

1 The Ocean Genome and Future Prospects for Conservation and Equity

2
3 Blasiak R.^{1,2}, Wynberg R.³, Grorud-Colvert K.⁴, Thambisetty S.⁵, Bandarra N.M.⁶, Canario A.V.M.⁷, da
4 Silva J.^{8,9}, Duarte C.M.¹⁰, Jaspars M.¹¹, Rogers A.¹², Sink K.⁸ and Wabnitz C.C.C.^{1,13}

5 **Life has evolved in the ocean for 3.7 billion years, resulting in a rich “ocean genome”, the**
6 **ensemble of genetic material present in all marine biodiversity, including both the physical**
7 **genes and the information they encode. Rapid advances in sequencing technologies and**
8 **bioinformatics have enabled exploration of the ocean genome and are informing innovative**
9 **approaches to conservation and a growing number of commercial biotechnology applications.**
10 **However, the capacity to undertake genomic research and to access and use sequence data is**
11 **inequitably distributed among countries, highlighting an urgent need to build capacity,**
12 **promote inclusive innovation, and increase access to affordable technologies.**

13 The ocean is a vast and diverse habitat that covers 70% of the Earth’s surface. Although estimates of
14 extant species are based on indirect approaches and extrapolations can vary widely, some 2.2
15 million (range 0.3-10 million) eukaryotic marine species likely exist in the ocean, of which 230,000
16 are confirmed^{1,2}. Comparisons with terrestrial life underscore the striking diversity of marine life: for
17 instance, of the 34 major animal phyla, only 12 are found on land, while 33 have been recorded in the
18 ocean³. The abundance and diversity of marine prokaryotes (bacteria and archaea) and viruses
19 reaches monumental orders of magnitude, collectively accounting for the majority of living mass in
20 the ocean, with estimates, extrapolated from mean values per unit volume of seawater, of 1.2×10^{29}
21 prokaryote cells and 1.3×10^{30} virus particles found in ocean waters^{4,5}. Some 24-98% of eukaryotic
22 marine species, depending on the taxon group, remain undescribed, while even less is known about
23 prokaryotic marine life, with estimates extrapolated using scaling laws, ranging from $1.0 \cdot 10^6$ to
24 $3.0 \cdot 10^{27}$ operational taxonomic units comparable, in taxonomic terms, to species^{2,6,7}.

25 The diversity of marine life is closely associated with and dependent upon underlying genetic
26 diversity, namely the total number of genetic characters in the genetic makeup of each species.
27 Genetic diversity encodes the functional attributes of species, and their distribution and adaptability.
28 Conserving genetic diversity provides more opportunities for evolution, and helps to foster the
29 fitness of populations and their potential to recover from and adapt to threats ranging from disease
30 to environmental changes⁸.

31 We define the “ocean genome” as the ensemble of genetic material present in all marine
32 biodiversity, including both the genes and the information they encode⁹. The explicit reference to
33 the physical resources and informational component of genes reflects technological advances as
34 well as the regulatory efforts striving to govern them. In recent decades, it has become possible not
35 only to store the nucleotide sequences of DNA and RNA as digital information, but to then use this
36 information to synthesize proteins, create molecular processes and innovation, and modify or even
37 create organisms^{10,11}. Genetic sequence data and innovations based on such digital information are
38 now the subject of patent and ownership claims¹². The complexity of regulating access to both
39 informational and physical resources and equitably sharing benefits from the vast potential

¹ Author affiliations: (1) Stockholm Resilience Centre, Stockholm University, Sweden; (2) University of Tokyo, Japan; (3) University of Cape Town, South Africa; (4) Oregon State University, USA; (5) London School of Economics, UK; (6) Portuguese Institute of Sea and Atmosphere, Portugal; (7) CCMAR, University of Algarve, Portugal; (8) South African National Biodiversity Institute, South Africa; (9) Centre for Ecological Genomics and Wildlife Conservation, Department of Zoology, University of Johannesburg, South Africa; (10) Red Sea Research Center and Computational Bioscience Research Center, King Abdullah University of Science and Technology, Saudi Arabia; (11) Marine Biodiscovery Centre, Department of Chemistry, University of Aberdeen, UK; (12) REV Ocean, Lysaker, Norway and University of Oxford, UK; (13) University of British Columbia, Canada

40 applications of these genetic resources across multiple industries remains unresolved and is the
41 subject of negotiations in multiple international fora¹³.

42 In this review, we address three questions. What are the benefits to the biosphere, to humanity and
43 to other living organisms that arise from the ocean genome? What are the threats eroding genetic
44 diversity in the ocean? How can the ocean genome be conserved and used in a more sustainable, fair
45 and equitable manner?

46 Ecological benefits

47 Most attributes of organisms are encoded within their genomes, which determine much of their
48 morphology, biology, behavior and physiology. High levels of genetic variability and the presence of
49 multiple genotypes within a species can result in functional redundancy that supports species
50 resilience and adaptive capacity under environmental pressures and anomalous conditions^{14,15}.
51 Within the context of complex and dynamic systems, genetic diversity is therefore a crucial
52 stabilizing factor. Such benefits have been of interest to fishery managers, as genetically diverse fish
53 populations are better positioned to exploit a range of habitats, which adds flexibility in their
54 responses to environmental change¹⁶. Alaska's Bristol Bay salmon, for instance, is a highly
55 heterogeneous population that includes over 100 discrete sub-populations, resulting in a portfolio
56 effect, whereby the associated diversity has led not only to a more stable population, but also less
57 frequent closures for fishing communities¹⁵. Elsewhere, the benefits of genetic variability have been
58 recorded in restoration projects. For instance, in North America and Indonesia, plots of seagrass
59 with higher levels of genetic diversity also exhibited higher rates of survival, plant density and
60 growth¹⁷. The ecological benefits of genetic diversity extend beyond the resilience of individual
61 populations. In both of the above cases, positive impacts were recorded – in the stability of
62 populations feeding on salmon during spawning, and in increased levels of primary production and
63 nutrient retention in restored seagrass beds in the Chesapeake Bay^{15,18}.

64 Genetic variability also drives adaptive potential, which not only enhances resilience to anomalous
65 conditions, but also enables persistence as environmental conditions change and evolve over time.
66 Recent studies have demonstrated that this adaptive potential is of relevance even over short
67 timeframes, for instance within the span of 200 to 600 generations (6 months) of certain tropical
68 diatoms¹⁹. Due to the prominence of coral reef ecosystems as hotspots of marine biodiversity and a
69 crucial element of marine food webs, the bleaching and loss of corals is of special concern. There is
70 evidence suggesting that some corals may already have begun adapting to ocean warming caused
71 by anthropogenic activity, rendering them more resistant in the context of mass-bleaching events.
72 This relatively rapid response is a function of genetic diversity and phenotypic plasticity at the
73 holobiont level. Likewise, current changes in ocean conditions could alter the functional
74 composition of marine phytoplankton communities, the foundation of virtually all marine food webs
75 and the source of roughly half of the oxygen on the planet. In an experimental setting, cultures of
76 marine phytoplankton with higher genetic diversity outperformed less diverse cultures with regard
77 to their ability to withstand low salinities and maintain nitrogen uptake levels²³.

78 Closely studied ecosystems and commercial fisheries are already providing some evidence of how
79 genetic diversity contributes to ecosystem function and enhances adaptive potential. Yet the full
80 value of marine genetic diversity for the ocean and the biosphere will become increasingly apparent
81 as ocean systems continue to change and additive and synergistic impacts are better understood.

