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Conserving Genetic and Genomic Diversity in Accordance with the Global Biodiversity Framework

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Abstract

Adopted in December 2022, the Kunming–Montreal Global Biodiversity Framework (KMGBF) under the Convention on Biological Diversity outlines a visionary road map guiding humanity's relationship with nature. KMGBF commitments require active intervention, sustained monitoring and scientific reporting, capacity building for tools and technologies, and cooperation among 196 signatories. Genetic diversity, which underlies adaptation and fitness, is a core tenet of the KMGBF. This article aims to distill the KMGBF to help researchers, practitioners, and other interested parties achieve its commitments. In five sections, we address (*a*) the KMGBF's terminology and scope, (*b*) the intersection of KMGBF targets with genetic diversity, (*c*) genetic monitoring for tracking its progress, (*d*) paradigms and decision frameworks to guide genetic conservation actions, and (*e*) emerging frontiers. A better understanding of the KMGBF will help researchers, practitioners, and other interested parties more effectively engage and fulfill global, national, and local commitments to the conservation of our planet's biodiversity.

1. INTRODUCTION

Genetic/genomic diversity (GD; see the sidebar titled What We Mean by "Genetic Diversity" in This Article) is important for individual fitness (1, 2), adaptation within species in response to changing environments (3), and resilience of ecosystem processes (4, 5). GD (e.g., heterozygosity and allelic richness) of many wild species has declined in recent decades (e.g., 6), and models predict greater upcoming declines through habitat loss and population size reductions (7, 8). Local extinctions, reduced population sizes, and disruption of genetic connectivity mean that many remaining populations have insufficient genetically effective population sizes (Ne) to maintain adaptive evolution (e.g., 9, 10).

The need for policy and legal frameworks to better conserve GD has been highlighted increasingly for more than 15 years (e.g., 11). A landmark step occurred in December 2022 when the Convention on Biological Diversity (CBD)'s Kunming–Montreal Global Biodiversity Framework (KMGBF) made commitments to conserve and restore GD within and among populations of all species—an outcome that was the consequence of 3+ years of sustained outreach, advising, relationship building, and advocacy by a group of conservation geneticists (12). These commitments will require active intervention and sustained monitoring and reporting, leveraging scientific knowledge, new and emerging tools, capacity building, and cooperation. This article first explains the KMGBF's terminology and scope (in Section 2) and how its various targets (especially Target 4) are an important, albeit imperfect, step change for conservation (Section 3). In Section 4 we explain monitoring approaches for tracking progress toward KMGBF commitments, under the categories of DNA-based monitoring and proxy- or indicator-based monitoring. Section 5 explains the current state of knowledge on how a continuum of actions can help achieve the goals of the KMGBF, as well as paradigms and practices to guide those actions. Section 6 summarizes

Kunming–Montreal Global Biodiversity Framework (KMGBF): international agreement to halt and reverse biodiversity loss, with four global goals for 2050 and 23 targets for 2030

Indicator: a simple summary of the state of a system, in this context a component of biodiversity; may leverage and summarize EBVs

WHAT WE MEAN BY "GENETIC DIVERSITY" IN THIS ARTICLE

In this article we use "genetic diversity," or GD, as in Article 2 of the Convention for Biological Diversity, "diversity within species." This article does not cover genetic variation above the species level, such as phylogenetic diversity. We also note that not all aspects of GD relate to DNA sequencing techniques (e.g., GD can be assessed in some cases by measuring phenotypes, tracking pedigrees), and not all DNA sequencing techniques relate to GD within species. For example, molecular methods for detecting environmental DNA (eDNA), like metabarcoding and metagenomics, usually use DNA sequences to assess presence/absence of biological entities at or above the species level, typically with insufficient resolution to quantify GD within species. Very few studies have estimated diversity within species from eDNA samples, nor is it yet possible to use eDNA in the field to reliably obtain even coarse measures of population abundance (149).

a few key emerging frontiers and tools that could significantly advance GD conservation. It is important for researchers to understand this policy landscape in order to effectively contribute to biodiversity commitments at global, national, and local levels. This can result in science-informed policy and policy-relevant science.

UN Framework Convention on Climate Change (UNFCCC): UN convention to combat climate change and limit greenhouse gas emissions

2. GLOBAL BIODIVERSITY FRAMEWORK

2.1. Structure of the CBD

In this section, we cover the history of the CBD, the major components of the KMGBF and similar multinational environmental agreements, and important terminology throughout the article.

The CBD is an international treaty devised in 1992 at the Earth Summit in Rio de Janeiro, Brazil. It has been ratified by 196 parties (195 countries and the European Union), making it the foremost mechanism for global biodiversity policy. It has three objectives: conservation of biological diversity; sustainable use of biodiversity; and fair, equitable sharing of the benefits arising from the use of genetic resources. The CBD is analogous to the UN Framework Convention on Climate Change (UNFCCC): Both are framework conventions that define overall goals, procedures, and guidance for addressing their respective global challenges. Implementation of these and similar conventions is guided by several governing bodies, whose members are primarily political appointees representing each party: the Conference of the Parties (COP) and two subsidiary bodies [Subsidiary Body on Scientific, Technical and Technological Advice (SBSTTA) and Subsidiary Body on Implementation (SBI)] (see **Figure 1** and **Supplemental Table 1**). Other constituent groups, such as academia and research, Indigenous Peoples and Local Communities

