal expertise.</p>

Table A1. Opportunities for Action to Conserve and Use Marine Genetic Resources Fairly, Equitably and Sustainably (Cont'd)

THEME	OPPORTUNITIES FOR ACTION	BARRIERS TO IMPLEMENTATION	OVERCOMING BARRIERS
5.	<p>Disclose the origins (species and geographical area where organisms were extracted) of genetic material as a norm across all associated commercial and noncommercial activities.</p> <p>International level</p> <p>Modify procedural aspects of international patent law to require the disclosure of the origins (species and geographical area where organisms were extracted) of genetic material in patent filings. This could be achieved through either in-application disclosure or the development of new categories in the international patent classification system. Such measures could help identify cases of noncompliance with the Nagoya Protocol and ensure compliance with existing and emerging access and benefit-sharing obligations.</p> <p>National, regional and local levels</p> <p>Regardless of legal obligations, funding bodies, genetic sequence database administrators and journal editors should require disclosure of origin.</p>	<p>Slow pace of consensus building within relevant international forums.</p>	<p>Reputational benefits accrued by voluntary disclosure of origin by scientists, with potential to shape norms of best practice.</p>
6.	<p>Increase financial and political support to improve knowledge of the ocean genome.</p> <p>International level</p> <p>Build support for taxonomic research aimed at understanding the ocean genome by making this a key element of the UN Decade of Ocean Science.</p> <p>National, regional and local levels</p> <p>Responsible ministries, departments, research councils and other relevant actors should support research needed for basic taxonomic knowledge, genetic monitoring as part of existing environmental assessments, and research on the links between genetic diversity and adaptive capacity in the context of global change.</p> <p>All levels</p> <p>Funding agencies should prioritise the allocation of resources to support the building of scientific capacity to enhance understanding using the range of available resources, including environmental DNA, DNA metabarcoding and other emerging techniques to enable genetic monitoring.</p>	<p>Convincing policymakers and funding bodies to prioritise taxonomic research and genetic monitoring approaches.</p>	<p>Communicate the range of benefits associated with improved knowledge of the ocean genome (for both conservation and commercial purposes).</p> <p>See Opportunity for Action 8.</p>

Table A1. Opportunities for Action to Conserve and Use Marine Genetic Resources Fairly, Equitably and Sustainably (Cont'd)

	THEME	OPPORTUNITIES FOR ACTION	BARRIERS TO IMPLEMENTATION	OVERCOMING BARRIERS
7.	Comprehensively assess the risks and benefits of transgenic marine organisms as well as the use of new technologies—such as CRISPR-Cas (gene editing) and gene drives—in the marine environment.	<p>International level</p> <p>Initiate a deliberative process or ‘observatory’ think tank to bring together scientists, ethicists, environmentalists, policymakers and other actors to develop principles and debate approaches to using genetic technologies in the marine environment, and to engender robust conversations about the limits and directions of research and development, risk assessments, and wider impacts as well as ethical considerations.</p>	<p>Different worldviews and knowledge systems are difficult to bring together.</p> <p>Rigid positions may be adopted by different actors.</p> <p>Communication between actors remains a major challenge.</p>	<p>Ensure that scientific information is effectively translated into accessible language; improve interdisciplinary understandings; build awareness among policymakers.</p>
8.	Increase the role of philanthropy in providing infrastructure and funding for marine science.	<p>International level</p> <p>Establish a network to better coordinate privately funded initiatives with those of states that are acquiring knowledge for societal needs, as outlined by global agendas such as the SDGs and the UN Decade of Ocean Science.</p> <p>Financial supporters of ocean science, including philanthropies, sign a ‘Declaration for Coordinated Ocean Action’ that is based on the principles set forth in the Paris Declaration on Aid Effectiveness and the Accra Agenda for Action to ensure that support is aligned and coordinated with the objectives of the UN Decade of Ocean Science and the SDGs.</p> <p>Communicate with the Organisation for Economic Co-operation and Development’s Development Assistance Committee for data illustrating the impact of the Paris Declaration on Aid Effectiveness and Accra Agenda for Action, and use these experiences to communicate the added value of a coordinated approach.</p>	<p>Hesitance by national research councils, philanthropies or others to commit to a coordinated and aligned approach in their financial support.</p>	<p>Take a stepwise approach, first asking signatories to recommit to existing development frameworks, and then seeking more ambitious commitments to align and coordinate support over time.</p>

Abbreviations

ABNJ	areas beyond national jurisdiction	LBSAP	Local Biodiversity Strategy and Action Plan
ABS	access and benefit sharing	MGR	marine genetic resources
antiSMASH	antibiotics & Secondary Metabolite Analysis Shell	MPA	marine protected area
BBNJ	biodiversity in areas beyond national jurisdiction	NBA	National Biodiversity Assessment
CBA	Critical Biodiversity Area	NBSAP	National Biodiversity Strategy and Action Plan
CBD	Convention on Biological Diversity	NGS	next-generation sequencing
cDNA	complementary DNA	OECD	other effective area-based conservation measure
CRISPR	Clustered Regularly Interspaced Short Palindromic Repeats	RNA	ribonucleic acid
DHA	docosahexaenoic acid	RRI	responsible research and innovation
DNA	deoxyribonucleic acid	SDG	Sustainable Development Goal
eDNA	environmental DNA	SEA	strategic environmental assessment
EEZ	exclusive economic zone	TALENs	transcription activator-like effector nucleases
EIA	environmental impact assessment	TRIPS	The Agreement on Trade-Related Aspects of Intellectual Property Rights
EPA	eicosapentaenoic acid	UN	United Nations
EPS	extracellular polymeric substances	UNCLOS	United Nations Convention on the Law of the Sea
ESA	Ecological Support Area	WIPO	World Intellectual Property Organization
GFP	green fluorescent protein		
IPBES	Intergovernmental Science-Policy Platform on Biodiversity and Ecosystem Services		
IUCN	International Union for the Conservation of Nature		

References

- Abberton, M., J. Batley, A. Bentley, J. Bryant, H. Cai, J. Cockram, A. Costa de Oliveira, et al. 2016. "Global Agricultural Intensification during Climate Change: A Role for Genomics." *Plant Biotechnology Journal* 14 (4): 1095–98. <https://doi.org/10.1111/pbi.12467>.
- Aburto-Oropeza, O., A. Rogers, et al. 2020. *Critical Habitats and Biodiversity: Inventory, Thresholds and Governance*. Washington, DC: World Resources Institute.
- Ahmed, N., and M. Glaser. 2016. "Coastal Aquaculture, Mangrove Deforestation and Blue Carbon Emissions: Is REDD+ a Solution?" *Marine Policy* 66: 58–66.
- Ainsworth, T.D., S.F. Heron, J.C. Ortiz, P.J. Mumby, A. Grech, D. Ogawa, C.M. Eakin, et al. 2016. "Climate Change Disables Coral Bleaching Protection on the Great Barrier Reef." *Science* 352 (6283): 338–42. <https://doi.org/10.1126/science.aac7125>.
- Algenesis Materials. n.d. "Our Technology." <https://www.algenesismaterials.com/technology>.
- Allendorf, F.W., P.R. England, G. Luikart, P.A. Ritchie and N. Ryman. 2008. "Genetic Effects of Harvest on Wild Animal Populations." *Trends in Ecology & Evolution* 23 (6): 327–37. <https://doi.org/10.1016/j.tree.2008.02.008>.
- Allison, G.W., S.D. Gaines, J. Lubchenco and H.P. Possingham. 2003. "Ensuring Persistence of Marine Reserves: Catastrophes Require Adopting an Insurance Factor." *Ecological Applications* 13 (1): S8–24.
- Allott, P. 1992. "Mare Nostrum: A New International Law of the Sea." *American Journal of International Law* 86 (4): 764–87.
- Almany, G.R., S.R. Connolly, D.D. Heath, J.D. Hogan, G.P. Jones, L.J. McCook, M. Mills, et al. 2009. "Connectivity, Biodiversity Conservation and the Design of Marine Reserve Networks for Coral Reefs." *Coral Reefs* 28 (2): 339–51.
- Alves, C., J. Silva, S. Pinteus, H. Gaspar, M.C. Alpoim, L.M. Botana and R. Pedrosa. 2018. "From Marine Origin to Therapeutics: The Antitumor Potential of Marine Algae-Derived Compounds." *Frontiers in Pharmacology* 9. <https://doi.org/10.3389/fphar.2018.00777>.
- Andruszkiewicz, E.A., H.A. Starks, F.P. Chavez, M. Sassoubre, B.A. Block and A.B. Boehm. 2017. "Biomonitoring of Marine Vertebrates in Monterey Bay Using eDNA Metabarcoding." *PLOS ONE* 12 (4): e0176343. <https://doi.org/10.1371/journal.pone.0176343>.
- Ardura, A., A. Zaiko, J.L. Martinez, A. Samulioviene, A. Semenova and E. Garcia-Vazquez. 2015. "eDNA and Specific Primers for Early Detection of Invasive Species—A Case Study on the Bivalve *Rangia Cuneata*, Currently Spreading in Europe." *Marine Environmental Research* 112: 48–55. <https://doi.org/10.1016/j.marenvres.2015.09.013>.
- Arismendi, I., D. Soto, B. Penaluna, C. Jara, C. Leal and J. León-Muñoz. 2009. "Aquaculture, Non-native Salmonid Invasions and Associated Declines of Native Fishes in Northern Patagonian Lakes." *Freshwater Biology* 54 (5): 1135–47.
- Arnaud-Haond, S., J.M. Arrieta and C.M. Duarte. 2011. "Marine Biodiversity and Gene Patents." *Science* 331 (6024): 1521–22.
- Arrieta, J.M., S. Arnaud-Haond and C.M. Duarte. 2010. "What Lies underneath: Conserving the Oceans' Genetic Resources." *Proceedings of the National Academy of Sciences* 107 (43): 18318–24.
- Arulandhu, A.J., M. Staats, R. Hagelaar, M.M. Voorhuijzen, T.W. Prins, I. Scholtens, A. Costessi, et al. 2017. "Development and Validation of a Multi-Locus DNA Metabarcoding Method to Identify Endangered Species in Complex Samples." *Gigascience* 6 (10): 1–18. <https://doi.org/10.1093/gigascience/gix080>.
- Aylagas, E., Á. Borja, X. Irigoien and N. Rodríguez-Ezpeleta. 2016. "Benchmarking DNA Metabarcoding for Biodiversity-Based Monitoring and Assessment." *Frontiers in Marine Science* 3. <https://doi.org/10.3389/fmars.2016.00096>.
- Baird, D.J., and M. Hajibabaei. 2012. "Biomonitoring 2.0: A New Paradigm in Ecosystem Assessment Made Possible by Next-Generation DNA Sequencing." *Molecular Ecology* 21: 2039–44.
- Bakker, J., O.S. Wangenstein, D.D. Chapman, G. Boussarie, D. Buddo, T.L. Guttridge, H. Hertler, et al. 2017. "Environmental DNA Reveals Tropical Shark Diversity in Contrasting Levels of Anthropogenic Impact." *Scientific Reports* 7: 1–11. <https://doi.org/10.1038/s41598-017-17150-2>.
- Baldanzi, S., R. Watson, C.D. McQuaid, G. Gouws and F. Porri. 2017. "Epigenetic Variation among Natural Populations of the South African Sandhopper *Talorchestia Capensis*." *Evolutionary Ecology* 31 (1): 77–91. <https://doi.org/10.1007/s10682-016-9877-9>.
- Ban, N.C., G.G. Gurney, N.A. Marshall, C.K. Whitney, M. Mills, S. Gelcich, N.J. Bennett, et al. 2019. "Well-Being Outcomes of Marine Protected Areas." *Nature Sustainability* 2 (6): 524.
- Barbuto, M., A. Galimberti, E. Ferri, M. Labra, R. Malandra, P. Galli and M. Casiraghi. 2010. "DNA Barcoding Reveals Fraudulent Substitutions in Shark Seafood Products: The Italian Case of 'Palombo' (*Mustelus* Spp.)." *Food Research International* 43 (1): 376–81. <https://doi.org/10.1016/j.foodres.2009.10.009>.
- Barendse, J., A. Roel, C. Longo, L. Andriessen, L.M.I. Webster, R. Ogden and F. Neat. 2019. "DNA Barcoding Validates Species Labelling of Certified Seafood." *Current Biology* 29 (6): R198–99. <https://doi.org/10.1016/j.cub.2019.02.014>.
- Bar-On, Y.M., R. Phillips and R. Milo. 2018. "The Biomass Distribution on Earth." *Proceedings of the National Academy of Sciences* 115 (25): 6506–11.
- Barshis, D.J., J.T. Ladner, T.A.A. Oliver, F.O. Seneca, N. Traylor-Knowles and S.R. Palumbi. 2013. "Genomic Basis for Coral Resilience to Climate Change." *Proceedings of the National Academy of Sciences* 110 (4): 1387–92. <https://doi.org/10.1073/pnas.1210224110>.
- Barton, A.D., A.J. Irwin, Z.V. Finkel and C.A. Stock. 2016. "Anthropogenic Climate Change Drives Shift and Shuffle in North Atlantic Phytoplankton Communities." *Proceedings of the National Academy of Sciences* 113 (11): 2964–69.
- Béné, C., R. Arthur, H. Norbury, E.H. Allison, M. Beveridge, S. Bush, L. Campling, et al. 2016. "Contribution of Fisheries and Aquaculture to Food Security and Poverty Reduction: Assessing the Current Evidence." *World Development* 79: 177–96.
- Bester-van der Merwe, A.E., R. Roodt-Wilding, F.A.M. Volckaert and M.E. D'Amato. 2011. "Historical Isolation and Hydrodynamically Constrained Gene Flow in Declining Populations of the South-African Abalone, *Haliotis Midas*." *Conservation Genetics* 12 (2): 543–55. <https://doi.org/10.1007/s10592-010-0162-0>.