82

83 Commercial benefits

84 While the ocean genome provides the ecological foundation that sustains major commercial
85 industries such as marine fisheries and tourism, commercial benefits are also derived directly from
86 marine genes. Marine organisms, from microbes to large vertebrates, establish complex intra- and
87 interspecific interactions mostly mediated by a variety of chemicals. These chemicals serve multiple
88 purposes, including communication, chemical defense to predators, allelopathy, antifouling and
89 many others^{24,25}. These chemicals, also called secondary metabolites, are small molecules of a
90 diverse nature (e.g. peptides, sterols, phenols, terpenoids, alkaloids) often with a biological function
91 yet to be resolved. The continuum of “omic” approaches, extending from genomics and functional
92 genomics to transcriptomics, proteomics and metabolomics provides a mechanistic pathway linking
93 the ocean genome to the metabolites that play an important role as potential natural products for
94 human applications, as well as a key role in modulating interactions among organisms. Much
95 research has focused on finding useful biological activities for biomedical, cosmetic and other
96 commercial purposes. With the recent advances in analytical techniques (mass spectrometry,
97 nuclear magnetic resonance), new high throughput metabolomics approaches are able to
98 simultaneously unravel hundreds of novel compounds. When coupled to other omics technologies,
99 such as Next-Generation Sequencing (NGS), in a systems biology approach, insights of the complex
100 picture of interaction among organisms can be obtained. Furthermore, the pathways for production
101 of the metabolites can be obtained, which opens the way to their mass production using
102 biotechnological methods²⁶.

103 Perhaps the hallmark of human benefit from a marine gene is the discovery of green fluorescent
104 protein, which produces bioluminescence in the jellyfish *Aequorea victoria* and has been used across
105 a range of applications from protein tagging to identifying levels of environmental toxicity,
106 contributions ultimately recognized with the 2008 Nobel Prize in Chemistry²⁷. Further examples
107 include bioprospecting for novel antifoulants and adhesives, and the search for novel antibiotics,
108 which has increasingly focused on the bioactive compounds produced by marine invertebrates and
109 microorganisms associated with sea sponges²⁸⁻³⁰. Other marine microorganisms produce a type of
110 naturally occurring polymer (extracellular polymeric substance) that is of interest in bioremediation
111 efforts due to its capacity to detoxify pollutants such as heavy metals³¹, while *Pseudomonas spp.* and
112 *Ideonella sakaiensis* have the capacity to biodegrade certain plastics³². Additional categories of
113 commercial activity focused on marine genetic resources are briefly introduced below.
114 Controversies over the ownership and exclusive use of these genetic resources have persisted and
115 present some unique challenges to existing international frameworks, as well as to potential pace of
116 discovery.

117 **Marine drug discovery**

118 The marine environment has been an attractive source of bioactive compounds for the development
119 of novel drugs. The approximately 34,000 marine natural products³³ that have been reported have
120 resulted in 8 clinically-approved drugs, with a further 28 in clinical trials and 250 under preclinical
121 investigation³⁴. Compared with drug development from terrestrial natural products, this is a
122 remarkable success rate³⁵. A driving force behind the development of marine drugs has been
123 extensive funding from the US National Cancer Institute and prospective efforts by private
124 companies, as well as a focus on the collection of marine genetic resources globally, particularly
125 from shallow tropical reefs and marine invertebrates. Consequently, five of the eight clinically-
126 approved drugs are treatments for cancer, with the remainder comprising treatments for
127 neuropathic pain, the *Herpes simplex* virus and hypertriglyceridemia. Seven of the eight drugs were
128 derived from sessile marine invertebrates, whose tendency to produce highly bioactive compounds
129 – a virtual chemical arsenal – may be related to their lack of an adaptive immune system, predation
130 pressure, and intense competition for space and resources, although the majority of these
131 compounds have no apparent defensive function³⁶.

132 **Nutraceuticals and cosmeceuticals**

133 With properties that provide medical or health benefits and also serve cosmetic or nutritional
134 purposes, cosmeceuticals and nutraceuticals are a growing industry, with marine resources
135 comprising an attractive source due to the wide range of exhibited metabolic pathways. The
136 resulting diversity of bioactive compounds includes vitamins, carbohydrates, proteins and peptides,
137 and – perhaps most prominently – omega-3 fatty acids³⁷. While fish and crustaceans have long been
138 exploited as sources of eicosapentaenoic acid and docosahexaenoic acid, overexploitation of fish
139 stocks has led to research in alternative sources of omega-3 fatty acids, and the subsequent
140 development of algal oils that can be produced in industrial quantities using phototrophic
141 microalgae^{38,39}. Cosmeceutical skin creams with purported anti-inflammatory and detoxifying
142 agents have been developed from species as diverse as the Caribbean gorgonian (*Pseudopterogorgia*
143 *elisabethae*) and bacteria isolated from deep-sea hydrothermal vents (*Altermonas macleodi* subsp.
144 *fijiensis* biovar *deepsane*; *Thermus thermophilus*)^{40,41}.

145 **Aquaculture and new food products**

146 While genetic modification has been used on a variety of commercial land crops, it remains in its
147 infancy in the aquaculture industry. To date, only the Atlantic salmon (*Salmo salar*) has been
148 commercialized using genetic engineering, namely through the insertion of growth hormone cDNA
149 from Chinook salmon (*Oncorhynchus tshawytscha*) and regulated with antifreeze protein promoter
150 sequences from the Ocean pout (*Zoarces americanus*) that enable it to survive in near-freezing
151 temperatures⁴². The resulting transgenic salmon, which reached the market for the first time in
152 2017⁴³, can reach a marketable size within 16-18 months, as opposed to the three years it would
153 otherwise require. But with just 40 fish species having fully sequenced genomes, and the recent
154 advent of tools such as CRISPR (Clustered Regularly Interspaced Short Palindromic Repeats) and
155 associated enzymes (e.g. Cas9) allowing selective gene editing, the number of transgenic
156 aquaculture species is expected to increase, particularly due to a growing demand for seafood and
157 increasing focus on lower trophic level species like seaweeds and bivalve molluscs⁴⁴. However,
158 questions of consumer acceptability, environmental risk and social desirability remain paramount
159 and unresolved, alongside an uncertain regulatory framework^{45,46}. Parallel research has also
160 developed, focused on novel functional food ingredients with the potential to extend shelf-life and
161 prevent spoilage (e.g. chitosan and protein hydrolysates)⁴⁷, and the use of enzymes from marine
162 microorganisms as natural food processors⁴⁸.

163 **Bulk chemicals**

164 Products and processes derived from marine genetic resources are of growing importance for the
165 bulk chemical market, with applications ranging from novel laundry detergents to their use as
166 emulsifiers and stabilizers in food production. Bioplastics derived from seaweed polymers are being
167 used across a range of applications from straws and flip-flops to edible alternatives to plastic
168 packaging^{48,49}. The enzymes allowing species to flourish in extremely cold and hot marine
169 environments have also attracted commercial interest. For example, a genetically modified version
170 of a thermostable enzyme collected from a hydrothermal vent organism has been used for
171 bioethanol production due to its capacity to function across wide pH and temperature ranges⁵⁰. The
172 addition of certain red seaweeds (*Asparagopsis taxiformis* and *Asparagopsis armata*) to ruminant
173 feed has been shown to more than halve methane emissions, although concerns exist about the
174 ozone-depleting properties of bromoform, a secondary metabolite produced by these seaweeds, if
175 industrial-scale production for animal feed is pursued^{51,52}.

176 **Erosion of the ocean genome**

177 All of these benefits—including products from marine genetic resources and ecosystem services
178 delivered by diverse and fully functioning ocean systems—are predicated on the existing ocean
179 genome. Yet this is threatened by the intensification of human activity around the world, which is
180 contributing to a rapid loss of biodiversity in marine life and accelerating trends that are evident
181 across multiple ocean-based industries⁵³. Marine capture fisheries, coastal development and
182 pollution have contributed to the loss of (sub-) populations and in extreme cases, species extinction,
183 although these are rare in marine environments⁵⁴. This leads to a decline in genetic diversity in the
184 ocean, mostly concentrated, thus far, at the level of within species variability. The economic
185 importance of the salmon industry has spurred close monitoring of the population dynamics of
186 salmon, helping to understand the impact of human activities: within the Columbia River basin, for
187 example, dam construction has resulted in the extinction of several sockeye salmon subpopulations,
188 while chinook salmon have lost up to two-thirds of their genetic diversity⁵⁵. The decline in genetic
189 diversity has resulted in smaller and more variable salmon returns⁵⁵. Even within subpopulations
190 that persist, overfishing can result in the loss of genetic diversity over time, most likely reflected in
191 loss of allelic diversity for specific genes, as the prominence of certain genotypes fluctuates and
192 genetic drift reduces genetic diversity and lowers the capacity of species to persist and adapt to
193 changing conditions.