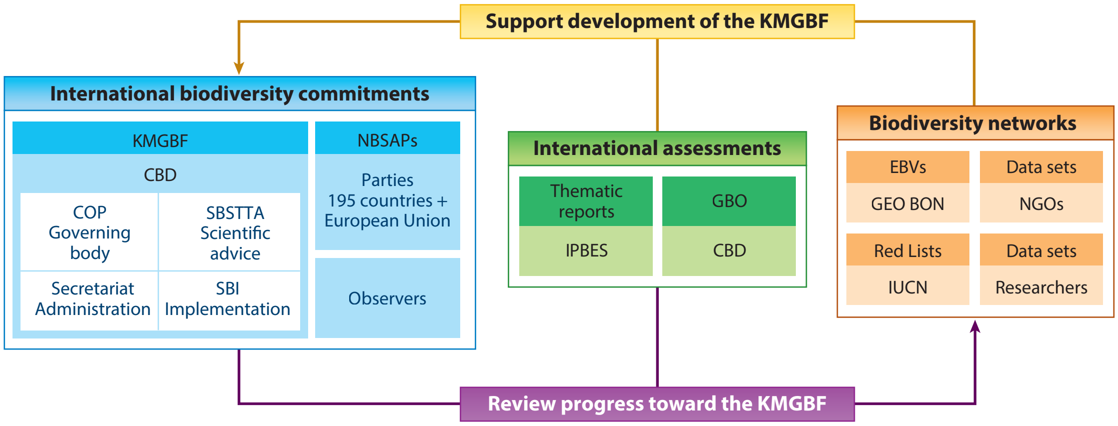


Figure 1

Connections among international biodiversity policy actors and outputs relevant to the KMGBF. Actors are denoted in light boxes, and outputs are denoted in dark boxes. International biodiversity commitments (*blue*), such as the KMGBF, are negotiated, adopted, and then implemented by parties. Implementation occurs through nationally set targets and activities (NBSAPs). Observers (non-party members) can inform the commitments and the NBSAPs. Global biodiversity assessments helped inform the KMGBF and will help ensure that parties progress toward KMGBF goals and targets, identify where data gaps exist, and subsequently revise strategies or develop tools to address gaps (*green*). Biodiversity networks help inform the development of the KMGBF with available science (*orange*). See **Supplemental Table 1** for more information on these actors, their roles, and the outputs they produce. Abbreviations: CBD, Convention on Biological Diversity; COP, Conference of the Parties; EBV, Essential Biodiversity Variable; GBO, Global Biodiversity Outlook; GEO BON, Group on Earth Observations Biodiversity Observation Network; IPBES, Intergovernmental Science-Policy Platform on Biodiversity and Ecosystem Services; IUCN, International Union for Conservation of Nature; KMGBF, Kunming–Montreal Global Biodiversity Framework; NBSAP, National Biodiversity Strategies and Action Plan; NGO, nongovernmental organization; SBI, Subsidiary Body on Implementation; SBSTTA, Subsidiary Body on Scientific, Technical and Technological Advice.

(IPLCs), nongovernmental organizations (NGOs), the private sector, and youth and women, may also participate as observers. The COP is the main decision-making body and meets (every two years for the CBD, and annually for the UNFCCC) to review progress toward biodiversity commitments, negotiate and adopt new policies, determine financial needs, and engage with civil society (including NGOs, business, academia and research, social movements, and individuals). The SBSTTA provides scientific and technical guidance to the COP, such as assessing biodiversity knowledge and its relation to biodiversity commitments and recommending monitoring strategies and tools. On occasion, the SBSTTA establishes short-term, smaller bodies called Ad Hoc Technical Expert Groups on specific topics. The SBI reviews how effectively parties contribute to CBD commitments, to help improve national biodiversity strategies and funding mechanisms.

Observer: in the context of the CBD, a non-party participant offers input, expertise, and stakeholder perspectives but does not have voting rights

Access and benefit sharing (ABS): specifically refers to how genetic resources may be accessed and the benefits that result from their use are shared

KMGBF targets: a set of 23 action-oriented measures to be implemented by 2030 aimed at halting biodiversity loss and ensuring sustainable ecosystem management

Cali Fund: established by the CBD in 2024 to finance biodiversity conservation by collecting contributions from companies using digital sequence information

Aichi Targets: established in 2010 by the CBD; set of 20 targets within the Strategic Plan for Biodiversity 2011–2020

Under the CBD, two supplementary legal agreements address specific challenges: the Cartagena Protocol on Biosafety (adopted in 2000) and the Nagoya Protocol on Access to Genetic Resources and the Fair and Equitable Sharing of Benefits Arising from their Utilization (adopted in 2010) (**Supplemental Table 1**). The Cartagena Protocol regulates handling and movement of genetically modified organisms (also known as living modified organisms). The Nagoya Protocol aims to ensure fair and equitable sharing of benefits arising from the use of genetic resources, including the use of traditional knowledge associated with these resources, through prior informed consent. Such benefits may be monetary (sharing of profits) or nonmonetary (e.g., building capacity, transferring technology, sharing and interpreting research findings). Genetic resources are defined under Nagoya as "any nonhuman material that contains functional units of heredity and has actual or potential value" (13).