- Beygmoradi, A., and A. Homaei. 2017. "Marine Microbes as a Valuable Resource for Brand New Industrial Biocatalysts." *Biocatalysis and Agricultural Biotechnology* 11: 131–52.
- Blasiak, R. 2019. "International Regulatory Changes Poised to Reshape Access to Marine Genes." *Nature Biotechnology* 37 (4): 357.
- Blasiak, R., J.-B. Jouffray, C.C.C. Wabnitz and H. Österblom. 2019. "Scientists Should Disclose Origin in Marine Gene Patents." *Trends in Ecology & Evolution* 34 (5): 392–95.
- Blasiak, R., J.-B. Jouffray, C.C.C. Wabnitz, E. Sundström and H. Österblom. 2018. "Corporate Control and Global Governance of Marine Genetic Resources." *Science Advances* 4 (6): eaar5237.
- Blowes, S.A., and S.R. Connolly. 2012. "Risk Spreading, Connectivity, and Optimal Reserve Spacing." *Ecological Applications* 22 (1): 311–21.
- Bockmann, F.A., M.T. Rodrigues, T. Kohlsdorf, L. Cobra Straker, T. Grant, M.C. Cardoso de Pinna, F.L. Medina Mantelatto, et al. 2018. "Brazil's Government Attacks Biodiversity." *Science* 360 (6391): 865.
- Bonfanti, C., C. Cardoso, C. Afonso, J. Matos, T. Garcia, S. Tanni and N.M. Bandarra. 2018. "Potential of Microalga Isochrysis Galbana: Bioactivity and Bioaccessibility." *Algal Research* 29: 242–48.
- Boussarie, G., J. Bakker, O.S. Wangensteen, S. Mariani, L. Bonnin, J.-B. Juhel, J.J. Kiszka, et al. 2018. "Environmental DNA Illuminates the Dark Diversity of Sharks." *Science Advances* 4 (5): eaap9661. May. <https://doi.org/10.1126/sciadv.aap9661>.
- Broggiato, A., S. Arnaud-Haond, C. Chiarolla and T. Greiber. 2014. "Fair and Equitable Sharing of Benefits from the Utilization of Marine Genetic Resources in Areas beyond National Jurisdiction: Bridging the Gaps between Science and Policy." *Marine Policy* 49 (November): 176–85. <https://doi.org/10.1016/j.marpol.2014.02.012>.
- Broggiato, A., T. Vanagt, L.E. Lallier, M. Jaspars, G. Burton and D. Muyldermans. 2018. "Mare Geneticum: Balancing Governance of Marine Genetic Resources in International Waters." *The International Journal of Marine and Coastal Law* 33 (1): 3–33. <https://doi.org/10.1163/15718085-13310030>.
- Bruckner, A.W. 2002. "Life-Saving Products from Coral Reefs." *Issues in Science and Technology* 18 (3). https://issues.org/p_bruckner/.
- Buchanan, J.R., G.M. Ralph, F. Krupp, H. Harwell, M. Abdallah, E. Abdulqader, M. Al-Husaini, et al. 2019. "Regional Extinction Risks for Marine Bony Fishes Occurring in the Persian/Arabian Gulf." *Biological Conservation* 230: 10–19.
- Caicedo, J.C., S. Cooper, F. Heigwer, S. Warchal, P. Qiu, C. Molnar, A.S. Vasilevich, et al. 2017. "Data-Analysis Strategies for Image-Based Cell Profiling." *Nature Methods* 14 (9): 849.
- Campbell, L., H.A. Nolla and D. Vaulot. 1994. "The Importance of Prochlorococcus to Community Structure in the Central North Pacific Ocean." *Limnology and Oceanography* 39 (4): 954–61.
- Caplan, A.L., B. Parent, M. Shen and C. Plunkett. 2015. "No Time to Waste—The Ethical Challenges Created by CRISPR." *EMBO Reports* 16 (11): 1421–26.
- Carpenter, K.E., M. Abrar, G. Aeby, R.B. Aronson, S. Banks, A. Bruckner, A. Chiriboga, et al. 2008. "One-Third of Reef-Building Corals Face Elevated Extinction Risk from Climate Change and Local Impacts." *Science* 321 (5888): 560–63.
- Carpenter, L.J., and P.S. Liss. 2000. "On Temperate Sources of Bromoform and Other Reactive Bromine Gases." *Journal of Geophysical Research: Atmospheres* 105: 20539–47.
- Carr, M.H., S.P. Robinson, C. Wahle, G. Davis, S. Kroll, S. Murray, E.J. Schumacker, et al. 2017. "The Central Importance of Ecological Spatial Connectivity to Effective Coastal Marine Protected Areas and to Meeting the Challenges of Climate Change in the Marine Environment." *Aquatic Conservation: Marine and Freshwater Ecosystems* 27: 6–29.
- Carradec, Q., E. Pelletier, C. Da Silva, A. Alberti, Y. Seeleuthner, R. Blanc-Mathieu, G. Lima-Mendez, et al. 2018. "A Global Ocean Atlas of Eukaryotic Genes." *Nature Communications* 9 (1): 1–13. <https://doi.org/10.1038/s41467-017-02342-1>.
- Carroll, A.R., B.R. Copp, R.A. Davis, R.A. Keyzers and M.R. Prinsep. 2019. "Marine Natural Products." *Natural Product Reports* 36: 122–73.
- Carugati, L., C. Corinaldesi, A. Dell'Anno and R. Danovaro. 2015. "Metagenetic Tools for the Census of Marine Meiofaunal Biodiversity: An Overview." *Marine Genomics* 24: 11–20. <https://doi.org/10.1016/j.margen.2015.04.010>.
- Cawthorn, D.-M., H.A. Steinman and R.C. Witthuhn. 2012. "DNA Barcoding Reveals a High Incidence of Fish Species Misrepresentation and Substitution on the South African Market." *Food Research International* 46 (1): 30–40.
- CBD (Convention on Biological Diversity). 2018. "Protected Areas and Other Effective Area-Based Conservation Measures. Recommendation Adopted by the Subsidiary Body on Scientific, Technical, and Technological Advice. CBD/SBSTTA/REC/22/5." Convention on Biological Diversity.
- Ceci, S.J., and W.M. Williams. 2011. "Understanding Current Causes of Women's Underrepresentation in Science." *Proceedings of the National Academy of Sciences* 108 (8): 3157–62.
- Cerezo Valverde, J., T. Rodríguez-González, M.D. Granero-Fernández, F. Aguado-Giménez and B. García García. 2019. "Successful Rearing of Common Octopus (*Octopus Vulgaris*) Fed a Formulated Feed in an Offshore Cage." *Aquaculture Research* 50 (3): 968–72.
- Chan, F.T., E. Briski and F. Chan. 2017. "An Overview of Recent Research in Marine Biological Invasions." *Marine Biology* 164 (6): 1–10. <https://doi.org/10.1007/s00227-017-3155-4>.
- Chang, F.-Y., and S.F. Brady. 2012. "Cloning and Characterization of an eDNA Derived Gene Cluster that Encodes the Biosynthesis of the Antitumor Substance BE-54017." *Journal of the American Chemistry Society* 133 (26): 9996–99. <https://doi.org/10.1021/ja2022653>.
- Chapin III, F.S., E.S. Zavaleta, V.T. Eviner, R.L. Naylor, P.M. Vitousek, H.L. Reynolds, D.U. Hooper, et al. 2000. "Consequences of Changing Biodiversity." *Nature* 405 (6783): 234.
- Chauton, M.S., K. Inge Reitan, N.H. Norsker, R. Tveterås and H.T. Kleivdal. 2015. "A Techno-Economic Analysis of Industrial Production of Marine Microalgae as a Source of EPA and DHA-Rich Raw Material for Aquafeed: Research Challenges and Possibilities." *Aquaculture* 436: 95–103.
- Cheng, B.S., A.H. Altieri, M.E. Torchin and G.M. Ruiz. 2019. "Can Marine Reserves Restore Lost Ecosystem Functioning? A Global Synthesis." *Ecology* 100 (4): e02617. <https://doi.org/10.1002/ecs.2617>.
- Chhetri, B.K., S. Lavoie, A.M. Sweeney-Jones and J. Kubanek. 2018. "Recent Trends in the Structural Revision of Natural Products." *Natural Product Reports* 35 (6): 514–31.
- Chiarolla, C. 2019. "Intellectual Property from a Global Environmental Law Perspective: Lessons from Patent Disclosure Requirements for Genetic Resources and Traditional Knowledge." *Transnational Environmental Law* 8 (3): 503–21.

- Claudet, J., C.W. Osenberg, L. Benedetti-Cecchi, P. Domenici, J.A. Garcia-Charton, A. Perez-Ruzafa, F. Badalamenti, et al. 2008. "Marine Reserves: Size and Age Do Matter." *Ecology Letters* 11 (5): 481–89.
- Cobián Güemes, A.G., M. Youle, V.A. Cantú, B. Felts, J. Nulton and F. Rohwer. 2016. "Viruses as Winners in the Game of Life." *Annual Review of Virology* 3 (1): 197–214. <https://doi.org/10.1146/annurev-virology-100114-054952>.
- Collins, J.E., H. Harden-Davies, M. Jaspars, T. Thiele, T. Vanagt and I. Huys. 2019. "Inclusive Innovation: Enhancing Global Participation in and Benefit Sharing Linked to the Utilization of Marine Genetic Resources from Areas beyond National Jurisdiction." *Marine Policy* 109 (November): 103696. <https://doi.org/10.1016/j.marpol.2019.103696>.
- Corkeron, P., P. Hamilton, J. Bannister, P. Best, C. Charlton, K.R. Groch, K. Findlay, et al. 2018. "The Recovery of North Atlantic Right Whales, *Eubalaena Glacialis*, Has Been Constrained by Human-Caused Mortality." *Royal Society Open Science* 5 (11): 180892. <https://doi.org/10.1098/rsos.180892>.
- Cornwall, W. 2019. "The Reef Builders." *Science* 363 (6433): 1264–69. <https://doi.org/10.1126/science.363.6433.1264>.
- Costanza, R. 1999. "The Ecological, Economic, and Social Importance of the Oceans." *Ecological Economics* 31 (2):199–213.
- Costello, M.J. 2014. "Long Live Marine Reserves: A Review of Experiences and Benefits." *Biological Conservation* 176 (August): 289–96. <https://doi.org/10.1016/j.biocon.2014.04.023>.
- Costello, M.J., S. Wilson and B. Houlding. 2012. "Predicting Total Global Species Richness Using Rates of Species Description and Estimates of Taxonomic Effort." *Systematic Biology* 61 (5): 871.
- Cowie, R.H., C. Regnier, B. Fontaine and P. Bouchet. 2017. "Measuring the Sixth Extinction: What Do Mollusks Tell Us." *Nautilus* 131 (1): 3–41.
- CSS, ENSSER and VDW (Critical Scientists Switzerland, European Network of Scientists for Social and Environmental Responsibility and Vereinigung Deutscher Wissenschaftler). 2019. *Gene Drives: A Report on Their Science, Applications, Social Aspects, Ethics and Regulation*.
- Cuevas, C., and A. Francesch. 2009. "Development of Yondelis® (Trabectedin, ET-743): A Semisynthetic Process Solves the Supply Problem." *Natural Product Reports* 26 (3): 322–37. <https://doi.org/10.1039/B808331M>.
- Czorlich, Y., T. Aykanat, J. Erkinaro, P. Orell and C.R. Primmer. 2018. "Rapid Sex-Specific Evolution of Age at Maturity Is Shaped by Genetic Architecture in Atlantic Salmon." *Nature Ecology & Evolution* 2 (11): 1800–07. <https://doi.org/10.1038/s41559-018-0681-5>.
- da Silva, J., and B. van Vuuren. 2019. *South African National Biodiversity Assessment 2018 Technical Report Volume 4: Marine Realm*. Pretoria, South Africa: South African National Biodiversity Institute.
- Davidson, A.D., A.G. Boyer, H. Kim, S. Pompa-Mansilla, M.J. Hamilton, D.P. Costa, G. Ceballos, et al. 2012. "Drivers and Hotspots of Extinction Risk in Marine Mammals." *Proceedings of the National Academy of Sciences* 109 (9): 3395–3400. <https://doi.org/10.1073/pnas.1121469109>.
- Dawson, T.P., S.T. Jackson, J.I. House, I.C. Prentice and G.M. Mace. 2011. "Beyond Predictions: Biodiversity Conservation in a Changing Climate." *Science* 332 (6025): 53–58. <https://doi.org/10.1126/science.1200303>.
- De Leo, G.A., and F. Micheli. 2015. "The Good, the Bad and the Ugly of Marine Reserves for Fishery Yields." *Philosophical Transactions of the Royal Society B: Biological Sciences* 370 (1681): 20140276. <https://doi.org/10.1098/rstb.2014.0276>.
- de Mitcheson, Y.S., M.T. Craig, A.A. Bertoni, K.E. Carpenter, W.W.L. Cheung, J.H. Choat, A.S. Cornish, et al. 2013. "Fishing Groupers towards Extinction: A Global Assessment of Threats and Extinction Risks in a Billion Dollar Fishery." *Fish and Fisheries* 14 (2): 119–36. <https://doi.org/10.1111/j.1467-2979.2011.00455.x>.
- Deiner, K., E.A. Fronhofer, E. Mächler, J.-C. Walser and F. Altermatt. 2016. "Environmental DNA Reveals that Rivers Are Conveyor Belts of Biodiversity Information." *Nature Communications* 7: 12544. <https://doi.org/10.1038/ncomms12544>.
- Deiner, K., H.M. Bik, E. Mächler, M. Seymour, A. Lacoursière-Roussel, F. Altermatt, S. Creer, et al. 2017. "Environmental DNA Metabarcoding: Transforming How We Survey Animal and Plant Communities." *Molecular Ecology* 26 (21): 5872–95. <https://doi.org/10.1111/mec.14350>.
- Devine, J.A., K.D. Baker and R.L. Haedrich. 2006. "Deep-Sea Fishes Qualify as Endangered." *Nature* 439 (7072): 29. <https://doi.org/10.1038/439029a>.
- Di Lorenzo, M., J. Claudet and P. Guidetti. 2016. "Spillover from Marine Protected Areas to Adjacent Fisheries Has an Ecological and a Fishery Component." *Journal for Nature Conservation* 32 (July): 62–66. <https://doi.org/10.1016/j.jnc.2016.04.004>.
- Di Muri, C., S.G. Vandamme, C. Peace, W. Barnes and S. Mariani. 2018. "Biodiversity Defrosted: Unveiling Non-compliant Fish Trade in Ethnic Food Stores." *Biological Conservation* 217 (January): 419–27. <https://doi.org/10.1016/j.biocon.2017.11.028>.
- Di Pinto, A., P. Di Pinto, V. Terio, G. Bozzo, E. Bonerba, E. Ceci and G. Tantillo. 2013. "DNA Barcoding for Detecting Market Substitution in Salted Cod Fillets and Battered Cod Chunks." *Food Chemistry* 141 (3): 1757–62. <https://doi.org/10.1016/j.foodchem.2013.05.093>.
- Djurhuus, A., K. Pitz, N.A. Sawaya, J. Rojas-Márquez, B. Michaud, E. Montes, F. Muller-Karger, et al. 2018. "Evaluation of Marine Zooplankton Community Structure through Environmental DNA Metabarcoding." *Limnology and Oceanography: Methods* 16 (4): 209–21. <https://doi.org/10.1002/lom3.10237>.
- Dlugosch, K.M., and I.M. Parker. 2008. "Founding Events in Species Invasions: Genetic Variation, Adaptive Evolution, and the Role of Multiple Introductions." *Molecular Ecology* 17: 431–49. <https://doi.org/10.1111/j.1365-294X.2007.03538.x>.
- Doney, S.C., M. Ruckelshaus, J.E. Duffy, J.P. Barry, F. Chan, C.A. English, H.M. Galindo, et al. 2012. "Climate Change Impacts on Marine Ecosystems." *Annual Review of Marine Science* 4 (1): 11–37. <https://doi.org/10.1146/annurev-marine-041911-111611>.
- Doudna, J.A., and E. Charpentier. 2014. "Genome Editing. The New Frontier of Genome Engineering with CRISPR-Cas9." *Science* 346 (6213): 1258096. <https://doi.org/10.1126/science.1258096>.
- Du Preez, C., K.D. Swan and J.M.R. Curtis. 2020. "Cold-Water Corals and Other Vulnerable Biological Structures on a North Pacific Seamount after Half a Century of Fishing." *Frontiers in Marine Science* 7: 17.
- Duarte, C.M., N. Marbá and M. Holmer. 2007. "Rapid Domestication of Marine Species." *Science* 316 (5823): 382–83. <https://doi.org/10.1126/science.1138042>.
- Dulvy, N.K., S.L. Fowler, J.A. Musick, R.D. Cavanagh, P.M. Kyne, L.R. Harrison, J.K. Carlson, et al. 2014. "Extinction Risk and Conservation of the World's Sharks and Rays." *eLife* 3 (January): e00590. <https://doi.org/10.7554/eLife.00590>.
- Dulvy, N.K., and J.D. Reynolds. 2009. "Skates on Thin Ice." *Nature* 462 (7272): 417. <https://doi.org/10.1038/462417a>.