194 Although documented species extinction has been rare in the ocean compared with recent rates of
195 terrestrial species loss, climate change is expected to result in disproportionate levels of species loss
196 in the ocean due to the narrow thermal range tolerated by marine ectotherms^{54,56}. As the ocean
197 warms and becomes more acidic and less oxygenated with climate change, the geographic
198 distribution of species is also changing as they track their environmental niche⁵⁷. At a genetic level,
199 this implies an altered distribution of genetic variants in space and time, impacts on levels of
200 phenotypic plasticity and changes to connectivity and population size⁵⁸. Genetic variation is not
201 uniform across species ranges, with populations in historic refuges often characterized by greater
202 genetic diversity, and likewise threatened by shifts in distribution due to climate change⁵⁹.

203 Efforts to optimize marine aquaculture have included the selective breeding of species and their
204 introduction into non-native habitats. Careful monitoring and containment helps to maintain the
205 integrity of local ecosystems, but escape events do occur, and have led to farmed species
206 outcompeting native populations as well as the interbreeding of farmed and native species⁶⁰. This
207 results in genetic introgression and can lead to a rapid and irreversible loss of genetic diversity
208 among the native fish populations, thereby lowering their adaptive capacity⁶¹. Such impacts could
209 be accelerated by the accidental release of genetically modified strains in the ocean.

210 Much of the deep ocean and seabed remain unexplored, and scientific expeditions regularly result in
211 the discovery of new species. A tendency for deep-sea life to exhibit slow growth rates and long
212 lifespans renders deep-sea ecosystems particularly vulnerable to environmental disturbance⁶². The
213 potential for large-scale commercial mining of the international seabed has therefore drawn
214 particular concern within the scientific community due to uncertainty about the scale of physical and
215 geochemical disturbance caused by mining operations and resulting sediment plumes in the deep
216 sea, which are expected to lead to the loss of habitat and a potentially irreversible loss of
217 biodiversity⁶². The scaly-foot snail (*Chrysomallon squamiferum*), for instance, is found exclusively on
218 three hydrothermal vent systems in the Indian Ocean at depths of over 2400 meters, and was placed
219 on the IUCN Red List in June 2019 due to two of the three systems falling within the boundaries of
220 exploratory mining licenses granted by the International Seabed Authority⁶³.

221 The acceleration of human activities on land and in the sea means that many marine species and
222 communities are simultaneously facing multiple pressures with cumulative or synergistic effects on
223 genetic structure and gene flow. Well-studied examples include the twin pressures of wild capture

224 salmon fisheries and aquaculture escapement, which undermine the genetic variability of wild
225 populations⁶⁴. Looking beyond individual populations or species, multiple pressures can also result
226 in a complete reordering of ecosystems into novel regimes. For instance, the combined and
227 interlinked pressures from eutrophication, overfishing and the introduction of invasive species into
228 the Black Sea led to abrupt transitions and the emergence of a new stable regime characterized by a
229 low-energy food web dominated by jellyfish and the dinoflagellate *Noctiluca scintillans*.⁶⁵

230 **A more sustainable and equitable future**

231 How can a growing understanding of the ecological and commercial benefits associated with the
232 ocean genome be leveraged to promote conservation efforts and mitigate the drivers of genetic
233 diversity loss in the ocean? Below, we detail not only what can be done to conserve the ocean
234 genome, but also avenues through improved regulatory frameworks and models of inclusive
235 innovation that can render use of the ocean genome more sustainable, equitable and fair.

236 **Towards conservation of the ocean genome**

237 In marine systems, there are opportunities for the conservation of genetic diversity via key tools,
238 among them ecosystem-based approaches to fisheries management, spatial planning, effective
239 quotas, marine protected areas (MPAs), protecting and managing key marine biodiversity areas,
240 reducing run-off pollution into oceans, and working closely with producers and consumers of ocean
241 products⁶⁶. Among these, the imperative of conserving the ocean genome would appear to be on
242 firm footing in existing international frameworks: the importance of genetic diversity was already
243 emphasized in the Convention on Biological Diversity (CBD) (1992), while the target of protecting at
244 least 10% of the ocean is found in both Sustainable Development Goal 14 and Aichi Target 11. Yet
245 genetic diversity has been largely overlooked in conservation policies and action plans, and only 8%
246 of the ocean is set aside for biodiversity conservation, while just 2.5% is considered fully or highly
247 protected⁶⁸.

248 MPAs are considered one of the most effective tools for achieving the conservation of genetic
249 diversity on an ecosystem scale⁶⁹. Fully or highly-protected large-scale MPAs and networks of MPAs
250 can encompass multiple sites of importance for the life-cycle of marine species. Well-managed
251 MPAs with adequate protection levels function as storehouses of genetic diversity that
252 simultaneously serve as important reference points for understanding changes to the ocean⁷⁰. MPA
253 networks can be designed with a specific focus on areas where genetic diversity is exceptionally high,
254 or where particular adaptation potential lies. Such MPA adaptation networks are relevant for
255 instance in coral reef systems⁷¹, which have been the focus of empirical work to map their
256 adaptation potential⁷². The capacity for a single coral species to inhabit a range of environments
257 characterized by high genetic diversity and on scales of less than 100 meters underscores the need
258 for protected areas to be designed with a consideration not only for potential shifts in species
259 distribution across latitudes, but also different water depths^{34,73} (Figure 1).

260 Recognizing the importance of MPAs and other effective area-based conservation measures
261 (OECMs) as tools for conserving the ocean genome, there is a particular need to optimize design to
262 also conserve the genetic component of marine biodiversity. This remains a substantial challenge
263 due to the rarity of temporal genetic diversity datasets or baselines, although a number of novel
264 genetic technologies are becoming available with the potential to overcome this barrier. These
265 include Sanger sequencing, with a history of applications ranging from wildlife conservation and
266 management to the identification of mislabeled seafood⁷⁴, as well as Next-Generation Sequencing
267 (NGS), a high-throughput DNA-sampling tool that can provide large-scale spatial and temporal
268 syntheses for both individual species and community assemblages⁷⁵. Several community initiatives

269 using NGS are starting to change this landscape, such as the Earth BioGenome Project which aims
270 to sequence, catalog, and characterize the genomes of all of Earth's eukaryotic biodiversity over a
271 period of 10 years⁷⁶, the sponge microbiome project a comprehensive resource of sponge-
272 associated microbial communities based on 16S rRNA gene sequences that can be used to address
273 overarching hypotheses regarding host-associated prokaryotes⁷⁷, and the Earth Microbiome Project
274 to characterize microbial life on the planet using DNA sequencing and mass spectrometry⁷⁸.
275 Emerging data on diversity within the microbiome of marine holobionts is revealing a vast reservoir
276 of hitherto largely ignored microbial biodiversity⁷⁹.

277 When coupled with another novel molecular approach, environmental DNA (eDNA) analysis, NGS
278 has also been used for the detection and monitoring of marine invasive species^{80,81}. The passive
279 sampling techniques employed for eDNA analysis provide multiple benefits of interest to marine
280 conservation. Due to the constant shedding of DNA by species as they interact with their
281 environment, analysis of eDNA samples can indicate whether certain species are present in a given
282 geography⁸². As a result of the rapid decomposition of eDNA over the span of days or even hours in
283 seawater, eDNA analysis provides an almost real-time picture of species presence, including rare or
284 elusive species, and invasive species^{83,84}. The flexibility of the approach allows for simultaneous
285 identification of hundreds of species in a single sample, providing insight into areas of particular
286 species richness and potential priority for area-based protection. Recent advances in interpreting
287 eDNA are also enabling quantification of population genetic structure and insights into trophic
288 connectivity⁸⁵. Sampling and analysis of eDNA is most powerful in well-studied marine ecosystems
289 with substantial barcode reference collections, but may become an increasingly useful tool for the
290 design of marine conservation interventions.