Typically, the term genetic resources has been associated with physical specimens (13); however, policy discussions have examined how digital sequence information (DSI; see **Figure 2** and the sidebar titled What Is DSI, and How Does It Relate to GD?) might be incorporated into access and benefit sharing (ABS) mechanisms given DSI's increasing utility in advancing science, medicine, agriculture, and industry. Consequently, at COP15 in 2022, after extensive discussions with the scientific community and considering various policy options, parties to the CBD established a multilateral mechanism (involving multiple countries) for benefit sharing from use of DSI instead of a bilateral one (country to country) typically applied under Nagoya. The goal is to maintain open access to DSI while ensuring benefit sharing (following FAIR and CARE data principles; see the sidebars titled FAIR and CARE Data Principles and Co-Creation of GD Research with IPLCs and **Supplemental Appendix 3**), supporting scientific research and allowing DSI to contribute to conservation and sustainable use of biodiversity (14). This is important because DSI has a role in achieving many of the 23 KMGBF targets (15). At COP16 in 2024, the CBD defined specific modalities of this mechanism, detailing how benefits from DSI use can be shared, and established the Cali Fund (16). For a more detailed history of DSI within the CBD, see **Supplemental Appendix 1**.

The KMGBF builds on two prior sets of negotiated goals and targets: Strategic Plan 2002–2010 (adopted at COP6 in 2002) (17) and Strategic Plan 2011–2020 (i.e., the Aichi Targets adopted at COP10 in 2010) (18). Alongside the KMGBF runs a set of complementary actions under the Global Strategy for Plant Conservation (GSPC) (19) (**Figure 1**). The targets from the 2002–2010 and 2011–2020 Strategic Plans and the GSPC were, at best, only partially achieved (e.g., 20, 21). Under increasing pressures (e.g., fish trawling, human appropriation of primary net productivity), downward trends continue in most biodiversity indicators (e.g., the Red List Index, sustainable fish stocks; see the sidebar titled What Is the Difference Between an Essential Biodiversity Variable and an Indicator?) despite increasing monetary investment in conservation and protected area coverage (e.g., 20, 22). This failure to stabilize humanity's impact on nature has been attributed to weak political commitment, inadequate funding and resources, interdependencies and sometimes

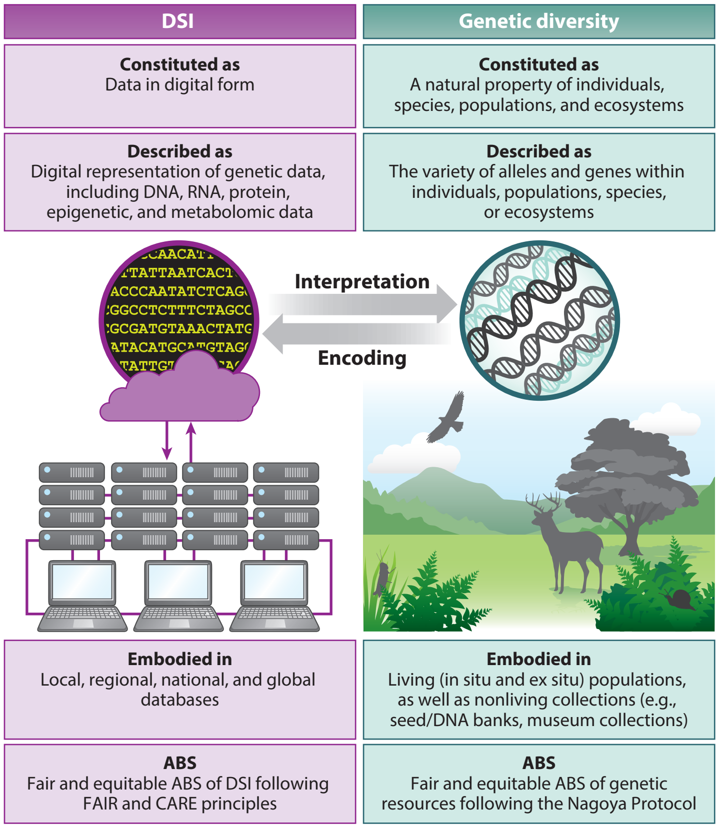


Figure 2

Distinctions between DSI (*left*) and genetic diversity (*right*). Gray arrows show information flow between the two (e.g., interpretation means the analysis, interpretation, and use for conservation and management of genetic diversity; encoding means the transcription of genetic diversity data into readable computer files; also see the sidebar titled What Is DSI, and How Does It Relate to GD?). Abbreviations: ABS, access and benefit sharing; CARE, collective benefit, authority to control, responsibility, and ethics; DSI, digital sequence information; FAIR, findable, accessible, interoperable, and reusable.

conflicts among targets, vague language in commitments, insufficient or absent indicators to measure progress, and the CBD Frameworks' failures to address the underlying drivers of biodiversity loss (e.g., 11, 23, 24). The KMGBF was envisioned to address some of these failures, although it is an imperfect attempt to do so (e.g., 25).

2.2. The KMGBF Commitments and Biodiversity Reporting Mechanisms

The KMGBF was referred to as "the Paris moment for biodiversity," referencing the UNFCCC Paris 2016 climate commitments. The KMGBF vision is to live in harmony with nature by 2050, with four long-term goals: (*a*) protect and restore ecosystems, species, and genetic diversity; (*b*) sustainably use and manage biodiversity; (*c*) fairly and equitably share benefits arising from the use of biodiversity; and (*d*) sustainably finance and support the implementation of the KMGBF through capacity building, technical and scientific cooperation, and access to technology (12). These goals are linked with the UN Sustainable Development Goals in that biodiversity supports food and water security, health and well-being, climate resilience, sustainable economies, and reducing poverty

Sustainable Development Goals (SDGs): global targets set by the United Nations in 2015 to end poverty, protect the planet, and ensure prosperity for all

WHAT IS DSI, AND HOW DOES IT RELATE TO GD?