- Duncan, M.I., A.E. Bates, N.C. James and W.M. Potts. 2019. "Exploitation May Influence the Climate Resilience of Fish Populations through Removing High Performance Metabolic Phenotypes." *Scientific Reports* 9 (1): 1–10.
- Echeverría, F., R. Valenzuela, M.C. Hernandez-Rodas and A. Valenzuela. 2017. "Docosahexaenoic Acid (DHA), a Fundamental Fatty Acid for the Brain: New Dietary Sources." *Prostaglandins, Leukotrienes and Essential Fatty Acids* 124 (September): 1–10. <https://doi.org/10.1016/j.plefa.2017.08.001>.
- El Samak, M., S.M. Solyman and A. Hanora. 2018. "Antimicrobial Activity of Bacteria Isolated from Red Sea Marine Invertebrates." *Biotechnology Reports* 19 (July): e00275. <https://doi.org/10.1016/j.btre.2018.e00275>.
- Elbe, S., and G. Buckland-Merrett. 2017. "Data, Disease and Diplomacy: GISAID's Innovative Contribution to Global Health." *Global Challenges* 1 (January): 33–46. <https://doi.org/10.1002/gch.2.1018>.
- Elkin-Koren, N., and N.W. Netanel, eds. 2002. *The Commodification of Information*. First edition. The Hague: Kluwer Law International.
- Ellegren, H., and N. Galtier. 2016. "Determinants of Genetic Diversity." *Nature Reviews Genetics* 17 (7): 422–33. <https://doi.org/10.1038/nrg.2016.58>.
- FAO (Food and Agriculture Organization of the United Nations). 2016. "Voluntary Guidelines for Mainstreaming Biodiversity into Policies, Programmes and National and Regional Plans of Action on Nutrition." Rome: Commission on Genetic Resources for Food and Agriculture. <http://www.fao.org/family-farming/detail/en/c/416118/>.
- FAO. 2018. *The State of World Fisheries and Aquaculture: Meeting the Sustainable Development Goals*. Rome: FAO.
- Fauchald, P. 2010. "Predator–Prey Reversal: A Possible Mechanism for Ecosystem Hysteresis in the North Sea?" *Ecology* 91 (8): 2191–97. <https://doi.org/10.1890/09-1500.1>.
- Fleming, I.A., K. Hindar, I.B. Mjølnerød, B. Jonsson, T. Balstad and A. Lamberg. 2000. "Lifetime Success and Interactions of Farm Salmon Invading a Native Population." *Proceedings of the Royal Society Series B: Biological Sciences* 267 (1452): 1517–23. <https://doi.org/10.1098/rspb.2000.1173>.
- Fleming, I.A., T. Agustsson, B. Finstad, J.I. Johnsson and B. Thrandur Björnsson. 2002. "Effects of Domestication on Growth Physiology and Endocrinology of Atlantic Salmon (*Salmo Salar*)." *Canadian Journal of Fisheries and Aquatic Sciences* 59 (8): 1323–30.
- Foster, C., and R. Heeks. 2013. "Conceptualising Inclusive Innovation: Modifying Systems of Innovation Frameworks to Understand Diffusion of New Technology to Low-Income Consumers." *The European Journal of Development Research* 25 (3): 333–55. <https://doi.org/10.1057/ejdr.2013.7>.
- Frankham, R. 2005. "Stress and Adaptation in Conservation Genetics." *Journal of Evolutionary Biology* 18 (4): 750–55. <https://doi.org/10.1111/j.1420-9101.2005.00885.x>.
- Fung, T., R.M. Seymour and C.R. Johnson. 2011. "Alternative Stable States and Phase Shifts in Coral Reefs under Anthropogenic Stress." *Ecology* 92 (4): 967–82. <https://doi.org/10.1890/10-0378.1>.
- Gaines, S.D., C. White, M.H. Carr and S.R. Palumbi. 2010. "Designing Marine Reserve Networks for Both Conservation and Fisheries Management." *Proceedings of the National Academy of Sciences* 107 (43): 18286–93.
- Garriy, G.M., L.M. Thompson, D.W. Ussery, N. Paskin, D. Baker, P. Desmeth, D.E. Schindel, et al. 2009. "Studies on Monitoring and Tracking Genetic Resources: An Executive Summary." *Standards in Genomic Sciences* 1 (1): 78–86. <https://doi.org/10.4056/sigs.1491>.
- Gerber, L.R., M. Del Mar Mancha-Cisneros, M.I. O'Connor and E.R. Selig. 2014. "Climate Change Impacts on Connectivity in the Ocean: Implications for Conservation." *Ecosphere* 5 (3): 1–18.
- Gerwick, W.H., and B.S. Moore. 2012. "Lessons from the Past and Charting the Future of Marine Natural Products Drug Discovery and Chemical Biology." *Chemistry & Biology* 19 (1): 85–98. <https://doi.org/10.1016/j.chembiol.2011.12.014>.
- Giakoumi, S., C. Scianna, J. Plass-Johnson, F. Micheli, K. Grorud-Colvert, P. Thiriet, J. Claudet, et al. 2017. "Ecological Effects of Full and Partial Protection in the Crowded Mediterranean Sea: A Regional Meta-Analysis." *Scientific Reports* 7 (1): 8940. <https://doi.org/10.1038/s41598-017-08850-w>.
- Giakoumi, S., J. McGowan, M. Mills, M. Beger, R.H. Bustamante, A. Charles, P. Christie, et al. 2018. "Revisiting 'Success' and 'Failure' of Marine Protected Areas: A Conservation Scientist Perspective." *Frontiers in Marine Science* 5. <https://doi.org/10.3389/fmars.2018.00223>.
- Gibson, D.G., J.I. Glass, C. Lartigue, V.N. Noskov, R.-Y. Chuang, M.A. Algire, G.A. Benders, et al. 2010. "Creation of a Bacterial Cell Controlled by a Chemically Synthesized Genome." *Science* 329 (5987): 52–56. <https://doi.org/10.1126/science.1190719>.
- Giles, P.B. 2011. "How to Claim a Gene: Application of the Patent Disclosure Requirements to Genetic Sequences." *Georgia State University Law Review* 27: 35.
- Gill, D.A., M.B. Mascia, G.N. Ahmadi, L. Glew, S.E. Lester, M. Barnes, I. Craigie, et al. 2017. "Capacity Shortfalls Hinder the Performance of Marine Protected Areas Globally." *Nature* 543 (7647): 665–69. <https://doi.org/10.1038/nature21708>.
- Giusti, A., L. Tinacci, C.G. Sotelo, M. Marchetti, A. Guidi, W. Zheng and A. Armani. 2017. "Seafood Identification in Multispecies Products: Assessment of 16SrRNA, Cytb, and COI Universal Primers' Efficiency as a Preliminary Analytical Step for Setting Up Metabarcoding Next-Generation Sequencing Techniques." *Journal of Agricultural and Food Chemistry* 65 (13): 2902–12. <https://doi.org/10.1021/acs.jafc.6b05802>.
- Glover, K.A., M.F. Solberg, P. McGinnity, K. Hindar, E. Verspoor, M.W. Coulson, M.M. Hansen, et al. 2017. "Half a Century of Genetic Interaction between Farmed and Wild Atlantic Salmon: Status of Knowledge and Unanswered Questions." *Fish and Fisheries* 18 (5): 890–927. <https://doi.org/10.1111/faf.12214>.
- Green, E.D., E.M. Rubin and M.V. Olson. 2017. "The Future of DNA Sequencing." *Nature News* 550 (7675): 179.
- Green, S.J., J.L. Akins, A. Maljković and I.M. Côté. 2012. "Invasive Lionfish Drive Atlantic Coral Reef Fish Declines." *PLOS ONE* 7 (3): e32596. <https://doi.org/10.1371/journal.pone.0032596>.
- Gregory, A.C., A.A. Zayed, N. Conceição-Neto, B. Temperton, B. Bolduc, A. Alberti, M. Ardyna, et al. 2019. "Marine DNA Viral Macro- and Microdiversity from Pole to Pole." *Cell* 177 (5): 1109–23.e14. <https://doi.org/10.1016/j.cell.2019.03.040>.
- Greiber, T. 2012. *An Explanatory Guide to the Nagoya Protocol on Access and Benefit-Sharing*. 83. Gland, Switzerland: International Union for Conservation of Nature.
- Grigg, R.W., and S.J. Dollar. 1990. "Natural and Anthropogenic Disturbance on Coral Reefs." In *Ecosystem of the World 25*, edited by Z. Dubinsky, 439–52. New York: Elsevier.
- Grorud-Colvert, K., J. Claudet, B.N. Tissot, J.E. Caselle, M.H. Carr, J.C. Day, A.M. Friedlander, et al. 2014. "Marine Protected Area Networks: Assessing Whether the Whole Is Greater than the Sum of Its Parts." *PLOS ONE* 9 (8): e102298. <https://doi.org/10.1371/journal.pone.0102298>.