291 Some have touted the potential of new genome-editing techniques such as CRISPR for conservation,
292 but their application remains theoretical. Extensive work done on corals, for example, reveals
293 limited knowledge about potential candidate genes to target, whether this would result in
294 phenotypic changes, whether the modified genome would be stable, and what unintended
295 consequences gene editing could generate^{86,87}. Moreover, a scarcity of information about the
296 environmental, social and ethical risks of existing and new genetic engineering tools, especially in
297 marine environments, have raised important questions about the governance and regulation of such
298 technologies, necessitating a precautionary approach to the introduction of such technologies for
299 conservation and fisheries management.

300 Although genetic techniques are rapidly evolving, policymakers do not have the luxury of waiting to
301 make interventions until comprehensive inventories of marine genetic diversity are available, or
302 until the extent of varied threats are fully understood. A delayed response risks resulting in the loss
303 of rapidly deteriorating storehouses of genetic information due to over-harvesting of species and
304 habitat degradation. Scientific recommendations to protect 30% of the ocean from all but the most
305 minimal extraction focus on encompassing sufficient biodiversity, species biomass, and
306 representative habitats⁸⁸. This requires that ongoing management outside protected areas
307 complements these efforts by ensuring sustainable use, minimizing habitat destruction and
308 avoiding overexploitation of resources. Such strategies include sustainable management of fisheries
309 with a focus on ecosystem-based fisheries management, affording special protections for rare,
310 vulnerable, threatened or endangered genotypes, populations and species, and using precautionary
311 approaches when initiating exploitation of previously unexploited species or places.

312 **Towards equitable benefit sharing**

313 Investments in marine biodiscovery are typically extremely costly and risky due in part to the high
314 costs of sampling in areas like the deep sea, the low chances of success, the technical, financial and

315 scientific investments required, and the significant regulatory hurdles for product approval (Figure
316 3)^{89,90}. The nature of the research enterprise is also changing, as research shifts towards
317 bioinformatics and the mining and exploration of these vast and growing datasets of genetic
318 information, which requires advanced computational resources that are not broadly available⁹¹. As a
319 result, most exploration has been undertaken by high-income countries, especially with regard to
320 deep-sea research^{36,92,93}. Disparities in research capacity, technology, finances and intellectual
321 property rights represent major constraints that prevent the inclusion of low and middle-income
322 countries in marine biotechnology efforts. Biodiversity and molecular expertise is unevenly spread⁹⁴,
323 and research vessels or submersibles are typically owned only by a few high-income nations, and
324 require substantial operational costs⁹⁵, representing a major barrier to sampling of the deep ocean
325 or in areas beyond national jurisdiction (see Box 1). While there are growing numbers of
326 collaborations between high-income and lower-income countries⁹⁶, the model of international
327 collaboration is still characterized by a pharmaceutical or biotech company working with established
328 centers of excellence located in high-income countries.

329 A number of international governance instruments and bodies provide an important platform where
330 new models of equitable benefit sharing and research partnerships can evolve, and conservation of
331 the ocean genome can be strengthened. These include the CBD, its Nagoya and Cartagena
332 (Biosafety) Protocols, the International Treaty on Plant Genetic Resources for Food and Agriculture,
333 the United Nations Convention on the Law of the Sea (UNCLOS) and the World Intellectual Property
334 Organization (WIPO). Among other provisions, these agreements place the responsibility on states
335 to conserve their biological diversity or to enter into meaningful management discussions with other
336 countries with which they share resources (e.g. transboundary fish stocks). In the context of genetic
337 resource use, the CBD's Nagoya Protocol sets forth the requirement for provider countries (where
338 genetic resources are located) and user countries (those accessing and developing the genetic
339 resources) to enter into mutually agreed terms based on prior informed consent before access to
340 genetic resources is granted. In areas beyond national jurisdiction (ABNJ), roughly 64% of the ocean,
341 no restrictions currently exist on access to genetic resources, or regulations for the sharing of
342 benefits based on their potential commercialization. However, this is one of four main elements of
343 ongoing UN treaty negotiations of cross-cutting importance for the ocean genome (Box 1).

344 A further complication is the so-called "definitional mistake" of the CBD and Nagoya Protocol,
345 whereby focus is placed on genetic resources in terms of their physical form rather than explicitly
346 including the intangible informational aspects⁹⁷. The development of novel genomic techniques has
347 contributed to a 4,000-fold drop in sequencing costs over the past decade⁹⁸, and has resulted in vast
348 and exponentially growing databases of genetic sequence data and hundreds of millions of
349 predicted genes (Figure 2)⁹⁹⁻¹⁰¹. While many of these databases are in the public domain and freely
350 accessible, the growing tendency towards "big data" applications means that leveraging novel
351 genomic techniques for conservation or other uses is becoming increasingly dependent on
352 computational and bioinformatics capacity, including access to technologies protected by
353 intellectual property rights. Additionally, the private appropriation of genetic resources through
354 intellectual property rights such as patents, because they result in exclusivity of use, can exacerbate
355 existing gaps in the ability to benefit from their exploitation¹⁰². Because countries of the global
356 North and South do not have equal capacities or technologies to exploit these resources, there is a
357 risk of inequitable outcomes out of sync with the 2030 Agenda for Sustainable Development and the
358 CBD and its Nagoya Protocol¹⁰³.

359 One opportunity rests in the development of research partnerships that connect countries that have
360 high molecular research capacity and biotechnology infrastructure with those that do not, with such
361 partnerships guided by norms of inclusive innovation and those of responsible research and
362 innovation^{90,104}. Taking an explicit focus on those excluded from the development mainstream,
363 inclusive innovation is a conceptual approach for ensuring that innovation both addresses the

364 problems faced by the poorest and most marginalized communities, and also involves these
365 communities in crafting a range of legal, technical and governance-based solutions^{101,102}. The related
366 concept of responsible research and innovation (RRI) envisages a transparent, interactive process by
367 which societal actors and innovators become mutually responsive to each other with a view to the
368 (a) ethical acceptability, (b) sustainability and (c) societal desirability of the innovation process and
369 its marketable products¹⁰⁶.

370 Historically, the majority of exploration of the ocean genome has been funded by high-income
371 countries such as the USA, Japan, Russia and EU states, and commercial activities and benefits
372 continue to be concentrated within a handful of highly-industrialized countries^{12,50}. However,
373 sustained commitments to research partnerships and inclusive and responsible research and
374 innovation, including through capacity building and the transfer of marine technology, could result
375 over time in a growing number of dynamic knowledge hubs and diffuse scientific collaborations
376 outside the Global North¹⁰⁷. Indeed, it may well be that enabling virtual access to data and the ability
377 to use it might prove an easier task than equalizing physical access to marine genetic resources.

378 While the concept of inclusive and responsible research and innovation is appealing and in line with
379 existing governance and regulatory frameworks, there are substantial and unresolved legal and
380 ethical issues related to the use and sharing of genomic information. The science bodies of the EU,
381 USA and Australia, for instance, require genomic data collected over the course of funded projects
382 to be deposited in open access databases. While regulations on disclosure of origin and other
383 measures aimed at increasing transparency in the use of genetic sequence data are being
384 negotiated within multiple international fora¹⁰⁸, the informational component of the ocean genome
385 is increasingly entering the public domain and becoming a *de jure* universal resource, that is *de facto*
386 only accessible to those with corresponding capacity. The capacity for industry actors to access
387 public databases, while remaining unbound by benefit-sharing requirements, has compounded
388 concerns among some countries of both a loss of control over national patrimony and the
389 management of global resources and a loss of opportunity to reap benefits¹⁰⁹.