Digital sequence information (DSI) refers to digital representations of genetic data (e.g., DNA, RNA, protein, epigenetic, metabolomic) from genetic resources like plants, animals, fungi, and microbes. Genetic diversity (GD) is the genetic variation found in individuals, populations, species, and ecosystems (see **Figure 2**). Researchers can generate estimates of GD from DSI to understand how genetic variation is distributed across space and time, making DSI an invaluable tool for informing conservation strategies.

The relevance of DSI extends to international policy on fair and equitable access and benefit sharing (ABS) (see the sidebars titled FAIR and CARE Data Principles and Co-Creation of GD Research with IPLCs and **Supplemental Appendix 1** for the history of DSI within the Convention on Biological Diversity). The recently established DSI multilateral mechanism means that all researchers can support fair and equitable ABS by providing country of origin and traditional knowledge information when submitting DSI, following FAIR and CARE data principles (see the sidebar titled Fair and Care Data Principles), involving local researchers and knowledge holders (see the sidebar titled Co-Creation of GD Research with IPLCs), translating their findings to the public, and supporting capacity building (see 150 for more practical research implications).

FAIR AND CARE DATA PRINCIPLES

Researchers are increasingly called upon to enable fair and equitable collection, storage, access, and use of data. Findable, accessible, interoperable, and reusable (FAIR) data principles were developed to enable data reuse, transparency, and innovation (151) and have been translated into best practices for genetic/genomic diversity (GD) data (62). However, FAIR data principles do not account for Indigenous data sovereignty: the right for Indigenous Peoples and Local Communities to control how their data—including the knowledge associated with it—are collected, stored, accessed, and used. Such omission increases the risk of biopiracy (unauthorized commercialization of Indigenous genetic resources), data misuse (use of Indigenous genetic resources beyond the original intent), and loss of control (unauthorized distribution of Indigenous genetic resources). In response, CARE (collective benefit, authority to control, responsibility, and ethics) data principles were developed to be people and purpose orientated (152, 153), enabling ethical research partnerships and benefit sharing beyond monetary compensation (154–156). FAIR and CARE are reflected in the Nagoya Protocol and in research practice (157–159; see the sidebar titled Co-Creation of GD Research with IPLCs).

and inequality (see **Supplemental Appendix 2**). To help meet these goals, 23 ambitious, measurable, and diverse action targets were formulated, covering areas such as actions to halt and reverse biodiversity loss; enhance financial commitments; eliminate harmful subsidies; acknowledge and protect the rights of IPLCs; and engage all of society, including the private sector, civil society, academia, and government. Of note, although the CBD is an international treaty, there is no cost or penalty for noncompliance; the CBD was put into place to enable, foster, and track collective voluntary action in good faith. Achieving the KMGBF requires the resources (financial, capacity, skills) and political will of each party.

To track progress toward KMGBF goals and targets, a Monitoring Framework comprising measurable indicators was developed (26). Indicators were chosen under criteria including scientific rigor (well-defined and tested methods, transparency, peer-review, repeatability, robustness), ease of understanding and interpretation, applicability at national and global scales, and clear alignment with associated goals or targets (27). Indicators from previous CBD Frameworks lacked some of these attributes (28). Parties are expected to report on the state of indicators from

CO-CREATION OF GD RESEARCH WITH IPLCS

Effective research partnerships are built on trust and respect, which includes embracing diverse knowledge systems and valuing the contributions of diverse knowledge holders, including Indigenous Peoples and Local Communities (IPLCs) (160, 161). Established biocultural protocols (which reflect biological, cultural, and linguistic diversity; 162) exist to help define customary laws, values, and traditions and can help guide such partnerships (e.g., 163–165). When absent, research teams may co-adapt existing frameworks or cocreate new ones. For example, an iterative decision-making framework was cocreated that embedded Indigenous principles across the research cycle to ensure that research was responsive to the needs and aspirations of the Indigenous research partners (166). This included generating genetic/genomic diversity (GD) data to inform translocations of a Critically Endangered freshwater fish endemic to Aotearoa, New Zealand. Researchers adapted existing frameworks to weave place-based knowledge and Western science to help interpret GD data for a culturally significant freshwater crayfish (156). For further details, see **Supplemental Appendix 3**.

WHAT IS THE DIFFERENCE BETWEEN AN ESSENTIAL BIODIVERSITY VARIABLE AND AN INDICATOR?

Essential Biodiversity Variables (EBVs) and biodiversity indicators serve different but complementary roles. EBVs are standardized measurements that capture key aspects of biodiversity (e.g., species abundance, ecosystem structure, genetic diversity). They provide a consistent framework to integrate and compare data across regions, timescales, and monitoring programs. EBVs are directly calculated from raw data on biodiversity (e.g., genetic EBVs are calculated from a data set of DNA data).

In contrast, indicators are higher-level metrics designed to be simple and easily communicable, helping policymakers and the public understand trends and make informed decisions. They are often derived from EBVs or other data, sometimes through models or comparisons to thresholds. They may be tailored to assess progress toward specific conservation goals (e.g., Kunming–Montreal Global Biodiversity Framework goals or Sustainable Development Goals).