- Grorud-Colvert, K., V. Constant, J. Sullivan-Stack, K. Dziedzic, S.L. Hamilton, Z. Randell, H. Fulton-Bennett, et al. 2019. "High-Profile International Commitments for Ocean Protection: Empty Promises or Meaningful Progress?" *Marine Policy* 105 (July): 52–66. <https://doi.org/10.1016/j.marpol.2019.04.003>.
- Gu, H., X. Chen, F. Chen, X. Zhou and Z. Parsaee. 2018. "Ultrasound-Assisted Biosynthesis of CuO-NPs Using Brown Alga *Cystoseira Trinodis*: Characterization, Photocatalytic AOP, DPPH Scavenging and Antibacterial Investigations." *Ultrasonics Sonochemistry* 41 (March): 109–19. <https://doi.org/10.1016/j.ultsonch.2017.09.006>.
- Guedes, A.C., H.M. Amaro, I. Sousa-Pinto and F.X. Malcata. 2019. "Algal Spent Biomass—A Pool of Applications." In *Biofuels from Algae*, edited by A. Pandey, et al., 397–433. Second edition. Elsevier.
- Gupta, A., C.J. Barrow and M. Puri. 2012. "Omega-3 Biotechnology: Thraustochytrids as a Novel Source of Omega-3 Oils." *Biotechnology Advances* 30 (6): 1733–45. <https://doi.org/10.1016/j.biotechadv.2012.02.014>.
- Hafsa, A.B., N. Nabi, M. Salem Zellama, K. Said and M. Chaouachi. 2016. "A New Specific Reference Gene Based on Growth Hormone Gene (GH1) Used for Detection and Relative Quantification of Aquadvantage® GM Salmon (*Salmo Salar L.*) in Food Products." *Food Chemistry* 190: 1040–45.
- Halpern, B.S., M. Frazier, J. Afflerbach, J.S. Lowndes, F. Micheli, C. O'Hara, C. Scarborough, et al. 2019. "Recent Pace of Change in Human Impact on the World's Ocean." *Scientific Reports* 9 (1): 1–8. <https://doi.org/10.1038/s41598-019-47201-9>.
- Halpern, B.S., S.E. Lester and J.B. Kellner. 2009. "Spillover from Marine Reserves and the Replenishment of Fished Stocks." *Environmental Conservation* 36 (4): 268–76.
- Halpern, B.S., S. Walbridge, K.A. Selkoe, C.V. Kappel, F. Micheli, C. D'Agrosa, J.F. Bruno, et al. 2008. "A Global Map of Human Impact on Marine Ecosystems." *Science* 319 (5865): 948–52. <https://doi.org/10.1126/science.1149345>. Hamilton, S. 2013. "Assessing the Role of Commercial Aquaculture in Displacing Mangrove Forest." *Bulletin of Marine Science* 89 (2): 585–601.
- Hampe, A., and R.J. Petit. 2005. "Conserving Biodiversity under Climate Change: The Rear Edge Matters." *Ecology Letters* 8 (5): 461–67. <https://doi.org/10.1111/j.1461-0248.2005.00739.x>.
- Hansen, B.K., D. Bekkevold, L. Worsøe Clausen and E.E. Nielsen. 2018. "The Sceptical Optimist: Challenges and Perspectives for the Application of Environmental DNA in Marine Fisheries." *Fish and Fisheries* 19 (5): 751–68. <https://doi.org/10.1111/faf.12286>.
- Hare, M.P., L. Nunney, M.K. Schwartz, D.E. Ruzzante, M. Burford, R.S. Waples, K. Ruegg, et al. 2011. "Understanding and Estimating Effective Population Size for Practical Application in Marine Species Management." *Conservation Biology: The Journal of the Society for Conservation Biology* 25 (3): 438–49. <https://doi.org/10.1111/j.1523-1739.2010.01637.x>.
- Hastings, A., and L.W. Botsford. 2006. "Persistence of Spatial Populations Depends on Returning Home." *Proceedings of the National Academy of Sciences* 103 (15): 6067–72.
- Hastings, A., S.D. Gaines and C. Costello. 2017. "Marine Reserves Solve an Important Bycatch Problem in Fisheries." *Proceedings of the National Academy of Sciences* 114 (34): 8927–34. <https://doi.org/10.1073/pnas.1705169114>.
- Hauser, L., G.J. Adcock, P.J. Smith, J.H. Bernal Ramírez and G.R. Carvalho. 2002. "Loss of Microsatellite Diversity and Low Effective Population Size in an Overexploited Population of New Zealand Snapper (*Pagrus Auratus*)." *Proceedings of the National Academy of Sciences* 99 (18): 11742–47. <https://doi.org/10.1073/pnas.172242899>.
- He, Y., T. Wu, H. Sun, P. Sun, B. Liu, M. Luo and F. Chen. 2019. "Comparison of Fatty Acid Composition and Positional Distribution of Microalgae Triacylglycerols for Human Milk Fat Substitutes." *Algal Research* 37 (January): 40–50. <https://doi.org/10.1016/j.algal.2018.11.004>.
- Heeks, R., M. Amalia, R. Kintu and N. Shah. 2013. "Inclusive Innovation: Definition, Conceptualisation and Future Research Priorities." Working Paper No. 53. Manchester, England: Centre for Development Informatics.
- Heidelberg, K.B., J.A. Gilbert and I. Joint. 2010. "Minireview Marine Genomics: At the Interface of Marine Microbial Ecology and Biodiscovery." *Microbial Biotechnology* 3 (5): 531–43. <https://doi.org/10.1111/j.1751-7915.2010.00193.x>.
- Hellberg, M.E. 2009. "Gene Flow and Isolation among Populations of Marine Animals." *Annual Review of Ecology, Evolution, and Systematics* 40: 291–310.
- Hendriks, I.E., and C.M. Duarte. 2008. "Allocation of Effort and Imbalances in Biodiversity Research." *Journal of Experimental Marine Biology and Ecology* 360 (1): 15–20. <https://doi.org/10.1016/j.jembe.2008.03.004>.
- Henriques, R., E.S. Nielsen, D. Durholtz, D. Japp and S. von der Heyden. 2017. "Genetic Population Sub-structuring of Kingklip (*Genypterus Capensis*—Ophidiidae), a Commercially Exploited Demersal Fish off South Africa." *Fisheries Research* 187: 86–95.
- Herrera, H., and E. Schroth. 2000. "Profitable Innovation without Patent Protection: The Case of Credit Derivatives." Working Paper 01–02. Berkeley Center for Entrepreneurial Studies.
- High Seas Alliance. 2019. *Strategic Environmental Assessments (SEAs) under the New BBNJ Instrument*. HSA Briefing. <http://highseasalliance.org/sites/highseasalliance.org/files/SEA%20brief%20final2.clean.pdf>.
- Hilborn, R., T.P. Quinn, D.E. Schindler and D.E. Rogers. 2003. "Biocomplexity and Fisheries Sustainability." *Proceedings of the National Academy of Sciences* 100 (11): 6564–68. <https://doi.org/10.1073/pnas.1037274100>.
- Hill, R.T., and W. Fenical. 2010. "Pharmaceuticals from Marine Natural Products: Surge or Ebb?" *Current Opinion in Biotechnology* 21 (6): 777–79. <https://doi.org/10.1016/j.copbio.2010.10.007>.
- Hoffmann, A.A., and C.M. Sgrò. 2011. "Climate Change and Evolutionary Adaptation." *Nature* 470 (7335): 479–85. <https://doi.org/10.1038/nature09670>.
- Houssen, W.E., A.F. Bent, A.R. McEwan, N. Pieiller, J. Tabudravu, J. Koehnke, G. Mann, et al. 2014. "An Efficient Method for the In Vitro Production of Azol(in)e-Based Cyclic Peptides." *Angewandte Chemie International Edition* 53 (51): 14171–74. <https://doi.org/10.1002/anie.201408082>.
- Hughes, T.P., J.T. Kerry, A.H. Baird, S.R. Connolly, A. Dietzel, C.M. Eakin, S.F. Heron, et al. 2018. "Global Warming Transforms Coral Reef Assemblages." *Nature* 556 (7702): 492. <https://doi.org/10.1038/s41586-018-0041-2>.
- Hurwitz, B.L., and M.B. Sullivan. 2013. "The Pacific Ocean Virome (POV): A Marine Viral Metagenomic Dataset and Associated Protein Clusters for Quantitative Viral Ecology." *PLOS ONE* 8 (2): e57355. <https://doi.org/10.1371/journal.pone.0057355>.
- Hutchings, J.A., and D.J. Fraser. 2008. "The Nature of Fisheries- and Farming-Induced Evolution." *Molecular Ecology* 17 (1): 294–313. <https://doi.org/10.1111/j.1365-294X.2007.03485.x>.
- Hutchings, J.A., and J.D. Reynolds. 2004. "Marine Fish Population Collapses: Consequences for Recovery and Extinction Risk." *BioScience* 54 (4): 297–309. [https://doi.org/10.1641/0006-3568\(2004\)054\[0297:MFFC CF\]2.0.CO;2](https://doi.org/10.1641/0006-3568(2004)054[0297:MFFC CF]2.0.CO;2).

- Hutchison, C.A., R.-Y. Chuang, V.N. Noskov, N. Assad-Garcia, T.J. Deerinck, M.H. Ellisman, J. Gill, et al. 2016. "Design and Synthesis of a Minimal Bacterial Genome." *Science* 351 (6280). <https://doi.org/10.1126/science.aad6253>.
- Ingeman, K.E., J.F. Samhoury and A.C. Stier. 2019. "Ocean Recoveries for Tomorrow's Earth: Hitting a Moving Target." *Science* 363 (6425): eaav1004. <https://doi.org/10.1126/science.aav1004>.
- IPBES (Intergovernmental Science-Policy Platform on Biodiversity and Ecosystem Services). 2019. *Summary for Policymakers of the Global Assessment Report on Biodiversity and Ecosystem Services – Unedited Advance Version*. Bonn, Germany: IPBES.
- IUCN (International Union for Conservation of Nature). 2019. *The IUCN Red List of Threatened Species*. Gland, Switzerland: IUCN.
- IUCN and WCPA (International Union for Conservation of Nature and World Commission on Protected Areas). 2018. "Applying IUCN's Global Conservation Standards to Marine Protected Areas (MPAs). Delivering Effective Conservation Action through MPAs, to Secure Ocean Health & Sustainable Development. Version 1.0." Gland, Switzerland: IUCN and WCPA.
- Jasanoff, S., J.B. Hurlbut and K. Saha. 2015. "CRISPR Democracy: Gene Editing and the Need for Inclusive Deliberation." *Issues in Science and Technology* 32 (1). <https://issues.org/crispr-democracy-gene-editing-and-the-need-for-inclusive-deliberation/>.
- Jaume, D., and C.M. Duarte. 2006. "General Aspects Concerning Marine and Terrestrial Biodiversity." In *The Exploration of Marine Biodiversity—Scientific and Technological Challenges*, edited by C.M. Duarte, 17–30. Bilbao, Spain: Fundación BBVA. http://imedea.uib-csic.es/damiajaume/DamiaJaumewebpage_archivos/PDFs/BBVA-ingles.pdf.
- Jeunen, G.-J., M. Knapp, H.G. Spencer, M.D. Lamare, H.R. Taylor, M. Stat, M. Bunce, et al. 2019. "Environmental DNA (eDNA) Metabarcoding Reveals Strong Discrimination among Diverse Marine Habitats Connected by Water Movement." *Molecular Ecology Resources* 19 (2): 426–38. <https://doi.org/10.1111/1755-0998.12982>.
- Jin, P., and S. Agustí. 2018. "Fast Adaptation of Tropical Diatoms to Increased Warming with Trade-Offs." *Scientific Reports* 8 (1): 17771. <https://doi.org/10.1038/s41598-018-36091-y>.
- Jinek, M., K. Chylinski, I. Fonfara, M. Hauer, J.A. Doudna and E. Charpentier. 2012. "A Programmable Dual-RNA-Guided DNA Endonuclease in Adaptive Bacterial Immunity." *Science* 337 (6096): 816–21. <https://doi.org/10.1126/science.1225829>.
- Johannes, R.E. 1975. "Pollution and Degradation of Coral Reef Communities." In *Tropical Marine Pollution*, edited by E.J. Ferguson Wood and R.E. Johannes, 13–50. Amsterdam: Elsevier.
- Johnson, B.M., B.M. Kemp and G.H. Thorgaard. 2018. "Increased Mitochondrial DNA Diversity in Ancient Columbia River Basin Chinook Salmon *Oncorhynchus Tshawytscha*." *PLOS ONE* 13 (1): e0190059. <https://doi.org/10.1371/journal.pone.0190059>.
- Johnson, J.A., R. Altwegg, D.M. Evans, J.G. Ewen, I.J. Gordon, N. Pettorelli and J.K. Young. 2016. "Is There a Future for Genome-Editing Technologies in Conservation?" *Animal Conservation* 19: 97–101. <https://doi.org/10.1111/acv.12273>.
- Jonsson, P.R., M.N. Jacobi and P.-O. Moksnes. 2016. "How to Select Networks of Marine Protected Areas for Multiple Species with Different Dispersal Strategies." *Diversity and Distributions* 22 (2): 161–73.
- Jouffray, J.-B., R. Blasiak, A.V. Norström, H. Österblom and M. Nyström. 2020. "The Blue Acceleration – The Trajectory of Human Expansion into the Ocean." *One Earth*. <https://doi.org/10.1016/j.oneear.2019.12.016>.
- Karlsson, S., O.H. Diserud, P. Fiske and K. Hindar. 2016. "Widespread Genetic Introgression of Escaped Farmed Atlantic Salmon in Wild Salmon Populations." *ICES Journal of Marine Science* 73 (10): 2488–98. <https://doi.org/10.1093/icesjms/fsw121>.
- Kitada, M., E. Williams and L.L. Froholdt, eds. 2015. *Maritime Women: Global Leadership*. Berlin: Springer.
- Kraus, S.D., M.W. Brown, H. Caswell, C.W. Clark, M. Fujiwara, P.K. Hamilton, R.D. Kenney, et al. 2005. "North Atlantic Right Whales in Crisis." *Science* 309 (5734): 561–62. <https://doi.org/10.1126/science.1111200>.
- Kyeremeh, K., A. Flint, M. Jaspars, S.N. Sunassee, R. Amewu, G.A. Dziwornu, K.S. Acquah, et al. 2020. "Making North–South Collaborations Work: Facilitating Natural Product Drug Discovery in Africa." In *Africa and the Sustainable Development Goals*, edited by M. Ramutinsindela and D. Mickler, 257–66. Sustainable Development Goals Series. Cham, Switzerland: Springer International Publishing. https://doi.org/10.1007/978-3-030-14857-7_24.
- Laikre, L. 2010. "Genetic Diversity Is Overlooked in International Conservation Policy Implementation." *Conservation Genetics* 11 (2): 349–54.
- Laikre, L., and N. Ryman. 1996. "Effects on Intraspecific Biodiversity from Harvesting and Enhancing Natural Populations." *Ambio* 25 (8): 504–9.
- Laird, S., and R. Wynberg. 2012. *Bioscience at a Crossroads: Implementing the Nagoya Protocol on Access and Benefit Sharing in a Time of Scientific, Technological and Industry Change*. Montreal: Secretariat of the Convention on Biological Diversity.
- Laird, S., and R. Wynberg. 2018. *A Fact-Finding and Scoping Study on Digital Sequence Information on Genetic Resources in the Context of the Convention on Biological Diversity and the Nagoya Protocol*, 2–79. Montreal: Secretariat of the Convention on Biological Diversity.
- Laird, S., C. Monagle, S. Johnston and Queensland Biodiscovery Collaboration. 2008. *The Griffith University AstraZeneca Partnership for Natural Product Discovery. An Access and Benefit Sharing Case Study*. Tokyo: United Nations University, Institute for the Advanced Study of Sustainability.
- Laird, S., R. Wynberg, M. Rourke, F. Humphries, M.R. Muller and C. Lawson. 2020. "Rethink the expansion of access and benefit sharing." *Science*, 367(6483), pp.1200-1202.
- Lasker, H.R. 2013. "Recruitment and Resilience of a Harvested Caribbean Octocoral." *PLOS ONE* 8 (9): e74587. <https://doi.org/10.1371/journal.pone.0074587>.
- Lautenschlager, R.A. 1997. "Biodiversity Is Dead." *Wildlife Society Bulletin (1973-2006)* 25 (3): 679–685.
- Law, R. 2007. "Fisheries-Induced Evolution: Present Status and Future Directions." *Marine Ecology Progress Series* 335: 271–78.
- Leal, M.C., J. Puga, J. Serôdio, N.C.M. Gomes and R. Calado. 2012. "Trends in the Discovery of New Marine Natural Products from Invertebrates over the Last Two Decades – Where and What Are We Bioprospecting?" *PLOS ONE* 7 (1): e30580. <https://doi.org/10.1371/journal.pone.0030580>.
- Leary, D. 2018. "Marine Genetic Resources in Areas beyond National Jurisdiction: Do We Need to Regulate Them in a New Agreement?" *Maritime Safety and Security Law Journal* 19.
- Leary, D., M. Vierros, G. Hamon, S. Arico and C. Monagle. 2009. "Marine Genetic Resources: A Review of Scientific and Commercial Interest." *Marine Policy* 33 (2): 183–94. <https://doi.org/10.1016/j.marpol.2008.05.010>.