390 Scientists and policymakers have noted the importance of respecting such concerns and avoiding
391 inequitable exploitation – commercial or otherwise – while also ensuring that scientific progress can
392 continue with as few impediments as possible. Some have criticized the Nagoya Protocol for
393 inadvertently hampering taxonomic research and international collaborations¹¹⁰, while being unable
394 to enforce meaningful benefits sharing. Others have underscored that UNCLOS ensures freedom to
395 undertake scientific research, including in ABNJ (Articles 256-257)¹¹¹ while still others have rejected
396 the legitimacy of legal claims that arise from marine scientific research (Article 241), including in the
397 form of intellectual property rights¹¹². The outcome of the BBNJ negotiations (see Box 1) has the
398 potential to not only strike this balance for ABNJ, but also to illustrate alternative pathways for
399 regulating the use and circulation of genetic resources internationally.

400 Conclusion

401 The future state of ocean ecosystems will depend in large part on recognizing that human activity
402 has already substantially eroded the ocean genome and that this has been to the detriment of the
403 biosphere, humanity and other life forms. Encouraging signals are emerging, including recent calls
404 to move beyond current international targets by ensuring that in the future at least 30% of the
405 ocean is fully or highly protected⁸⁸, the declaration of a UN Decade of Ocean Science for Sustainable
406 Development (2021-2030), and the consensus decision among UN member states to move forward
407 with negotiating a legally-binding instrument for conservation and sustainable use of BBNJ. Yet
408 human impacts on the ocean are growing alongside accelerating commercial use of its resources
409 and space^{53,113}, while the potential for new industries such as mining of the international seabed and

410 methane hydrates pose vast risks for the ocean genome⁶². Ensuring that the ocean genome is
411 conserved will require effective regulation and governance based on inclusive and iterative dialogue
412 processes that connect diverse stakeholders, are based on principles of fairness, equity and
413 inclusivity, and are informed by the latest scientific techniques and knowledge of the ocean genome.

414

415

BOX 1: Negotiations on Biodiversity in Areas Beyond National Jurisdiction (BBNJ)

Some 36% of the ocean falls within exclusive economic zones (EEZs) within which states are granted a broad range of sovereign rights to make decisions related to the conservation and management of resources (UNCLOS, Article 57). The remaining 64% of the ocean is described as areas beyond national jurisdiction (ABNJ), comprised of the water column (“The High Seas”) and the seabed and ocean floor beyond the limits of national jurisdiction (“The Area”). Multiple sectoral organizations exist with mandates to govern resources or activities in ABNJ, including a network of regional fisheries management organizations (RFMOs) under the Food and Agriculture Organization of the UN, the International Seabed Authority (for seabed mining), and the International Maritime Organization (for shipping). Recognizing that this landscape of sectoral organizations has been insufficient for addressing the full range of issues of relevance to BBNJ, states reached consensus with a UN General Assembly resolution (72/249) in December 2017 to initiate an intergovernmental conference with the aim to “elaborate the text of an international legally-binding instrument on the conservation and sustainable use of [BBNJ]”. The BBNJ negotiations are focused around a “package” of four topics, all of relevance to the ocean genome, namely:

- marine genetic resources (MGR), including questions on the sharing of benefits;
- measures such as area-based management tools, including MPAs;
- environmental impact assessments;
- capacity-building and the transfer of marine technology.

Negotiations related to MGR have proven complex due to the issues covered in this review relating to informational and physical aspects of MGR and conditions for equitable access and benefit sharing. The latter has been further hampered by a tendency for States to view MGR through the lens of contrasting regimes, namely “freedom of the high seas” or the “common heritage of [hu]mankind”. The former implies a continuation of the liberal access regime that currently prevails in ABNJ and an absence of benefit-sharing obligations, while the latter would see changes to both to reflect a view that MGR from ABNJ are owned by all. Pragmatic approaches have sought to establish common ground between these positions, particularly by shifting focus from sharing of potential monetary benefits of commercial activity to emphasize the range of associated non-monetary benefits. For a detailed account of the BBNJ negotiations, their history, and negotiating positions, see Wright et al⁹¹.

416

417

418

419

420

BOX 2: The future of the ocean genome

Ensuring that the ocean genome is both preserved and used in a sustainable, fair and equitable manner is critical and requires effective conservation in both protected areas and beyond. It will also depend on operative national and transnational legal measures being in place to ensure incentives for research and development as well as equitable technology diffusion. Within this space, emerging opportunities exist for exploration, research, innovation, and investment. These include:

- 1) **Building knowledge of the ocean genome:** Increasing governmental and philanthropic support for basic taxonomic research as well as comprehensive assessments of the risks of transgenic marine organisms and other uses of new technologies to facilitate both effective conservation and sustainable use.
- 2) **Protecting marine genetic diversity and monitoring outcomes:** Management efforts that conserve marine genetic diversity should be supported by existing international commitments, including a particular focus on protecting areas of high biodiversity via fully and highly protected areas. Strategic Environmental Assessments and monitoring programs provide opportunities to report and revise national biodiversity strategies and action plans.
- 3) **Embedding ocean genome conservation within research and commercialization:** Benefits from ocean genome exploration and use would be enhanced by requiring equitable research partnerships between high- and low-income countries and through disclosure of the origin of genetic material as well as an explanation of the potential conservation and equity outcomes of commercialization.
- 4) **Supporting greater equity in genomics research and commercialization:** Incorporating marine science capacity building, information exchange, collaboration, and appropriate technology transfer into national research policies, plans and programs can benefit from the involvement of users and providers of marine genetic resources, who can work to set fair agreements on benefit sharing and technology transfer.
- 5) **Promoting inclusive and responsible research and innovation:** A transparent and interactive process can facilitate benefit-sharing and equitable outcomes by engaging multiple stakeholders, including private sector entities and scientists, with a view to the ethical acceptability, environmental sustainability and social desirability of the innovation process, and a focus on benefits for under-represented, marginalized, and vulnerable communities.

421

422 Acknowledgement

423 The author group was assembled under the auspices of the High-Level Panel for a Sustainable
424 Ocean Economy, and provided with support to produce a paper titled "The ocean genome:
425 conservation and the fair equitable and sustainable use of marine genetic resources", on which this
426 review heavily draws. The authors wish to thank the editors as well as three anonymous reviewers
427 for constructive input, and J. Lokrantz (Azote) and J.B. Jouffray for their support with
428 conceptualizing and designing figures.
429

430 Correspondence

431 All correspondence and requests for materials should be addressed to Robert Blasiak
432 (robert.blasiak@su.se)
433

434 **Competing interests**

435 M.J. is founder of, shareholder in and consultant for 'GyreOx Ltd' which uses marine and terrestrial
436 enzymes for the rapid production of complex molecules to target protein-protein interactions
437 involved in disease. S.T. has participated in the BBNJ negotiations as a Pacific Islands Forum Adviser.

438 **Author contributions**

439 R.B., R.W., K.G.-C., S.T., N.M.B., A.V.M.C., J.D.S., C.M.D., M.J., A.R., K.S. and C.C.C.W. all
440 contributed to the writing and reviewing of this manuscript.

441

442

443 **REFERENCES**

444

445 1. Strother, P. K., Battison, L., Brasier, M. D. & Wellman, C. H. Earth's earliest non-marine
446 eukaryotes. *Nature* **473**, 505–509 (2011).

447 2. Louca, S., Mazel, F., Doebeli, M. & Parfrey, L. A census-based estimate of Earth's
448 bacterial and archaeal diversity. *PLOS Biology* **17**, (2019).

449 3. Jaume, D. & Duarte, C. M. General aspects concerning marine and terrestrial biodiversity.
450 *The Exploration of Marine Biodiversity—Scientific and Technological Challenges. Bilbao:*
451 *Fundación BBVA* 17–30 (2006).

452 4. Bar-On, Y. M., Phillips, R. & Milo, R. The biomass distribution on Earth. *Proceedings of*
453 *the National Academy of Sciences* **115**, 6506–6511 (2018).

454 5. Cobián Güemes, A. G. *et al.* Viruses as Winners in the Game of Life. *Annual Review of*
455 *Virology* **3**, 197–214 (2016).

456 6. Locey, K. J. & Lennon, J. T. Scaling laws predict global microbial diversity. *Proceedings*
457 *of the National Academy of Sciences* **113**, 5970–5975 (2016).