Whereas EBVs are used mainly by scientists and data managers to harmonize biodiversity observations and advance biodiversity science, indicators are used mainly by governments, nongovernmental organizations, and international organizations for reporting and policy evaluation and for biodiversity management and decision-making. EBVs emphasize ecological accuracy and scientific rigor, whereas indicators prioritize clarity, relevance, and usability for nonexpert audiences. Effective population size (Ne) is an EBV, whereas the proportion of populations with Ne > 500 is an indicator.

the Monitoring Framework (26) by submitting National Reports to the CBD in 2026 and 2029. To facilitate progress toward the KMGBF via setting of national priorities and initiatives, parties must also develop and submit National Biodiversity Strategy and Action Plans (NBSAPs), which include nationally relevant targets aligned to the KMGBF, plans for achieving them, and national institutions responsible for implementation (**Figure 1**). As of May 2025, 53 post-2020 NBSAPs have been submitted (**https://ort.cbd.int/nbsaps**).

At critical time points, another important document, the Global Biodiversity Outlook (GBO), produced by the CBD Secretariat (permanent UN staff and contractors in Montreal, Canada), summarizes current data on biodiversity status and trends and draws conclusions relevant to further the Convention's implementation (**Figure 1**). This report draws on scientific reports; NBSAPs; National Reports submitted by parties, including reported indicators; and reports from the Intergovernmental Science-Policy Platform on Biodiversity and Ecosystem Services (IPBES),

National Reports: official documents submitted to the CBD every 4–6 years detailing each party's progress in implementing biodiversity commitments

International Union for Conservation of Nature (IUCN), Group on Earth Observations Biodiversity Observation Network (GEO BON), and others (**Figure 1**; see **Supplemental Table 1** for details on IPBES, IUCN, GEO BON, and other actors).

National Biodiversity Strategy and Action Plan (NBSAP): national strategy outlining how a country will conserve and sustainably use biodiversity; updated versions must be submitted to the CBD following the adoption of a new global framework

Aichi Target 13: Aichi target on GD of cultivated species and wild relatives, including socioeconomically and culturally valuable species

Global Biodiversity Information Facility (GBIF): international network and research infrastructure making species biodiversity data freely and universally available, including taxonomic classification and georeferenced occurrence data (gbif.org)

3. WHERE GENETIC DIVERSITY FITS IN THE KMGBF

This section focuses on where and how GD is explicitly mentioned in, or relevant to, KMGBF targets, including where GD conservation or knowledge of GD are not mentioned but could help achieve a target.

3.1. Prior to and During Negotiations of the KMGBF

The conservation or maintenance of GD was part of the 2002–2010 and 2010–2020 Strategic Plans, especially Aichi Target 13. However, CBD commitments prior to 2020 were concerned primarily with the GD of cultivated plants, farmed and domesticated animals, their wild relatives, and other socioeconomically or culturally valuable species. Likewise, indicators for GD prior to 2020 focused on varieties of crops and domesticated animals and long-term, ex situ storage of genetic resources. This limited scope neglected wild populations' GD and evolutionary processes, meaning that conserving the GD of the vast majority of species on earth was not part of international commitments.

Conservation geneticists have worked intensively for 15 years to engage with policy such as the CBD. Since 2010, researchers have pointed out opportunities for including GD processes, knowledge, or data in IUCN Red List Assessments, Global Biodiversity Information Facility (GBIF) data storage, the Millenium Ecosystem Assessment, the CBD, the United Nations (UN) Environment Program, Global Environment Facility funding mechanisms, EU legislation, and indicator development initiatives (29). An assessment of National Reports submitted to the CBD found that countries acknowledged the importance of gene-level variation for species' survival and evolution, but most did not explicitly include GD in conservation strategies and monitoring programs (11). Reasons for this included lack of relevant indicators, limited recognition of the need for genetic monitoring, and inadequate support from international authorities. Likewise, impediments and opportunities were identified within international and EU biodiversity policies for conserving the evolutionary processes that generate and maintain GD with implications for biodiversity, climate change, agriculture, fisheries, and water management (30). The underrepresentation of evolutionary concepts in policy was also quantified in a survey of conservation policy documents: While ∼75% mentioned GD, only 17% discussed evolution and adaptation (31).

Leading up to the KMGBF, an evaluation was undertaken to assess how 57 countries reported on GD in 114 National Reports (submitted between 2014 and 2020) to the CBD (32). Although most countries recognized the importance of GD, they often considered it only in the context of agricultural species and undertook little to no DNA-based monitoring. Moreover, countries mostly reported on actions focused on ex situ gene banks or research institutes, rather than in situ actions for genetic management, with some notable exceptions.

Motivated by the fact that negotiations of the framework started in early 2020 with no mention of GD in the first (i.e., zero) draft of the post-2020 Targets, several conservation genetic networks (IUCN, Society of Conservation Biology, GEO BON, G-BiKE) formed the Coalition for Conservation Genetics [CCG (33)] and worked in two ways to help ensure that the framework would conserve GD of wild populations of all species.