- Ledford, H. 2015. "Salmon Approval Heralds Rethink of Transgenic Animals." *Nature News* 527 (7579): 417.
- Lester, S.E., B.S. Halpern, K. Grorud-Colvert, J. Lubchenco, B.I. Ruttenberg, S.D. Gaines, S. Airame, et al. 2009. "Biological Effects within No-Take Marine Reserves: A Global Synthesis." *Marine Ecology Progress Series* 384 (May): 33–46.
- Levin, P.S., and M.H. Schiewe. 2001. "Preserving Salmon Biodiversity: The Number of Pacific Salmon Has Declined Dramatically. But the Loss of Genetic Diversity May Be a Bigger Problem." *American Scientist* 89 (3): 220–27.
- Li, L., T.J. Pitcher and R.H. Devlin. 2015. "Potential Risks of Trophic Impacts by Escaped Transgenic Salmon in Marine Environments." *Environmental Conservation* 42 (2): 152–61. <https://doi.org/10.1017/S0376892914000319>.
- Lindeque, P.K., H.E. Parry, R.A. Harmer, P.J. Somerfield and A. Atkinson. 2013. "Next Generation Sequencing Reveals the Hidden Diversity of Zooplankton Assemblages." *PLOS ONE* 8 (11): 1–14. <https://doi.org/10.1371/journal.pone.0081327>.
- Locey, K.J., and J.T. Lennon. 2016. "Scaling Laws Predict Global Microbial Diversity." *Proceedings of the National Academy of Sciences* 113 (21): 5970–75.
- Logan, C.A., J.P. Dunne, C.M. Eakin and S.D. Donner. 2014. "Incorporating Adaptive Responses into Future Projections of Coral Bleaching." *Global Change Biology* 20 (1): 125–39. <https://doi.org/10.1111/gcb.12390>.
- Louca, S., F. Mazel, M. Doebeli and L. Parfrey. 2019. "A Census-Based Estimate of Earth's Bacterial and Archaeal Diversity." *PLOS Biology* 17.
- Lubchenco, J., and K. Grorud-Colvert. 2015. "Making Waves: The Science and Politics of Ocean Protection." *Science* 350 (6259): 382–83. <https://doi.org/10.1126/science.aad5443>.
- Lubchenco, J., and S.D. Gaines. 2019. "A New Narrative for the Ocean." *Science* 364 (6444): 911. <https://doi.org/10.1126/science.aay2241>.
- Lubchenco, J., E.B. Cerny-Chipman, J.N. Reimer and S.A. Levin. 2016. "The Right Incentives Enable Ocean Sustainability Successes and Provide Hope for the Future." *Proceedings of the National Academy of Sciences of the United States of America* 113 (51): 14507–14. <https://doi.org/10.1073/pnas.1604982113>.
- Madduppa, H.H., J. Timm and M. Kochzius. 2018. "Reduced Genetic Diversity in the Clown Anemonefish *Amphiprion Ocellaris* in Exploited Reefs of Spermonde Archipelago, Indonesia." *Frontiers in Marine Science* 5. <https://doi.org/10.3389/fmars.2018.00080>.
- Magris, R.A., M. Andrello, R.L. Pressey, D. Mouillot, A. Dalongeville, M.N. Jacobi and S. Manel. 2018. "Biologically Representative and Well-Connected Marine Reserves Enhance Biodiversity Persistence in Conservation Planning." *Conservation Letters* 11 (4): e12439. <https://doi.org/10.1111/conl.12439>.
- Mannon, M. 1998. "Nutraceutical Revolution Continues at Foundation for Innovation in Medicine Conference." *American Journal of Natural Medicine* 5: 30–3.
- Manson, J.E., N.R. Cook, I.-M. Lee, W. Christen, S.S. Bassuk, S. Mora, H. Gibson, et al. 2019. "Marine N-3 Fatty Acids and Prevention of Cardiovascular Disease and Cancer." *New England Journal of Medicine* 380 (1): 23–32. <https://doi.org/10.1056/NEJMoa1811403>.
- Manuel, J., K. Maze, M. Driver, A. Stephens, E. Botts, A. Parker, M. Tau, et al. 2016. "Key Ingredients, Challenges and Lessons from Biodiversity Mainstreaming in South Africa: People, Products, Processes." Environment Working Paper No. 107. Paris: Organisation for Economic Co-operation and Development, May. <https://doi.org/10.1787/5jlzgj1s4h5h-en>.
- Marine Conservation Institute. 2020. "Atlas of Marine Protection." <http://mpatlas.org>.
- MarinLit. 2020. "A Database of Marine Natural Products Literature." <http://pubs.rsc.org/marinlit/>.
- Marteinsson, V.T., J.L. Birrien, G. Raguénès, M.S. da Costa and D. Prieur. 1999. "Isolation and Characterization of *Thermus Thermophilus* Gy1211 from a Deep-Sea Hydrothermal Vent." *Extremophiles: Life under Extreme Conditions* 3 (4): 247–51.
- Mayer, A.M.S., A.D. Rodríguez, O. Tagliatalata-Scafati and N. Fusetani. 2017. "Marine Pharmacology in 2012–2013: Marine Compounds with Antibacterial, Antidiabetic, Antifungal, Anti-Inflammatory, Antiprotazoal, Antituberculosis, and Antiviral Activities; Affecting the Immune and Nervous Systems, and Other Miscellaneous Mechanisms of Action." *Marine Drugs* 15 (9). <https://doi.org/10.3390/md15090273>.
- Mayol, E., J.M. Arrieta, M.A. Jiménez, A. Martínez-Asensio, N. Garcías-Bonet, J. Dachs, B. González-Gaya, et al. 2017. "Long-Range Transport of Airborne Microbes over the Global Tropical and Subtropical Ocean." *Nature Communications* 8 (1): 1–9. <https://doi.org/10.1038/s41467-017-00110-9>.
- McCauley, D.J., M.L. Pinsky, S.R. Palumbi, J.A. Estes, F.H. Joyce and R.R. Warner. 2015. "Marine Defaunation: Animal Loss in the Global Ocean." *Science* 347 (6219): 1255641. <https://doi.org/10.1126/science.1255641>.
- McCook, L.J., G.R. Almany, M.L. Berumen, J.C. Day, A.L. Green, G.P. Jones, J.M. Leis, et al. 2009. "Management under Uncertainty: Guide-Lines for Incorporating Connectivity into the Protection of Coral Reefs." *Coral Reefs* 28 (2): 353–66.
- McCormack, J.E., F. Rodríguez-Gómez, W.L.E. Tsai and B.C. Faircloth. 2017. "Transforming Museum Specimens into Genomic Resources 1." In *The Extended Specimen: Emerging Frontiers in Collections-Based Ornithological Research*, edited by M.S. Webster, 143–156. Boca Raton, Florida: CRC Press.
- McGinnity, P., E. Jennings, E. deEyto, N. Allott, P. Samuelsson, G. Rogan, K. Whelan, et al. 2009. "Impact of Naturally Spawning Captive-Bred Atlantic Salmon on Wild Populations: Depressed Recruitment and Increased Risk of Climate-Mediated Extinction." *Proceedings of the Royal Society B: Biological Sciences* 276 (1673): 3601–10. <https://doi.org/10.1098/rspb.2009.0799>.
- McGinnity, P., P. Prodöhl, A. Ferguson, R. Hynes, N.Ó. Maoiléidigh, N. Baker, D. Cotter, et al. 2003. "Fitness Reduction and Potential Extinction of Wild Populations of Atlantic Salmon, *Salmo Salar*, as a Result of Interactions with Escaped Farm Salmon." *Proceedings of the Royal Society Series B: Biological Sciences* 270 (1532): 2443–50. <https://doi.org/10.1098/rspb.2003.2520>.
- McInerney, C.E., A.L. Allcock, M.P. Johnson and P.A. Prodöhl. 2012. "Ecological Coherence in Marine Reserve Network Design: An Empirical Evaluation of Sequential Site Selection Using Genetic Structure." *Biological Conservation* 152 (August): 262–70. <https://doi.org/10.1016/j.biocon.2012.03.009>.
- McNaughton, S.J. 1977. "Diversity and Stability of Ecological Communities: A Comment on the Role of Empiricism in Ecology." *The American Naturalist* 111 (979): 515–25. <https://doi.org/10.1086/283181>.
- Medema, M.H., K. Blin, P. Cimermancic, V. de Jager, P. Zakrzewski, M.A. Fischbach, T. Weber, et al. 2011. "antiSMASH: Rapid Identification, Annotation and Analysis of Secondary Metabolite Biosynthesis Gene Clusters in Bacterial and Fungal Genome Sequences." *Nucleic Acids Research* 39 (suppl 2): W339–46.