458 7. Mora, C., Tittensor, D. P., Adl, S., Simpson, A. G. B. & Worm, B. How Many Species
459 Are There on Earth and in the Ocean? *PLOS Biology* **9**, e1001127 (2011).

460 8. Reed, D. H. & Frankham, R. Correlation between Fitness and Genetic Diversity.
461 *Conservation Biology* **17**, 230–237 (2003).

- 462 9. Blasiak, R. *et al.* *The Ocean Genome: Conservation and the Fair, Equitable and*
463 *Sustainable Use of Marine Genetic Resources.* (High Level Panel for a Sustainable Ocean
464 Economy, 2020).
- 465 10. Gibson, D. G. *et al.* Creation of a bacterial cell controlled by a chemically synthesized
466 genome. *Science* **329**, 52–56 (2010).
- 467 11. Hutchison, C. A. *et al.* Design and synthesis of a minimal bacterial genome. *Science* **351**,
468 (2016).
- 469 12. Blasiak, R., Jouffray, J.-B., Wabnitz, C. C., Sundström, E. & Österblom, H. Corporate
470 control and global governance of marine genetic resources. *Science advances* **4**, eaar5237
471 (2018).
- 472 13. Blasiak, R. International regulatory changes poised to reshape access to marine genes.
473 *Nature biotechnology* **37**, 357 (2019).
- 474 14. Webster, M. S. *et al.* Who Should Pick the Winners of Climate Change? *Trends in*
475 *Ecology & Evolution* **32**, 167–173 (2017).
- 476 15. Schindler, D. E. *et al.* Population diversity and the portfolio effect in an exploited species.
477 *Nature* **465**, 609–612 (2010).
- 478 16. Ruzzante, D. E. *et al.* Biocomplexity in a highly migratory pelagic marine fish, Atlantic
479 herring. *Proc. Biol. Sci.* **273**, 1459–1464 (2006).
- 480 17. Reynolds, P. L., Richardson, J. P. & Duffy, J. E. Field experimental evidence that grazers
481 mediate transition between microalgal and seagrass dominance. *Limnology and*
482 *Oceanography* **59**, 1053–1064 (2014).
- 483 18. Reynolds, L. K., McGlathery, K. J. & Waycott, M. Genetic Diversity Enhances
484 Restoration Success by Augmenting Ecosystem Services. *PLOS ONE* **7**, e38397 (2012).
- 485 19. Jin, P. & Agustí, S. Fast adaptation of tropical diatoms to increased warming with trade-
486 offs. *Sci Rep* **8**, 1–10 (2018).

- 487 20. Norström, A. V. *et al.* Guiding coral reef futures in the Anthropocene. *Frontiers in*
488 *Ecology and the Environment* **14**, 490–498 (2016).
- 489 21. Morikawa, M. K. & Palumbi, S. R. Using naturally occurring climate resilient corals to
490 construct bleaching-resistant nurseries. *Proceedings of the National Academy of Sciences*
491 **116**, 10586–10591 (2019).
- 492 22. Ziegler, M., Seneca, F. O., Yum, L. K., Palumbi, S. R. & Voolstra, C. R. *Bacterial*
493 *community dynamics are linked to patterns of coral heat tolerance. Nat Commun* **8**:
494 *14213*. (2017).
- 495 23. Sjöqvist, C. O. & Kremp, A. Genetic diversity affects ecological performance and stress
496 response of marine diatom populations. *ISME J* **10**, 2755–2766 (2016).
- 497 24. Brown, E. R., Cepeda, M. R., Mascuch, S. J., Poulson-Ellestad, K. L. & Kubanek, J.
498 Chemical ecology of the marine plankton. *Natural Product Reports* **36**, 1093–1116
499 (2019).
- 500 25. Puglisi, M. P., Sneed, J. M., Sharp, K. H., Ritson-Williams, R. & Paul, V. J. Marine
501 chemical ecology in benthic environments. *Natural Product Reports* **31**, 1510–1553
502 (2014).
- 503 26. Kuhlisch, C. & Pohnert, G. Metabolomics in chemical ecology. *Natural Product Reports*
504 **32**, 937–955 (2015).
- 505 27. Rogers, A. D. *The Deep: The Hidden Wonders of Our Oceans and How We Can Protect*
506 *Them*. (Wildfire, 2019).
- 507 28. El Samak, M., Solyman, S. M. & Hanora, A. Antimicrobial activity of bacteria isolated
508 from Red Sea marine invertebrates. *Biotechnol Rep (Amst)* **19**, e00275 (2018).
- 509 29. Tortorella, E. *et al.* Antibiotics from deep-sea microorganisms: Current discoveries and
510 perspectives. *Marine Drugs* **16**, 355 (2018).

- 511 30. Tincu, J. A. & Taylor, S. W. Antimicrobial peptides from marine invertebrates.
512 *Antimicrobial agents and chemotherapy* **48**, 3645–3654 (2004).
- 513 31. Pal, A. & Paul, A. K. Microbial extracellular polymeric substances: central elements in
514 heavy metal bioremediation. *Indian J Microbiol* **48**, 49–64 (2008).
- 515 32. Wilkes, R. A. & Aristilde, L. Degradation and metabolism of synthetic plastics and
516 associated products by *Pseudomonas* sp.: capabilities and challenges. *Journal of applied*
517 *microbiology* **123**, 582–593 (2017).
- 518 33. MarinLit. A database of marine natural products literature. (2019).
- 519 34. Clinical Pipeline.
520 <https://www.midwestern.edu/departments/marinepharmacology/clinical-pipeline.xml>.
- 521 35. Gerwick, W. H. & Moore, B. S. Lessons from the past and charting the future of marine
522 natural products drug discovery and chemical biology. *Chem. Biol.* **19**, 85–98 (2012).
- 523 36. Leal, M. C., Puga, J., Serôdio, J., Gomes, N. C. M. & Calado, R. Trends in the Discovery
524 of New Marine Natural Products from Invertebrates over the Last Two Decades – Where
525 and What Are We Bioprospecting? *PLOS ONE* **7**, e30580 (2012).
- 526 37. Suleria, H. A. R., Osborne, S., Masci, P. & Gobe, G. Marine-Based Nutraceuticals: An
527 Innovative Trend in the Food and Supplement Industries. *Mar Drugs* **13**, 6336–6351
528 (2015).
- 529 38. Rodolfi, L. *et al.* Microalgae for oil: strain selection, induction of lipid synthesis and
530 outdoor mass cultivation in a low-cost photobioreactor. *Biotechnol. Bioeng.* **102**, 100–112
531 (2009).
- 532 39. Chauton, M. S., Reitan, K. I., Norsker, N. H., Tveterås, R. & Kleivdal, H. T. A techno-
533 economic analysis of industrial production of marine microalgae as a source of EPA and
534 DHA-rich raw material for aquafeed: research challenges and possibilities. *Aquaculture*
535 **436**, 95–103 (2015).