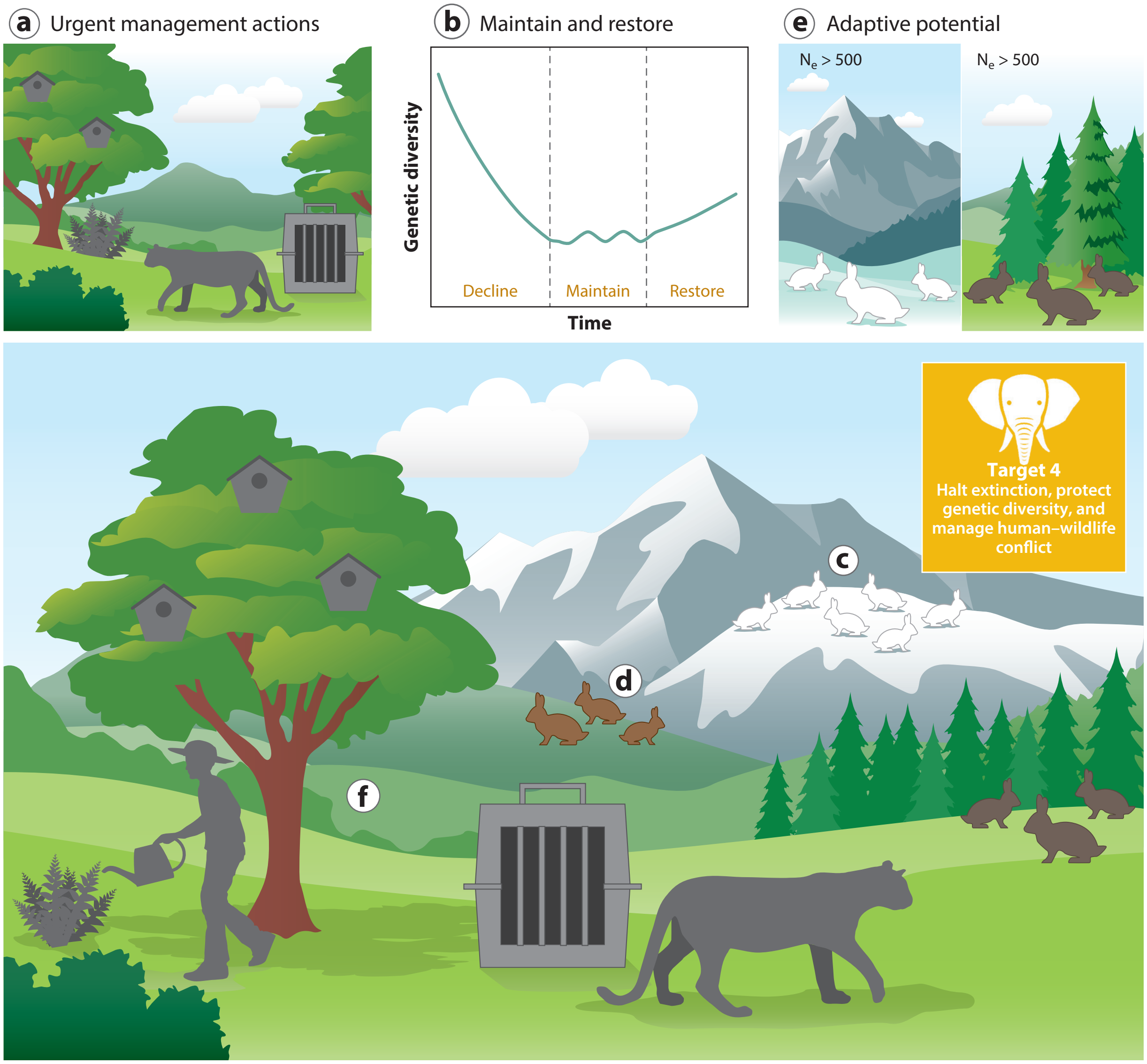
First, two indicators for GD within and among wild populations (8, 34) were designed, piloted, improved with stakeholder involvement, and upscaled to demonstrate their use in multiple countries on a scale approximating that needed for National Reports (10): (*a*) the proportion of populations maintained within species and (*b*) the proportion of populations with an Ne greater than 500 (Section 4.2 provides detail). These indicators had to be developed quickly and demonstrated in advance of COP15 (late 2022), because early negotiations (circa 2020) indicated that each target must have indicators ready for use with demonstrated affordability and feasibility for all countries, be established, and have peer-reviewed methodology. Without demonstrated indicators, it is unlikely GD would have been represented adequately in the KMGBF.

Second, the CCG actively interfaced with CBD decision-makers including parties, NGOs, and the CBD Secretariat to propose and advocate for clear wording of genetic goals and targets. Engagement included drafting potential target text, publishing and disseminating peer-reviewed scientific articles aimed at policy audiences and policy briefs in many languages (see Related Resources), hosting webinars and discussion panels, submitting responses to requests from CBD bodies (e.g., SBSTTA) for comments on draft target text, and liaising with CBD parties at in-person and hybrid meetings of SBSTTA and other CBD meetings (e.g., 32, 35, 36). It was vital for researchers to provide and revise possible text for the KMGBF, and reply to policymakers' requests, because GD's relative complexity meant that policymakers were challenged in composing scientifically defensible commitments around it.

3.2. Explicit References to Genetic Diversity in the Final Version of the KMGBF

The most explicit mention of GD in the KMGBF is in Goal A|Target 4: "Ensure urgent management actions. . .to maintain and restore the genetic diversity within and between populations of native, wild and domesticated species to maintain their adaptive potential." To "maintain genetic diversity" essentially means preserving current alleles, genotypes, and genetic differences among populations (**Figure 3**). However, biodiversity is naturally dynamic, and some level of genetic change is natural, including loss of alleles due to genetic drift and gain of alleles by mutation or immigration. Thus, "maintain and restore genetic diversity" also encompasses foundational concepts of conservation genetics: ensuring continued response to natural selection through sufficient levels of variation for adaptation and natural patterns of gene flow (37). The phrase "within and among populations" refers to two components of GD, variation within populations (e.g., levels of heterozygosity, Ne) and differences among populations (underpinning local adaptations and distinct evolutionary histories). "Adaptive potential" is the extent to which species or populations can respond to future environmental change. It is contributed to by within-population diversity, which (along with other factors, notably Ne, see Section 4) controls the speed of adaptation, as well as among-population diversity, which determines divergent natural selection and the total breadth of conditions in which a species can exist. Lastly, "active management" refers to actions such as conservation translocations, habitat restoration, and population size and/or genetic augmentation that help maintain, and in some cases restore, GD (Section 5).