- Merges, R.P. 2004. "A New Dynamism in the Public Domain." *The University of Chicago Law Review* 71: 183–203.
- Moberg, F., and C. Folke. 1999. "Ecological Goods and Services of Coral Reef Ecosystems." *Ecological Economics* 29 (2): 215–33. [https://doi.org/10.1016/S0921-8009\(99\)00009-9](https://doi.org/10.1016/S0921-8009(99)00009-9).
- Mora, C., D.P. Tittensor, S. Adl, A.G.B. Simpson and B. Worm. 2011. "How Many Species Are There on Earth and in the Ocean?" *PLOS Biology* 9 (8): e1001127. <https://doi.org/10.1371/journal.pbio.1001127>.
- Morgera, E. 2018. "Fair and Equitable Benefit-Sharing in a New Treaty on Marine Biodiversity: A Principled Approach towards Partnership Building?" Forthcoming in *Maritime Safety and Security Law Journal*. BENELEX Working Paper No. 16.
- Morikawa, M.K., and S.R. Palumbi. 2019. "Using Naturally Occurring Climate Resilient Corals to Construct Bleaching-Resistant Nurseries." *Proceedings of the National Academy of Sciences* 116 (21): 10586–91.
- Morley, J.W., R.L. Selden, R.J. Latour, T.L. Frölicher, R.J. Seagraves and M.L. Pinsky. 2018. "Projecting Shifts in Thermal Habitat for 686 Species on the North American Continental Shelf." *PLOS ONE* 13 (5): e0196127. <https://doi.org/10.1371/journal.pone.0196127>.
- Mühlroth, A., K. Li, G. Røkke, P. Winge, Y. Olsen, M.F. Hohmann-Marriott, O. Vadstein, et al. 2013. "Pathways of Lipid Metabolism in Marine Algae, Co-Expression Network, Bottlenecks and Candidate Genes for Enhanced Production of EPA and DHA in Species of Chromista." *Marine Drugs* 11 (11): 4662–97. <https://doi.org/10.3390/md11114662>.
- Muir, P., S. Li, S. Lou, D. Wang, D.J. Spakowicz, L. Salichos, J. Zhang, et al. 2016. "The Real Cost of Sequencing: Scaling Computation to Keep Pace with Data Generation." *Genome Biology* 17 (1): 53. <https://doi.org/10.1186/s13059-016-0917-0>.
- Munday, P.L., R.R. Warner, K. Monro, J.M. Pandolfi and D.J. Marshall. 2013. "Predicting Evolutionary Responses to Climate Change in the Sea." *Ecology Letters* 16 (12): 1488–1500. <https://doi.org/10.1111/ele.12185>.
- Musick, J.A., M.M. Harbin, S.A. Berkeley, G.H. Burgess, A.M. Eklund, L. Findley, R.G. Gilmore, et al. 2000. "Marine, Estuarine, and Diadromous Fish Stocks at Risk of Extinction in North America (Exclusive of Pacific Salmonids)." *Fisheries* 25 (11): 6–30. [https://doi.org/10.1577/1548-8446\(2000\)025<0006:MEADFS>2.0.CO;2](https://doi.org/10.1577/1548-8446(2000)025<0006:MEADFS>2.0.CO;2).
- National Academies of Sciences, Engineering, and Medicine. 2019. *A Research Review of Interventions to Increase the Persistence and Resilience of Coral Reefs*. Washington, DC: The National Academies Press. <https://doi.org/10.17226/25279>.
- Naylor, R., K. Hindar, I.A. Fleming, R. Goldberg, S. Williams, J. Volpe, F. Whoriskey, et al. 2005. "Fugitive Salmon: Assessing the Risks of Escaped Fish from Net-Pen Aquaculture." *BioScience* 55 (5): 427–37. [https://doi.org/10.1641/0006-3568\(2005\)055\[0427:FSATRO\]2.0.CO;2](https://doi.org/10.1641/0006-3568(2005)055[0427:FSATRO]2.0.CO;2).
- Nielsen, J., R.B. Hedeholm, J. Heinemeier, P.G. Bushnell, J.S. Christiansen, J. Olsen, C.B. Ramsey, et al. 2016. "Eye Lens Radiocarbon Reveals Centuries of Longevity in the Greenland Shark (*Somniosus Microcephalus*)." *Science* 353 (6300): 702–4. <https://doi.org/10.1126/science.aaf1703>.
- Norström, A.V., M. Nyström, J.-B. Jouffray, C. Folke, N.A.J. Graham, F. Moberg, P. Olsson, et al. 2016. "Guiding Coral Reef Futures in the Anthropocene." *Frontiers in Ecology and the Environment* 14 (9): 490–98. <https://doi.org/10.1002/fee.1427>.
- Oguz, T., and V. Velikova. 2010. "Abrupt Transition of the Northwestern Black Sea Shelf Ecosystem from a Eutrophic to an Alternative Pristine State." *Marine Ecology Progress Series* 405 (April): 231–42. <https://doi.org/10.3354/meps08538>.
- Oldham, P., S. Hall and O. Forero. 2013. "Biological Diversity in the Patent System." *PLOS ONE* 8 (11): e78737. <https://doi.org/10.1371/journal.pone.0078737>.
- Oldham, P., S. Hall, C. Barnes, C. Oldham, M. Cutter, N. Burns and L. Kindness. 2014. *Valuing the Deep: Marine Genetic Resources in Areas Beyond National Jurisdiction*. London, UK: Department for Environment, Food and Rural Affairs. http://randd.defra.gov.uk/Document.aspx?Document=12289_ValuingTheDeepDEFRAFinalVersionOne28092014.pdf
- O'Leary, B.C., M. Winther-Janson, J.M. Bainbridge, J. Aitken, J.P. Hawkins and C.M. Roberts. 2016. "Effective Coverage Targets for Ocean Protection." *Conservation Letters* 9 (6): 398–404.
- Ooho Water. n.d. "Home." <http://www.oohowater.com>.
- Oregon State University, World Database on Protected Areas, IUCN-Marine, National Geographic Pristine Seas, and Marine Conservation Institute's MPAtlas. 2019. "The MPA Guide." Wcmc.io/8408.
- Österblom, H., C.C.C. Wabnitz, D. Tladi, et al. 2020. *Towards Ocean Equity*. Washington, DC: World Resources Institute. www.oceanpanel.org/blue-papers/how-distribute-benefits-ocean-equitably.
- Oyinlola, M.A., G. Reygondeau, C.C.C. Wabnitz, M. Troell and W.W.L. Cheung. 2018. "Global Estimation of Areas with Suitable Environmental Conditions for Mariculture Species." *PLOS ONE* 13 (1): e0191086. <https://doi.org/10.1371/journal.pone.0191086>.
- Paddon, C.J., and J.D. Keasling. 2014. "Semi-Synthetic Artemisinin: A Model for the Use of Synthetic Biology in Pharmaceutical Development." *Nature Reviews Microbiology* 12 (5): 355–67. <https://doi.org/10.1038/nrmicro3240>.
- Pal, A., and A.K. Paul. 2008. "Microbial Extracellular Polymeric Substances: Central Elements in Heavy Metal Bioremediation." *Indian Journal of Microbiology* 48 (1): 49–64. <https://doi.org/10.1007/s12088-008-0006-5>.
- Palkovacs, E.P., B.A. Wasserman and M.T. Kinnison. 2011. "Eco-Evolutionary Trophic Dynamics: Loss of Top Predators Drives Trophic Evolution and Ecology of Prey." *PLOS ONE* 6 (4): e18879. <https://doi.org/10.1371/journal.pone.0018879>.
- Palstra, F.P., and D.E. Ruzzante. 2008. "Genetic Estimates of Contemporary Effective Population Size: What Can They Tell Us about the Importance of Genetic Stochasticity for Wild Population Persistence?" *Molecular Ecology* 17 (15): 3428–47. <https://doi.org/10.1111/j.1365-294x.2008.03842.x>.
- Palumbi, S.R. 2014. "Mechanisms of Reef Coral Resistance to Future Climate Change." *Science* 344 (6186): 895–98. <https://doi.org/10.1126/science.1251336>.
- Parsons, K.M., E. Meredith, D. Marilyn and P. Linda. 2019. "Water, Water Everywhere: Environmental DNA Can Unlock Population Structure in Elusive Marine Species." *Royal Society Open Science* 5 (8): 180537. <https://doi.org/10.1098/rsos.180537>.
- Pazos, G., J. Fernández, F. Linares, J. Sánchez, J.J. Otero, J. Iglesias and P. Domingues. 2018. "The Complete Life Cycle in Captivity of the Spider Crab, *Maja Brachydactyla*, Herbst 1788." *Aquaculture Research* 49 (7): 2440–45. <https://doi.org/10.1111/are.13703>.
- Pearce, B.K.D., A.S. Tupper, R.E. Pudritz and P.G. Higgs. 2018. "Constraining the Time Interval for the Origin of Life on Earth." *Astrobiology* 18 (3): 343–64. <https://doi.org/10.1089/ast.2017.1674>.
- Pecl, G.T., M.B. Araújo, J.D. Bell, J. Blanchard, T.C. Bonebrake, I.-C. Chen, T.D. Clark, et al. 2017. "Biodiversity Redistribution under Climate Change: Impacts on Ecosystems and Human Well-Being." *Science* 355 (6332): eaai9214. <https://doi.org/10.1126/science.aai9214>.

- Pedersen, E.J., P.L. Thompson, R.A. Ball, M.-J. Fortin, T.C. Gouhier, H. Link, C. Moritz, et al. 2017. "Signatures of the Collapse and Incipient Recovery of an Overexploited Marine Ecosystem." *Royal Society Open Science* 4 (7). <https://doi.org/10.1098/rsos.170215>.
- Perry, A.L., P.J. Low, J.R. Ellis and J.D. Reynolds. 2005. "Climate Change and Distribution Shifts in Marine Fishes." *Science* 308 (5730): 1912–15. <https://doi.org/10.1126/science.1111322>.
- Pevsner, J. 2015. *Bioinformatics and Functional Genomics*. Oxford: John Wiley & Sons.
- Phelps, M.P., L.W. Seeb and J.E. Seeb. 2019. "Transforming Ecology and Conservation Biology through Genome Editing." *Conservation Biology* 34 (1). <https://doi.org/10.1111/cobi.13292>.
- Piaggio, A.J., G. Segelbacher, P.J. Seddon, L. Alphey, E.L. Bennett, R.H. Carlson, R.M. Friedman, et al. 2017. "Is It Time for Synthetic Biodiversity Conservation?" *Trends in Ecology & Evolution* 32 (2): 97–107. <https://doi.org/10.1016/j.tree.2016.10.016>.
- Pikitch, E.K. 2018. "A Tool for Finding Rare Marine Species: Environmental DNA Analysis Shows Promise for Studying Rare and Elusive Marine Species." *Science* 360 (6394): 1180–82.
- Pinsky, M.L., A.M. Eikeset, D.J. McCauley, J.L. Payne and J.M. Sunday. 2019. "Greater Vulnerability to Warming of Marine versus Terrestrial Ectotherms." *Nature* 569 (7754): 108.
- Pinsky, M.L., and S.R. Palumbi. 2014. "Meta-Analysis Reveals Lower Genetic Diversity in Overfished Populations." *Molecular Ecology* 23 (1): 29–39. <https://doi.org/10.1111/mec.12509>.
- Pinsky, M.L., B. Worm, M.J. Fogarty, J.L. Sarmiento and S.A. Levin. 2013. "Marine Taxa Track Local Climate Velocities." *Science* 341 (6151): 1239–42. <https://doi.org/10.1126/science.1239352>.
- PISCO and UNS (Partnership for Interdisciplinary Studies of Coastal Oceans and University of Nice Sophia Antipolis). 2016. "The Science of Marine Reserves." Third edition. Mediterranean Version.
- Pitcher, G.C., and T.A. Probyn. 2016. "Suffocating Phytoplankton, Suffocating Waters—Red Tides and Anoxia." *Frontiers in Marine Science* 3. <https://doi.org/10.3389/fmars.2016.00186>.
- Pitz, K.J., C.J. Closek, A. Djurhuus, R.P. Michisaki, K. Walz, A.B. Boehm, M. Breitbart, et al. 2017. "Rewards and Challenges of eDNA Sequencing with Multiple Genetic Markers for Marine Observation Programs." *Biodiversity Information Science and Standards* 1 (August): e20548–e20548.
- Poloczanska, E.S., M.T. Burrows, C.J. Brown, J. García Molinos, B.S. Halpern, O. Hoegh-Guldberg, C.V. Kappel, et al. 2016. "Responses of Marine Organisms to Climate Change across Oceans." *Frontiers in Marine Science* 3. <https://doi.org/10.3389/fmars.2016.00062>.
- Pörtner, H.O., and M.A. Peck. 2010. "Climate Change Effects on Fishes and Fisheries: Towards a Cause-and-Effect Understanding." *Journal of Fish Biology* 77 (8): 1745–79. <https://doi.org/10.1111/j.1095-8649.2010.02783.x>.
- Pratchett, M.S., C.A. Thompson, A.S. Hoey, P.F. Cowman and S.K. Wilson. 2018. "Effects of Coral Bleaching and Coral Loss on the Structure and Function of Reef Fish Assemblages." In *Coral Bleaching: Patterns, Processes, Causes and Consequences*, edited by M.J.H. van Oppen and J.M. Lough, 265–93. Cham, Switzerland: Springer. https://doi.org/10.1007/978-3-319-75393-5_11.
- Prathapan, K.D., R. Pethiyagoda, K.S. Bawa, P.H. Raven and P.D. Rajan. 2018. "When the Cure Kills—CBD Limits Biodiversity Research." *Science* 360 (6396): 1405–06.
- Protected Planet. 2020. "Explore the World's Marine Protected Areas." <https://www.protectedplanet.net/marine>.
- Prouty, N.G., E.B. Roark, N.A. Buster and S.W. Ross. 2011. "Growth Rate and Age Distribution of Deep-Sea Black Corals in the Gulf of Mexico." *Marine Ecology Progress Series* 423: 101115. <https://doi.org/10.3354/meps08953>.
- Provan, J., and C.A. Maggs. 2012. "Unique Genetic Variation at a Species' Rear Edge Is under Threat from Global Climate Change." *Proceedings. Biological Sciences* 279 (1726): 39–47. <https://doi.org/10.1098/rspb.2011.0536>.
- Pujolar, J.M., M. Schiavina, A. Di Franco, P. Melià, P. Guidetti, M. Gatto, G.A. De Leo, et al. 2013. "Understanding the Effectiveness of Marine Protected Areas Using Genetic Connectivity Patterns and Lagrangian Simulations." *Diversity and Distributions* 19 (12): 1531–42.
- Qi, S.-H., and X. Ma. 2017. "Antifouling Compounds from Marine Invertebrates." *Marine Drugs* 15 (9). <https://doi.org/10.3390/md15090263>.
- Quah, D. 2002. "Technology Dissemination and Economic Growth: Some Lessons for the New Economy." *Technology and the New Economy* 3: 95–156.
- Quince, C., A.W. Walker, J.T. Simpson, N.J. Loman and N. Segata. 2017. "Shotgun Metagenomics, from Sampling to Analysis." *Nature Biotechnology* 35 (9): 833–44. <https://doi.org/10.1038/nbt.3935>.
- Rabone, M., H. Harden-Davies, J.E. Collins, S. Zajderman, W. Appeltans, G. Droege, A. Brandt, et al. 2019. "Access to Marine Genetic Resources (MGR): Raising Awareness of Best-Practice Through a New Agreement for Biodiversity beyond National Jurisdiction (BBNJ)." *Frontiers in Marine Science* 6. <https://doi.org/10.3389/fmars.2019.00520>.
- Ramesh, N., J.A. Rising and K.L. Oremus. 2019. "The Small World of Global Marine Fisheries: The Cross-Boundary Consequences of Larval Dispersal." *Science* 364 (6446): 1192–96. <https://doi.org/10.1126/science.aav3409>.
- Ramos, J.E., G.T. Pecl, N.A. Moltschanivskyj, J.M. Semmens, C.A. Souza and J.M. Strugnell. 2018. "Population Genetic Signatures of a Climate Change Driven Marine Range Extension." *Scientific Reports* 8 (1): 1–12. <https://doi.org/10.1038/s41598-018-27351-y>.
- Reed, D.H., and R. Frankham. 2003. "Correlation between Fitness and Genetic Diversity." *Conservation Biology* 17 (1): 230–37. <https://doi.org/10.1046/j.1523-1739.2003.01236.x>.
- Rees, H.C., B.C. Maddison, D.J. Middleditch, J.R.M. Patmore and K.C. Gough. 2014. "The Detection of Aquatic Animal Species Using Environmental DNA: A Review of eDNA as a Survey Tool in Ecology." *Journal of Applied Ecology* 51 (5): 1450–59. <https://doi.org/10.1111/1365-2664.12306>.
- Resplandy, L., R.F. Keeling, Y. Edebbbar, M.K. Brooks, R. Wang, L. Bopp, M.C. Long, et al. 2018. "Quantification of Ocean Heat Uptake from Changes in Atmospheric O₂ and CO₂ Composition." *Nature* 563 (7729): 105–8. <https://doi.org/10.1038/s41586-018-0651-8>.
- Reynolds, L.K., K.J. McGlathery and M. Waycott. 2012. "Genetic Diversity Enhances Restoration Success by Augmenting Ecosystem Services." *PLOS ONE* 7 (6): e38397. <https://doi.org/10.1371/journal.pone.0038397>.
- Reynolds, P.L., J.P. Richardson and J.E. Duffy. 2014. "Field Experimental Evidence that Grazers Mediate Transition between Microalgal and Seagrass Dominance." *Limnology and Oceanography* 59 (3): 1053–64. <https://doi.org/10.4319/lo.2014.59.3.1053>.
- Rhode, C., J.-A. Hepple, S. Jansen, T. Davis, J. Vervalle, A.E. Bester-van der Merwe and R. Roodt-Wilding. 2012. "A Population Genetic Analysis of Abalone Domestication Events in South Africa: Implications for the Management of the Abalone Resource." *Aquaculture* 356–57 (August): 235–42. <https://doi.org/10.1016/j.aquaculture.2012.05.012>.