- 536 40. Jaspars, M. *et al.* The marine biodiscovery pipeline and ocean medicines of tomorrow.
537 *Journal of the Marine Biological Association of the United Kingdom* **96**, 151–158 (2016).
- 538 41. Cambon-Bonavita, M. A., Raguenes, G., Vincent, P. & Guezennec, J. A novel polymer
539 produced by a bacterium isolated from a deep-sea hydrothermal vent polychaete annelid.
540 *Journal of Applied Microbiology* **93**, 310–315 (2002).
- 541 42. Smith, M. D., Asche, F., Guttormsen, A. G. & Wiener, J. B. Genetically modified salmon
542 and full impact assessment. *Science* **330**, 1052–1053 (2010).
- 543 43. Waltz, E. First genetically engineered salmon sold in Canada. *Nature News* **548**, 148
544 (2017).
- 545 44. Zhu, B. & Ge, W. Genome editing in fishes and their applications. *Gen. Comp.*
546 *Endocrinol.* **257**, 3–12 (2018).
- 547 45. Otts, S. S. US regulatory framework for genetic biocontrol of invasive fish. *Biological*
548 *invasions* **16**, 1289–1298 (2014).
- 549 46. Van Eenennaam, A. L., Wells, K. D. & Murray, J. D. Proposed US regulation of gene-
550 edited food animals is not fit for purpose. *npj Science of Food* **3**, 1–7 (2019).
- 551 47. Shahidi, F. & Ambigaipalan, P. Novel functional food ingredients from marine sources.
552 *Current Opinion in Food Science* **2**, 123–129 (2015).
- 553 48. Beygmoradi, A. & Homaei, A. Marine microbes as a valuable resource for brand new
554 industrial biocatalysts. *Biocatalysis and Agricultural Biotechnology* **11**, 131–152 (2017).
- 555 49. Guedes, A. C., Amaro, H. M., Sousa-Pinto, I. & Malcata, F. X. Chapter 16 - Algal spent
556 biomass—A pool of applications. in *Biofuels from Algae (Second Edition)* (eds. Pandey,
557 A., Chang, J.-S., Soccol, C. R., Lee, D.-J. & Chisti, Y.) 397–433 (Elsevier, 2019).
558 doi:10.1016/B978-0-444-64192-2.00016-0.
- 559 50. Leary, D., Vierros, M., Hamon, G., Arico, S. & Monagle, C. Marine genetic resources: A
560 review of scientific and commercial interest. *Marine Policy* **33**, 183–194 (2009).

- 561 51. Roque, B. M., Salwen, J. K., Kinley, R. & Kebreab, E. Inclusion of *Asparagopsis armata*
562 in lactating dairy cows' diet reduces enteric methane emission by over 50 percent.
563 *Journal of Cleaner Production* **234**, 132–138 (2019).
- 564 52. Carpenter, L. J. & Liss, P. S. On temperate sources of bromoform and other reactive
565 bromine gases. *Journal of Geophysical Research: Atmospheres* **105**, 20539–20547 (2000).
- 566 53. Jouffray, J.-B., Blasiak, R., Norström, A. V., Österblom, H. & Nyström, M. The Blue
567 Acceleration – The Trajectory of Human Expansion into the Ocean. *One Earth* (2020)
568 doi:10.1016/j.oneear.2019.12.016.
- 569 54. McCauley, D. J. *et al.* Marine defaunation: Animal loss in the global ocean. *Science* **347**,
570 1255641 (2015).
- 571 55. Johnson, B. M., Kemp, B. M. & Thorgaard, G. H. Increased mitochondrial DNA diversity
572 in ancient Columbia River basin Chinook salmon *Oncorhynchus tshawytscha*. *PLOS ONE*
573 **13**, e0190059 (2018).
- 574 56. Pinsky, M. L., Eikeset, A. M., McCauley, D. J., Payne, J. L. & Sunday, J. M. Greater
575 vulnerability to warming of marine versus terrestrial ectotherms. *Nature* **569**, 108 (2019).
- 576 57. Poloczanska, E. S. *et al.* Responses of Marine Organisms to Climate Change across
577 Oceans. *Front. Mar. Sci.* **3**, (2016).
- 578 58. Hoffmann, A. A. & Sgrò, C. M. Climate change and evolutionary adaptation. *Nature* **470**,
579 479–485 (2011).
- 580 59. Provan, J. & Maggs, C. A. Unique genetic variation at a species' rear edge is under threat
581 from global climate change. *Proc. Biol. Sci.* **279**, 39–47 (2012).
- 582 60. Fleming, I. A. *et al.* Lifetime success and interactions of farm salmon invading a native
583 population. *Proceedings of the Royal Society of London. Series B: Biological Sciences*
584 **267**, 1517–1523 (2000).

- 585 61. Glover, K. A. *et al.* Half a century of genetic interaction between farmed and wild
586 Atlantic salmon: Status of knowledge and unanswered questions. *Fish and Fisheries* **18**,
587 890–927 (2017).
- 588 62. Van Dover, C. L. *et al.* Biodiversity loss from deep-sea mining. *Nature Geoscience* **10**,
589 464–465 (2017).
- 590 63. Sigwart, J. D. *et al.* Red Listing can protect deep-sea biodiversity. *Nat Ecol Evol* **3**, 1134–
591 1134 (2019).
- 592 64. Waples, R. S., Hindar, K. & Hard, J. J. Genetic risks associated with marine aquaculture.
593 (2012).
- 594 65. Oguz, T. & Velikova, V. Abrupt transition of the northwestern Black Sea shelf ecosystem
595 from a eutrophic to an alternative pristine state. *Marine Ecology Progress Series* **405**,
596 231–242 (2010).
- 597 66. IPBES. *Summary for policymakers of the global assessment report on biodiversity and*
598 *ecosystem services – unedited advance version.* (2019).
- 599 67. Laikre, L. Genetic diversity is overlooked in international conservation policy
600 implementation. *Conservation Genetics* **11**, 349–354 (2010).
- 601 68. Sala, E. *et al.* Assessing real progress towards effective ocean protection. *Marine Policy*
602 **91**, 11–13 (2018).
- 603 69. Sala, E. & Giakoumi, S. No-take marine reserves are the most effective protected areas in
604 the ocean. *ICES J Mar Sci* **75**, 1166–1168 (2018).
- 605 70. Grorud-Colvert, K. *et al.* Marine Protected Area Networks: Assessing Whether the Whole
606 Is Greater than the Sum of Its Parts. *PLOS ONE* **9**, e102298 (2014).
- 607 71. Costello, M. J. Long live Marine Reserves: A review of experiences and benefits.
608 *Biological Conservation* **176**, 289–296 (2014).

- 609 72. Hughes, T. P. *et al.* Global warming transforms coral reef assemblages. *Nature* **556**, 492–
610 496 (2018).
- 611 73. Barshis, D. J. *et al.* Genomic basis for coral resilience to climate change. *Proceedings of*
612 *the National Academy of Sciences* **110**, 1387–1392 (2013).
- 613 74. Tinacci, L. *et al.* DNA barcoding for the verification of supplier’s compliance in the
614 seafood chain: How the lab can support companies in ensuring traceability. *Ital J Food*
615 *Saf* **7**, (2018).
- 616 75. Djurhuus, A. *et al.* Evaluation of marine zooplankton community structure through
617 environmental DNA metabarcoding. *Limnology and Oceanography: Methods* **16**, 209–
618 221 (2018).
- 619 76. Lewin, H. A., Robinson, G. E., Kress, W. J., Baker, W. J. & Coddington, J. Earth
620 Biogenome Project: Sequencing Life for the Future of Life. *Proceedings of the National*
621 *Academy of Sciences* **115**, 4325–4333.
- 622 77. Moitinho-Silva, L., Nielsen, S., Amir, A. & Gonzalez, A. The sponge microbiome project.
623 *GigaScience* **6**, (2017).
- 624 78. Thompson, L. R., Sanders, J. G., McDonald, D. & Amir, A. A communal catalogue
625 reveals Earth’s multiscale microbial diversity. *Nature* **551**, 457–463 (2017).
- 626 79. Ainsworth, T. D., Krause, L., Bridge, T., Torda, G. & Raina, J. B. The coral core
627 microbiome identifies rare bacterial taxa as ubiquitous endosymbionts. *The ISME journal*
628 **9**, 2261–2274 (2015).
- 629 80. Ardura, A. *et al.* eDNA and specific primers for early detection of invasive species—A
630 case study on the bivalve *Rangia cuneata*, currently spreading in Europe. *Marine*
631 *Environmental Research* **112**, 48–55 (2015).