Goal A and Target 4 represent a compromise of scientifically sound proposals and political requests reflecting each party's national priorities (25), which resulted in some deficiencies in the policy commitments. For example, key terms were omitted, such as protected (e.g., through policy or legislation), monitored (with indicators and/or DNA-based research), and gene flow/genetic connectivity (via genetic exchange among populations, via restoring habitat connectivity or implementing periodic translocations). The absence of these concepts, along with critical phenomena such as hybridization and inbreeding, from Target 4 and others (e.g., Targets 1–3, 5, 9, 12) could result in parties overlooking these elements (35, 36). Additionally, no quantitative targets (e.g., maintain X% of heterozygosity) are proposed for retaining GD, although these were suggested in early negotiations. Numerical levels are not present in most KMGBF targets, due to political resistance, the challenge of determining what level of loss is acceptable, and the complexity of biodiversity metrics.



Target 4

Ensure urgent management actions ⓐ to halt human-induced extinction of known threatened species and for the recovery and conservation of species, in particular threatened species, to significantly reduce extinction risk, as well as to **maintain and restore** ⓑ the genetic diversity **within** ⓒ **and between** ⓓ **populations** of native, wild and domesticated species to maintain their **adaptive potential** ⓔ, including through **in situ and ex situ conservation and sustainable management practices** ⓕ, and effectively manage human–wildlife interactions to minimize human–wildlife conflict for coexistence.

*(Caption for **Figure 3** appears on following page)*

Figure 3 (*Figure appears on preceding page*)

Visual depiction of key text in Kunming–Montreal Global Biodiversity Framework Target 4: Ensure urgent management actions (*a*) to halt human-induced extinction of known threatened species and for the recovery and conservation of species, in particular threatened species, to significantly reduce extinction risk, as well as to maintain and restore (*b*) the genetic diversity within (*c*) and between (*d*) populations of native, wild, and domesticated species to maintain their adaptive potential (*e*), including through in situ and ex situ conservation and sustainable management practices (*f*), and effectively manage human–wildlife interactions to minimize human–wildlife conflict for coexistence. Abbreviation: Ne, effective population size. The elephant head logo associated with Target 4, featured on the CBD official webpage (**https://www.cbd.int/gbf/targets/4**), is used with the permission of the CBD Secretariat.

3.3. How Genetic Diversity Relates to Elements of the KMGBF Other Than Goal A|Target 4

In addition to Target 4, GD and evolutionary processes are integral to achieving other KMGBF targets, with evolutionary considerations capable of benefiting numerous societal problems (e.g., 38). We first address targets falling under the theme "reducing threats to biodiversity" (Targets 1–8). Ecosystem restoration (Target 2) is typically more successful (greater population persistence) when restoration stocks have higher GD, originate from multiple source populations, and/or have larger Ne (e.g., 39–41). Mitigation of climate change (Target 8) can benefit from adaptation of wild and domestic populations, which is promoted by high GD (42, 43). Appropriate GD can also help reduce carbon emissions (e.g., via trees and other plants that sequester more carbon and animals that emit less methane). Protected areas (Target 3) could also be designed or enhanced to protect genetic biodiversity (44, 45).

Other examples of the relevance of evolutionary genetic concepts to KMGBF targets fall under sustainable use and benefit sharing (Targets 9–13) and tools and solutions for implementation and mainstreaming (e.g., putting into action and integrating biodiversity through all aspects of society, Targets 14–23). Sustainable harvest (Target 10) should not only avoid extinction of a given stock or population but also prevent major, human-induced phenotypic change [e.g., ovids evolving small horns under hunting pressure (46) or fish evolving small body size and shy behavior through harvesting (47)]. Strengthening capacity building, technology transfer, and scientific cooperation (Target 20) should include helping all countries to assess and interpret DNA-based data. Meanwhile, businesses that might directly impact GD (e.g., through habitat changes, deforestation, pollution including climate-changing emissions) could report GD as part of disclosure of their dependencies and impacts on biodiversity (Target 15) (48).

Further clues to how GD relates to KMGBF targets can be found in the NBSAPs that parties are required to submit. An examination of 12 recent (post-KMGBF) and older NBSAPs found numerous examples in which some countries strongly focused on genetic resources and agriculture, while other countries focused on conserving or restoring GD in wild populations (49). Some examples include mentioning genetic connectivity, managing adaptive capacity of populations, restoring ecosystems with genetically diverse individuals, and recognizing the importance of GD during a time of climate change. The authors then devised 10 suggestions on how countries can better account for GD in their NBSAPs, mapped to the CBD's policy cycle (setting national targets, actions and policies, monitoring and review).

4. MONITORING GENETIC DIVERSITY STATUS AND TRENDS FOR REPORTING UNDER THE KMGBF

This section explains how nations can effectively use two approaches in measuring and monitoring GD to achieve the KMGBF: direct assessment of DNA sequences with population genetic methods and indirect assessment based on measuring the processes that produce GD change (see 50 for advantages of each).