- Rincón-Cervera, M.Á., V. González-Barriga, R. Valenzuela, S. López-Arana, J. Romero and A. Valenzuela. 2019. "Profile and Distribution of Fatty Acids in Edible Parts of Commonly Consumed Marine Fishes in Chile." *Food Chemistry* 274 (February): 123–29. <https://doi.org/10.1016/j.foodchem.2018.08.113>.
- Rittschof, D. 2017. "Off the Shelf Fouling Management." *Marine Drugs* 15 (6). <https://doi.org/10.3390/md15060176>.
- Roark, E.B., T.P. Guilderson, R.B. Dunbar, S.J. Fallon and D.A. Mucciarone. 2009. "Extreme Longevity in Proteiaceous Deep-Sea Corals." *Proceedings of the National Academy of Sciences* 106 (13): 5204 LP–5208. <https://doi.org/10.1073/pnas.0810875106>.
- Roberts, C.M. 1995. "Effects of Fishing on the Ecosystem Structure of Coral Reefs." *Conservation Biology* 9 (5): 988–95.
- Roberts, C.M., B.C. O'Leary, D.J. McCauley, P.M. Cury, C.M. Duarte, J. Lubchenco, D. Pauly, et al. 2017. "Marine Reserves Can Mitigate and Promote Adaptation to Climate Change." *Proceedings of the National Academy of Sciences* 114 (24): 6167–75. <https://doi.org/10.1073/pnas.1701262114>.
- Roberts, C.M., G. Branch, R.H. Bustamante, J.C. Castilla, J. Dugan, B.S. Halpern, K.D. Lafferty, et al. 2003. "Application of Ecological Criteria in Selecting Marine Reserves and Developing Reserve Networks." *Ecological Applications* 13 (1): S215–28.
- Roche, R.C., C.V. Harvey, J.J. Harvey, A.P. Kavanagh, M. McDonald, V.R. Stein-Rostaing and J.R. Turner. 2016. "Recreational Diving Impacts on Coral Reefs and the Adoption of Environmentally Responsible Practices within the Scuba Diving Industry." *Environmental Management* 58 (1): 107–16. <https://doi.org/10.1007/s00267-016-0696-0>.
- Rodolfi, L., G. Chini Zittelli, N. Bassi, G. Padovani, N. Biondi, G. Bonini and M.R. Tredici. 2009. "Microalgae for Oil: Strain Selection, Induction of Lipid Synthesis and Outdoor Mass Cultivation in a Low-Cost Photobioreactor." *Biotechnology and Bioengineering* 102 (1): 100–112. <https://doi.org/10.1002/bit.22033>.
- Rogers, A.D. 2019. *The Deep: The Hidden Wonders of Our Oceans and How We Can Protect Them*. London: Wildfire.
- Rogers A.D., A. Brierley, P. Croot, M.R. Cunha, R. Danovaro, C. Devey, A.H. Hoel, H. Ruhl, P.-M. Sarradin, S. Trevisanut, S. van den Hove, H. Vieira and M. Visbeck. 2015. "Delving Deeper: Critical Challenges for 21st Century Deep-Sea Research." In *Position Paper 22 of the European Marine Board*, edited by K.E. Larkin, K. Donaldson and N. McDonough. Ostend, Belgium. 224 pp. ISBN 978-94-920431-1-5.
- Roman, J., and J.A. Darling. 2007. "Paradox Lost: Genetic Diversity and the Success of Aquatic Invasions." *Trends in Ecology & Evolution* 22 (9): 454–64. <https://doi.org/10.1016/j.tree.2007.07.002>.
- Roque, B.M., J.K. Salwen, R. Kinley and E. Kebreab. 2019. "Inclusion of Asparagopsis Armata in Lactating Dairy Cows' Diet Reduces Enteric Methane Emission by over 50 Percent." *Journal of Cleaner Production* 234 (October): 132–38. <https://doi.org/10.1016/j.jclepro.2019.06.193>.
- Ruiz-Frau, A., H.P. Possingham, G. Edwards-Jones, C.J. Klein, D. Segan and M.J. Kaiser. 2015. "A Multidisciplinary Approach in the Design of Marine Protected Areas: Integration of Science and Stakeholder Based Methods." *Ocean & Coastal Management* 103: 86–93.
- Ruiz Muller, M. 2015. *Genetic Resources as Natural Information. Implications for the Convention on Biological Diversity and Nagoya Protocol*. First edition. London: Routledge.
- Ruzzante, D.E., S. Mariani, D. Bekkevold, C. André, H. Mosegaard, L.A.W. Clausen, T.G. Dahlgren, et al. 2006. "Biocomplexity in a Highly Migratory Pelagic Marine Fish, Atlantic Herring." *Proceedings of the Royal Society B: Biological Sciences* 273 (1593): 1459–64. <https://doi.org/10.1098/rspb.2005.3463>.
- Ryckebosch, E., C. Bruneel, K. Muylaert and I. Foubert. 2012. "Microalgae as an Alternative Source of Omega-3 Long Chain Polyunsaturated Fatty Acids." *Lipid Technology* 24 (6): 128–30. <https://doi.org/10.1002/lite.201200197>.
- Sala, E., and S. Giakoumi. 2018. "No-Take Marine Reserves Are the Most Effective Protected Areas in the Ocean." *ICES Journal of Marine Science* 75 (3): 1166–68. <https://doi.org/10.1093/icesjms/fsx059>.
- Sala, E., C. Costello, D. Dougherty, G. Heal, K. Kelleher, J.H. Murray, A.A. Rosenberg, et al. 2013. "A General Business Model for Marine Reserves." *PLOS ONE* 8 (4): e58799.
- Sala, E., J. Lubchenco, K. Grorud-Colvert, C. Novelli, C. Roberts and U.R. Sumaila. 2018. "Assessing Real Progress towards Effective Ocean Protection." *Marine Policy* 91 (May): 11–13. <https://doi.org/10.1016/j.marpol.2018.02.004>.
- Sanger, F., S. Nicklen and A.R. Coulson. 1977. "DNA Sequencing with Chain-Terminating Inhibitors." *Proceedings of the National Academy of Sciences* 74 (12): 5463–67.
- Scheffers, B.R., L. De Meester, T.C.L. Bridge, A.A. Hoffmann, J.M. Pandolfi, R.T. Corlett, S.H.M. Butchart, et al. 2016. "The Broad Footprint of Climate Change from Genes to Biomes to People." *Science* 354 (6313): aaf7671. <https://doi.org/10.1126/science.aaf7671>.
- Schindler, D.E., and R. Hilborn. 2015. "Prediction, Precaution, and Policy under Global Change." *Science* 347 (6225): 953–54. <https://doi.org/10.1126/science.1261824>.
- Schindler, D.E., R. Hilborn, B. Chasco, C.P. Boatright, T.P. Quinn, L.A. Rogers and M.S. Webster. 2010. "Population Diversity and the Portfolio Effect in an Exploited Species." *Nature* 465 (7298): 609–12. <https://doi.org/10.1038/nature09060>.
- Schleicher, J., J.G. Zaehring, C. Fastré, B. Vira, P. Visconti and C. Sandbrook. 2019. "Protecting Half of the Planet Could Directly Affect over One Billion People." *Nature Sustainability* 2 (12): 1094–96.
- Shahidi, F., and P. Ambigaipalan. 2015. "Novel Functional Food Ingredients from Marine Sources." *Current Opinion in Food Science* 2 (April): 123–29. <https://doi.org/10.1016/j.cofs.2014.12.009>.
- Sherman, C.D.H., K.E. Lotterhos, M.F. Richardson, C.K. Tepolt, L.A. Rollins, S.R. Palumbi and A.D. Miller. 2016. "What Are We Missing about Marine Invasions? Filling in the Gaps with Evolutionary Genomics." *Marine Biology* 163 (10): 198. <https://doi.org/10.1007/s00227-016-2961-4>.
- Sigwart, J.D., C. Chen, E.A. Thomas, A.L. Allcock, M. Böhm and M. Seddon. 2019. "Red Listing Can Protect Deep-Sea Biodiversity." *Nature Ecology & Evolution* 3 (8): 1134. <https://doi.org/10.1038/s41559-019-0930-2>.
- Simmons, M., A. Tucker, W.L. Chadderton, C.L. Jerde and A.R. Mahon. 2015. "Active and Passive Environmental DNA Surveillance of Aquatic Invasive Species." *Canadian Journal of Fisheries and Aquatic Sciences* 73 (1): 76–83. <https://doi.org/10.1139/cjfas-2015-0262>.
- Sjöqvist, C.O., and A. Kremp. 2016. "Genetic Diversity Affects Ecological Performance and Stress Response of Marine Diatom Populations." *The ISME Journal* 10 (11): 2755–66. <https://doi.org/10.1038/ismej.2016.44>.
- Skowno, A.L., C.J. Poole, D.C. Raimondo, K.J. Sink, H. Van Deventer, L. Van Niekerk, L. Harris, et al. 2019. *National Biodiversity Assessment 2018: The Status of South Africa's Ecosystems and Biodiversity*. Synthesis Report. Pretoria: South African National Biodiversity Institute, an entity of the Department of Environment, Forestry and Fisheries.
- Slobodian, L., R. Kinna, A. Kambu and L. Ognibene. 2015. *Bioprospecting in the Global Commons: Legal Issues Brief*. Nairobi: United Nations Environment Programme. Division of Environmental Law and Conventions. Environmental Law and Governance Branch.