- 632 81. Simmons, M., Tucker, A., Chadderton, W. L., Jerde, C. L. & Mahon, A. R. Active and
633 passive environmental DNA surveillance of aquatic invasive species. *Can. J. Fish. Aquat.*
634 *Sci.* **73**, 76–83 (2015).
- 635 82. Baird, D. J. & Hajibabaei, M. Biomonitoring 2.0: a new paradigm in ecosystem
636 assessment made possible by next-generation DNA sequencing. *Molecular ecology* **21**,
637 2039–2044 (2012).
- 638 83. Bakker, J. *et al.* Environmental DNA reveals tropical shark diversity in contrasting levels
639 of anthropogenic impact. *Scientific reports* **7**, 16886 (2017).
- 640 84. Weltz, K. *et al.* Application of environmental DNA to detect an endangered marine skate
641 species in the wild. *PLOS ONE* **12**, e0178124 (2017).
- 642 85. Jeunen, G.-J. *et al.* Environmental DNA (eDNA) metabarcoding reveals strong
643 discrimination among diverse marine habitats connected by water movement. *Molecular*
644 *Ecology Resources* **19**, 426–438 (2019).
- 645 86. Caplan, A. L., Parent, B., Shen, M. & Plunkett, C. No time to waste—the ethical
646 challenges created by CRISPR. *EMBO reports* **16**, 1421–1426 (2015).
- 647 87. National Academies of Sciences, E. *A Research Review of Interventions to Increase the*
648 *Persistence and Resilience of Coral Reefs*. (2018). doi:10.17226/25279.
- 649 88. O’Leary, B. C. *et al.* Effective coverage targets for ocean protection. *Conservation Letters*
650 **9**, 398–404 (2016).
- 651 89. Laird, S. & Wynberg, R. Bioscience at a Crossroads: Implementing the Nagoya Protocol
652 on Access and Benefit Sharing in a Time of Scientific. *Technological and Industry*
653 *Change* (2012).
- 654 90. Morgera, E. Fair and equitable benefit-sharing in a new treaty on marine biodiversity: a
655 principled approach towards partnership building? *Maritime Safety and Security Law*
656 *Journal* **5**, 48–77 (2018).

- 657 91. Muir, P. *et al.* The real cost of sequencing: scaling computation to keep pace with data
658 generation. *Genome Biology* **17**, 53 (2016).
- 659 92. Greiber, T. *An explanatory guide to the Nagoya Protocol on access and benefit-sharing*.
660 (IUCN, 2012).
- 661 93. Oldham, P., Hall, S. & Forero, O. Biological Diversity in the Patent System. *PLOS ONE*
662 **8**, e78737 (2013).
- 663 94. Hendriks, I. E. & Duarte, C. M. Allocation of effort and imbalances in biodiversity
664 research. *Journal of Experimental Marine Biology and Ecology* **360**, 15–20 (2008).
- 665 95. Stokstad, E., 2018 & Pm, 12:00. Norwegian billionaire funds deluxe deep ocean research
666 ship. *Science / AAAS* [https://www.sciencemag.org/news/2018/11/norwegian-billionaire-](https://www.sciencemag.org/news/2018/11/norwegian-billionaire-funds-deluxe-deep-ocean-research-ship)
667 [funds-deluxe-deep-ocean-research-ship](https://www.sciencemag.org/news/2018/11/norwegian-billionaire-funds-deluxe-deep-ocean-research-ship) (2018).
- 668 96. Kyeremeh, K. *et al.* Making North–South Collaborations Work: Facilitating Natural
669 Product Drug Discovery in Africa. in *Africa and the Sustainable Development Goals* (eds.
670 Ramutsindela, M. & Mickler, D.) 257–266 (Springer International Publishing, 2020).
671 doi:10.1007/978-3-030-14857-7_24.
- 672 97. Mueller, M. R. *Genetic Resources as Natural Information Implications for the*
673 *Convention on Biological Diversity and Nagoya Protocol*. (Routledge, 2015).
- 674 98. Green, E. D., Rubin, E. M. & Olson, M. V. The future of DNA sequencing. *Nature News*
675 **550**, 179 (2017).
- 676 99. Laird, S. & Wynberg, R. A Fact-Finding and Scoping Study on Digital Sequence
677 Information on Genetic Resources in the Context of the Convention on Biological
678 Diversity and the Nagoya Protocol. *Secretariat of CBD* 2–79 (2018).
- 679 100. Carradec, Q. *et al.* A global ocean atlas of eukaryotic genes. *Nat Commun* **9**, 1–13
680 (2018).

- 681 101. Gregory, A. C. *et al.* Marine DNA Viral Macro- and Microdiversity from Pole to Pole.
682 *Cell* **177**, 1109-1123.e14 (2019).
- 683 102. Angrist, M. & Cook-Deegan, R. ‘Distributing the Future: The Weak Justifications for
684 Keeping Genomic Databases Secret and the Challenges and Opportunities in Reverse
685 Engineering them. *Applied and Translational Genomics* **3**, 124–127 (2014).
- 686 103. Österblom, H. *et al.* Towards Ocean Equity. (2020).
- 687 104. Heeks, R., Amalia, M., Kintu, R. & Shah, N. Inclusive innovation: definition,
688 conceptualisation and future research priorities. *development informatics working paper*
689 (2013).
- 690 105. Foster, C. & Heeks, R. Conceptualising Inclusive Innovation: Modifying Systems of
691 Innovation Frameworks to Understand Diffusion of New Technology to Low-Income
692 Consumers. *Eur J Dev Res* **25**, 333–355 (2013).
- 693 106. Von Schomberg, R. A Vision of Responsible Research and Innovation. in *Responsible*
694 *Innovation. Managing the responsible emergence of science and innovation in society* 51–
695 74 (Wiley, 2013).
- 696 107. Broggiato, A., Arnaud-Haond, S., Chiarolla, C. & Greiber, T. Fair and equitable
697 sharing of benefits from the utilization of marine genetic resources in areas beyond
698 national jurisdiction: Bridging the gaps between science and policy. *Marine Policy* **49**,
699 176–185 (2014).
- 700 108. Blasiak, R., Jouffray, J.-B., Wabnitz, C. C. & Österblom, H. Scientists Should
701 Disclose Origin in Marine Gene Patents. *Trends in ecology & evolution* **34**, 392–395
702 (2019).
- 703 109. Elbe, S. & Buckland-Merrett, G. Data, disease and diplomacy: GISAID’s innovative
704 contribution to global health. *Global Challenges* **1**, 33–46 (2017).

- 705 110. Deplazes-Zemp, A. *et al.* The Nagoya Protocol could backfire on the Global South.
706 *Nat Ecol Evol* **2**, 917–919 (2018).
- 707 111. Vierros, M., Suttle, C. A., Harden-Davies, H. & Burton, G. Who Owns the Ocean?
708 Policy Issues Surrounding Marine Genetic Resources. *Limnology and Oceanography*
709 *Bulletin* **25**, 29–35 (2016).
- 710 112. Thambisetty, S. 'Biodiversity Beyond National Jurisdiction: (Intellectual) Property
711 Heuristics. in *Biodiversity Beyond National Jurisdiction: Intractable Challenges &*
712 *Potential Solutions* (Brill Nijhoff, 2020).
- 713 113. Halpern, B. S. *et al.* Recent pace of change in human impact on the world's ocean. *Sci*
714 *Rep* **9**, 1–8 (2019).
- 715 114. NCBI. Sequence Read Archive. <https://trace.ncbi.nlm.nih.gov/Traces/sra/sra.cgi?>
716 (2020).
- 717 115. Wetterstrand, K. A. DNA Sequencing Costs: Data from the NHGRI Genome
718 Sequencing Program (GSP). (2020).

719

720

721 **Figure captions**

722 **FIGURE 1: A portfolio approach for conserving the ocean genome and its associated benefits.**
723 *Effective conservation hinges on using multiple tools, including area-based conservation measures such*
724 *as fully and highly protected marine protected areas (MPAs), that provide the greatest protection from*
725 *the impacts of extractive and destructive activities. Coupling these with effective management of*
726 *sustainable use can ensure wide-ranging benefits that are ecological, sustaining, provisional and*
727 *commercial.*

728

729 **FIGURE 2: (A) Decline in average sequencing costs (cost per raw megabase of DNA sequence)¹¹⁴; (B)**
730 **Growth in GenBank Sequence Read Archive (cumulative number of open access base pairs)¹¹⁵**

731

732 **FIGURE 3: Risk profit margins and timelines for commercial activities based on marine genetic resources**

733

734