- Smith, D., and J. Jabour. 2018. "MPAs in ABNJ: Lessons from Two High Seas Regimes." *ICES Journal of Marine Science* 75 (1): 417–25. <https://doi.org/10.1093/icesjms/fsx189>.
- Smith, M.D., F. Asche, A.G. Guttormsen and J.B. Wiener. 2010. "Genetically Modified Salmon and Full Impact Assessment." *Science* 330 (6007): 1052–53.
- Sorte, C.J.B., S.L. Williams and J.T. Carlton. 2010. "Marine Range Shifts and Species Introductions: Comparative Spread Rates and Community Impacts." *Global Ecology and Biogeography* 19 (3): 303–16. <https://doi.org/10.1111/j.1466-8238.2009.00519.x>.
- Spalding, M.D., and B.E. Brown. 2015. "Warm-Water Coral Reefs and Climate Change." *Science* 350 (6262): 769–71. <https://doi.org/10.1126/science.aad0349>.
- Stefanni, S., D. Stanko, D. Borme, A. De Olazabal, T. Juretić, A. Pallavicini and V. Tirelli. 2018. "Multi-Marker Metabarcoding Approach to Study Mesozooplankton at Basin Scale." *Scientific Reports* 8: 1–13. <https://doi.org/10.1038/s41598-018-30157-7>.
- Stephens, Z.D., S.Y. Lee, F. Faghri, R.H. Campbell, C. Zhai, M.J. Efron, R. Iyer, et al. 2015. "Big Data: Astronomical or Genomic?" *PLOS Biology* 13 (7): e1002195. <https://doi.org/10.1371/journal.pbio.1002195>.
- Stewart, K.A. 2019. "Understanding the Effects of Biotic and Abiotic Factors on Sources of Aquatic Environmental DNA." *Biodiversity and Conservation* 28 (5): 983–1001. <https://doi.org/10.1007/s10531-019-01709-8>.
- Stokstad, E. 2018. "Norwegian Billionaire Funds Deluxe Deep Ocean Research Ship." *Science*. <https://www.sciencemag.org/news/2018/11/norwegian-billionaire-funds-deluxe-deep-ocean-research-ship>.
- Strother, P.K., L. Battison, M.D. Brasier and C.H. Wellman. 2011. "Earth's Earliest Non-Marine Eukaryotes." *Nature* 473 (7348): 505–9. <https://doi.org/10.1038/nature09943>.
- Suleria, H.A.R., S. Osborne, P. Masci and G. Gobe. 2015. "Marine-Based Nutraceuticals: An Innovative Trend in the Food and Supplement Industries." *Marine Drugs* 13 (10): 6336–51. <https://doi.org/10.3390/md13106336>.
- Sunagawa, S., L.P. Coelho, S. Chaffron, J.R. Kultima, K. Labadie, G. Salazar, B. Djahanschiri, et al. 2015. "Structure and Function of the Global Ocean Microbiome." *Science* 348 (6237): 1261359. <https://doi.org/10.1126/science.1261359>.
- Taberlet, P., E. Coissac, F. Pompanon, C. Brochmann and E. Willerslev. 2012. "Towards Next-Generation Biodiversity Assessment Using DNA Metabarcoding." *Molecular Ecology* 21 (8): 2045–50. <https://doi.org/10.1111/j.1365-294X.2012.05470.x>.
- Taylor, M.L., and C.N. Roterman. 2017. "Invertebrate Population Genetics across Earth's Largest Habitat: The Deep-Sea Floor." *Molecular Ecology* 26 (19): 4872–96. <https://doi.org/10.1111/mec.14237>.
- Teske, P.R., S. von der Heyden, C.D. McQuaid and N.P. Barker. 2011. "A Review of Marine Phylogeography in Southern Africa Coastal Phylogeography." *South African Journal of Science* 107: 43–53. <https://doi.org/10.4102/sajs.v107i5/6.514>.
- Thambisetty, S. 2007. "Patents as Credence Goods." *Oxford Journal of Legal Studies* 27 (4): 707–40.
- Thambisetty, S. 2019. *Due Diligence and ABS Compliance under EUR 511/2014*. SSRN Scholarly Paper ID 3323389. Rochester, NY: Social Science Research Network. <https://papers.ssrn.com/abstract=3323389>.
- Thambisetty, S. 2020. "Biodiversity beyond National Jurisdiction: (Intellectual) Property Heuristics." In *Biodiversity beyond National Jurisdiction: Intractable Challenges & Potential Solutions*. Leiden, Netherlands: Brill Nijhoff.
- Thilsted, S.H., A. Thorne-Lyman, P. Webb, J.R. Bogard, R. Subasinghe, M.J. Phillips and E.H. Allison. 2016. "Sustaining Healthy Diets: The Role of Capture Fisheries and Aquaculture for Improving Nutrition in the Post-2015 Era." *Food Policy* 61 (May): 126–31. <https://doi.org/10.1016/j.foodpol.2016.02.005>.
- Thomsen, P.F., and E. Willerslev. 2015. "Environmental DNA: An Emerging Tool in Conservation for Monitoring Past and Present Biodiversity." *Biological Conservation* 183: 4–18. <https://doi.org/10.1016/j.biocon.2014.11.019>.
- Thornburg, C.C., J.R. Britt, J.R. Evans, R.K. Akee, J.A. Whitt, S.K. Trinh, M.J. Harris, et al. 2018. "NCI Program for Natural Product Discovery: A Publicly-Accessible Library of Natural Product Fractions for High-Throughput Screening." *ACS Chemical Biology* 13 (9): 2484–97. <https://doi.org/10.1021/acscchembio.8b00389>.
- Tinacci, L., A. Guidi, A. Toto, L. Guardone, A. Giusti, P. D'Amico and A. Armani. 2018. "DNA Barcoding for the Verification of Supplier's Compliance in the Seafood Chain: How the Lab Can Support Companies in Ensuring Traceability." *Italian Journal of Food Safety* 7 (2): 6894. <https://doi.org/10.4081/ijfs.2018.6894>.
- Tolley, K.A., and J. Šmíd. 2019. "Chapter 4: Evaluating the Status and Trends of Landscape Level Genetic Diversity: A Case Study Using South African Reptiles." In *National Biodiversity Assessment 2018 Technical Report Volume 7: Genetic Diversity*, edited by K.A. Tolley, J.M. da Silva and B. Jansen van Vuren. Pretoria: South African National Biodiversity Institute.
- Troell, M., R.L. Naylor, M. Metian, M. Beveridge, P.H. Tyedmers, C. Folke, K.J. Arrow, et al. 2014. "Does Aquaculture Add Resilience to the Global Food System?" *Proceedings of the National Academy of Sciences* 111 (37): 13257–63. <https://doi.org/10.1073/pnas.1404067111>.
- Twichell, J., R. Pollnac and P. Christie. 2018. "Lessons from Philippines MPA Management: Social Ecological Interactions, Participation, and MPA Performance." *Environmental Management* 61 (6): 916–27.
- UN (United Nations). 1995. *Agreement for the Implementation of the Provisions of the United Nations Convention on the Law of the Sea of 10 December 1982 Relating to the Conservation and Management of Straddling Fish Stocks and Highly Migratory Fish Stocks*. New York: United Nations, Division for Ocean Affairs and the Law of the Sea. <https://documents-dds-ny.un.org/doc/UNDOC/GEN/N95/274/67/PDF/N9527467.pdf>.
- Vandepierre, F., R.M. Higgins, J. Sánchez-Meca, F. Maynou, R. Goñi, P. Martín-Sosa, A. Pérez-Ruzafa, et al. 2011. "Effects of No-Take Area Size and Age of Marine Protected Areas on Fisheries Yields: A Meta-Analytical Approach." *Fish and Fisheries* 12 (4): 412–26.
- Van Dover, C.L. 2014. "Impacts of Anthropogenic Disturbances at Deep-Sea Hydrothermal Vent Ecosystems: A Review." *Marine Environmental Research*, Special Issue: Managing Biodiversity in a Changing Ocean, 102 (December): 59–72. <https://doi.org/10.1016/j.marenvres.2014.03.008>.
- Van Dover, C.L., J.A. Ardron, E. Escobar, M. Gianni, K.M. Gjerde, A. Jaeckel, D.O.B. Jones, et al. 2017. "Biodiversity Loss from Deep-Sea Mining." *Nature Geoscience* 10 (7): 464–65. <https://doi.org/10.1038/ngeo2983>.
- van Oppen, M.J.H., J.K. Oliver, H.M. Putnam and R.D. Gates. 2015. "Building Coral Reef Resilience through Assisted Evolution." *Proceedings of the National Academy of Sciences* 112 (8): 2307–13. <https://doi.org/10.1073/pnas.1422301112>.
- Van Soest, R.W.M., N. Boury-Esnault, J. Vacelet, M. Mohrmann, D. Erpenbeck, N.J. De Voogd, N. Santodomingo, et al. 2012. "Global Diversity of Sponges (Porifera)." *PLOS ONE* 7 (4): e35105. <https://doi.org/10.1371/journal.pone.0035105>.

- Villarino, E., J.R. Watson, B. Jönsson, J.M. Gasol, G. Salazar, S.G. Acinas, M. Estrada, et al. 2018. "Large-Scale Ocean Connectivity and Planktonic Body Size." *Nature Communications* 9 (1): 1–13. <https://doi.org/10.1038/s41467-017-02535-8>.
- Viteri, C., and C. Chávez. 2007. "Legitimacy, Local Participation, and Compliance in the Galápagos Marine Reserve." *Ocean & Coastal Management* 50 (3–4): 253–74.
- Volkman, L., I. Martyn, V. Moulton, A. Spillner and A.O. Mooers. 2014. "Prioritizing Populations for Conservation Using Phylogenetic Networks." *PLOS ONE* 9 (2).
- von der Heyden, S. 2009. "Why Do We Need to Integrate Population Genetics into South African Marine Protected Area Planning?" *African Journal of Marine Science* 31 (2): 263–69. <https://doi.org/10.2989/AJMS.2009.31.2.14.886>.
- von der Heyden, S., M.R. Lipinski and C.A. Matthee. 2007. "Mitochondrial DNA Analyses of the Cape Hakes Reveal an Expanding, Panmictic Population for Merluccius Capensis and Population Structuring for Mature Fish in Merluccius Paradoxus." *Molecular Phylogenetics and Evolution* 42 (2): 517–27. <https://doi.org/10.1016/j.ympev.2006.08.004>.
- von der Heyden, S., M.R. Lipinski and C.A. Matthee. 2010. "Remarkably Low MtDNA Control Region Diversity in an Abundant Demersal Fish." *Molecular Phylogenetics and Evolution* 55: 1183–88. <https://doi.org/10.1016/j.ympev.2009.09.018>.
- Von Schomberg, R. 2013. "A Vision of Responsible Research and Innovation." In *Responsible Innovation*, edited by R. Owen, J. Bessant and M. Heintz, 51–74. Hoboken, New Jersey: John Wiley & Sons, Ltd. <https://doi.org/10.1002/9781118551424.ch3>.
- Walsh, M.R., S.B. Munch, S. Chiba and D.O. Conover. 2006. "Maladaptive Changes in Multiple Traits Caused by Fishing: Impediments to Population Recovery." *Ecology Letters* 9 (2): 142–48. <https://doi.org/10.1111/j.1461-0248.2005.00858.x>.
- Waltz, E. 2016. *GM Salmon Declared Fit for Dinner Plates*. Nature Publishing Group.
- Waltz, E. 2017. "First Genetically Engineered Salmon Sold in Canada." *Nature News* 548 (7666): 148. <https://doi.org/10.1038/nature.2017.22116>.
- Wang, K-L., Z-H. Wu, Y. Wang, C-Y. Wang and Y. Xu. 2017. "Mini-Review: Antifouling Natural Products from Marine Microorganisms and Their Synthetic Analogs." *Marine Drugs* 15 (9). <https://doi.org/10.3390/md15090266>.
- Waples, R.S., and A. Audzijonyte. 2016. "Fishery-Induced Evolution Provides Insights into Adaptive Responses of Marine Species to Climate Change." *Frontiers in Ecology and the Environment* 14 (4): 217–24. <https://doi.org/10.1002/fee.1264>.
- Waples, R.S., K. Hindar and J.J. Hard. 2012. *Genetic Risks Associated with Marine Aquaculture*. U.S. Department of Commerce. NOAA Technical Memo NMFS-NWFSC-119.
- Ward, A. 2018. "Exploring a New Enzymatic Tool for AAV Production: Balancing Optimal Nuclease Activity with Effective DNA Digestion." *Genetic Engineering & Biotechnology News* 38 (3): 22.
- Webster, M.S., M.A. Colton, E.S. Darling, J. Armstrong, M.L. Pinsky, N. Knowlton and D.E. Schindler. 2017. "Who Should Pick the Winners of Climate Change?" *Trends in Ecology & Evolution* 32 (3): 167–73. <https://doi.org/10.1016/j.tree.2016.12.007>.
- Weeks, R., and S.D. Jupiter. 2013. "Adaptive Comanagement of a Marine Protected Area Network in Fiji." *Conservation Biology* 27 (6): 1234–44.
- Weir, L.K., and J.W.A. Grant. 2005. "Effects of Aquaculture on Wild Fish Populations: A Synthesis of Data." *Environmental Reviews* 13: 145–68.
- Weltz, K., J.M. Lyle, J. Ovenden, J.A.T. Morgan, A. Moreno and J.M. Semmens. 2017. "Application of Environmental DNA to Detect an Endangered Marine Skate Species in the Wild." *PLOS ONE* 12 (6): e0178124.
- Wetterstrand, K.A. 2019. "DNA Sequencing Costs: Data." National Human Genome Research Institute. <https://www.genome.gov/about-genomics/fact-sheets/DNA-Sequencing-Costs-Data>.
- Wilkinson, C.R., and R.W. Buddemeier. 1994. *Global Climate Change and Coral Reefs: Implications for People and Reefs*. Report of the UNEP-IUCN-ASPEI-IUCN Global Task Team on the Implications of Climate Change on Coral Reefs. Gland, Switzerland: IUCN.
- Worm, B., and D.P. Tittensor. 2011. "Range Contraction in Large Pelagic Predators." *Proceedings of the National Academy of Sciences* 108 (29): 11942–47.
- Worm, B., E.B. Barbier, N. Beaumont, J.E. Duffy, C. Folke, B.S. Halpern, J.B.C. Jackson, et al. 2006. "Impacts of Biodiversity Loss on Ocean Ecosystem Services." *Science* 314 (5800): 787–90. <https://doi.org/10.1126/science.1132294>.
- Wright, D., J.M. Bishop, C.A. Matthee and S. Von Der Heyden. 2015. "Genetic Isolation by Distance Reveals Restricted Dispersal across a Range of Life Histories: Implications for Biodiversity Conservation Planning across Highly Variable Marine Environments." *Diversity and Distributions* 21: 698–710. <https://doi.org/10.1111/ddi.12302>.
- Wynberg, R. 2016. "Marine Genetic Resources and Bioprospecting in the Western Indian Ocean." In *Regional State of the Coast Report*. United Nations Environment Programme, Nairobi Convention. <https://doi.org/10.18356/7a82e6cd-en>.
- Wynberg, R., and S.A. Laird. 2018. "Fast Science and Sluggish Policy: The Herculean Task of Regulating Biodiscovery." *Trends in Biotechnology* 36 (1): 1–3. <https://doi.org/10.1016/j.tibtech.2017.09.002>.
- Xiong, X., L. Guardone, A. Giusti, L. Castigliengo, D. Gianfaldoni, A. Guidi and A. Andrea. 2016. "DNA Barcoding Reveals Chaotic Labeling and Misrepresentation of Cod (, Xue) Products Sold on the Chinese Market." *Food Control* 60: 519–32. <https://doi.org/10.1016/j.foodcont.2015.08.028>.
- Young, T.R., and M. Walløe Tvedt. 2017. *Drafting Successful Access and Benefit-Sharing Contracts*. Leiden, Netherlands: Brill.
- Zachos, E. 2017. "To Fight Opioid Addiction, Scientists See Promise in Sea Snail Venom." *National Geographic*. <https://www.nationalgeographic.com/news/2017/12/fight-opioid-addiction-scientists-see-promise-in-sea-snail-venom-spd/>.
- Zaiko, A., X. Pochon, E. Garcia-Vazquez, S. Olenin and S.A. Wood. 2018. "Advantages and Limitations of Environmental DNA/RNA Tools for Marine Biosecurity: Management and Surveillance of Non-indigenous Species." *Frontiers in Marine Science* 5: 322.
- Zeng, C., A.A. Rowden, M.R. Clark and J.P.A. Gardner. 2017. "Population Genetic Structure and Connectivity of Deep-Sea Stony Corals (Order Scleractinia) in the New Zealand Region: Implications for the Conservation and Management of Vulnerable Marine Ecosystems." *Evolutionary Applications* 10 (10): 1040–54. <https://doi.org/10.1111/eva.12509>.
- Zhu, B., and W. Ge. 2018. "Genome Editing in Fishes and Their Applications." *General and Comparative Endocrinology* 257: 3–12. <https://doi.org/10.1016/j.ygcen.2017.09.011>.

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