4.1. Monitoring with DNA-Based Data

Single-nucleotide polymorphism (SNP): nucleotide variation in the DNA sequence within and between individuals, and therefore useful for genetic/genomic research

Essential Biodiversity Variables (EBVs): standardized and scalable metrics directly summarizing raw data to track core components (genetics, species, ecosystems) of biodiversity change

Resequenced genomes: the entire genome sequence of individuals or populations of a species to identify genetic variations compared to a reference genome

DNA sequences or other heritable molecular markers [e.g., isozymes, microsatellites, single-nucleotide polymorphisms (SNPs), insertions/deletions] have been used for ∼60 years to assess genetic variation. Briefly, this involves sampling biological material that contains DNA (blood, tissue, leaves, hair, feces), extracting DNA, sequencing or otherwise examining its variation, analyzing this variation statistically, and interpreting it. DNA-based approaches are often used for genetic assessment, especially in species of economic or ecological importance (e.g., large carnivores, harvested fish, game) and/or threatened species [e.g., *Lynx lynx* (Eurasian lynx; 51), various fishes (52)]. Levels of GD and degree of populations' genetic distinctiveness are often assessed to inform management and track gene flow, whether regarded as positive (genetic rescue) or harmful (swamping, whereby a target gene pool is overwhelmed, e.g., swamping of alleles, which is a concern in rare taxa, or the movement of alleles from domestic varieties into wild populations). For example, DNA-based data were used to monitor the genetic impacts of fencing and translocations of *Panthera leo* (lion) and guide future translocations (53). Monitoring is also important in captive populations and restocking to ensure recovery efforts, maintain GD, and prevent increased inbreeding (e.g., 54).

Most genetic assessments are snapshots of one time point. However, monitoring change in genetic parameters is achieved most readily with DNA from multiple time points, like from long-term studies or museum collections, in which levels of GD in historic samples are compared to levels of GD in contemporary samples, which may reveal loss, maintenance, or restoration (e.g., 55). Unfortunately, most investigators lack temporally stratified samples (from multiple generations), and specialized laboratories may be required to process ancient and historical samples (56, 57). Nonetheless, some species have attracted considerable genetic sampling over long periods (especially in some birds, and fish-scale collections) sufficient to detect changes in GD (e.g., 58, 59). Temporal studies have often found loss of GD driven by habitat degradation or direct exploitation such as whaling or industrial fishing (e.g., 60, 61). The frequency of temporal monitoring required varies depending on generation times; for long-lived species, monitoring GD of offspring can be useful.

The designation of four genetic Essential Biodiversity Variables (EBVs) [GD, genetic structure, inbreeding, and Ne (34)] advanced standardized reporting of GD statistics and change over time (see the sidebar titled What Is the Difference Between an Essential Biodiversity Variable and an Indicator?). EBVs are meant to represent basic dimensions of an element of biodiversity. EBV reporting can be standardized via the adoption of best practices developed to compare DNA data across studies, including data archiving (62).

Large-scale assessments of DNA data vary among taxonomic groups and by geographic locale. For example, genetic monitoring efforts are often lacking at species' climatic niche margins, which can be reservoirs of adaptive potential. This suggests a need for investments in GD monitoring (63, 64). There are challenges with DNA-based monitoring, including expense, time, equipment, and technical expertise (65). Initiatives are producing genomic data at large scales that can inform EBVs and establish baseline data for future comparisons, though still for relatively few species. For example, the Genomics of Brazilian Biodiversity initiative is sequencing >1,000 resequenced genomes in a country with more than 117,096 known animal species (66). Genetic information is available for less than 0.5% of species in major taxonomic groups (only ∼6% of mammal species), and genetic data are geographically biased, with 72% being from North America and Europe (based on >36,000 genotyped populations for terrestrial species) (67). An assessment of genetic indicators found that only 6% of species examined had DNA-based estimates of Ne (10), a moderate improvement over earlier assessments (68).

Even as DNA-based monitoring efforts grow, most countries still lack sufficient funds, infrastructure, and expertise, a situation that could be improved by enhanced collaboration and resource sharing (69). Additionally, with the growth of large genomic data sets, access to specialized infrastructure is still limited globally due to its cost and the expertise needed for data production and processing (70). Global South countries face larger costs for producing and storing DNA data (66, 71) and limited funding for genomic research compared to the Global North (e.g., 70). Upscaling GD monitoring must also overcome challenges including data interoperability, storage, and standard setting in data reporting and processing, including with new workflows and tools (e.g., 72). If DNA-based monitoring is not possible for economic, logistic, or other reasons, viable alternatives exist that can help address KMGBF obligations.

Headline Indicator: high-level indicator used for planning and tracking the progress of KMGBF's goals and targets; mandatory to report on

4.2. Monitoring Using Process-Based Indicators

Considering the challenges for large-scale DNA-based analysis—expense, complexity of statistics, and paucity of temporal samples—scientists devised simple, affordable, easily explained metrics reflecting GD, based on summarizing the major processes that impact GD (35, 73). In addition to being more affordable, monitoring proxies or processes may sometimes reveal genetic health issues more quickly than metrics from DNA-based studies (e.g., changes in genetic structure), because changes in DNA patterns resulting from evolutionary processes can show significant time lags (e.g., 74).

The KMGBF genetic indicators include the proportion of (genetically distinct) populations maintained (PM) and the proportion of populations with an Ne greater than 500 (Ne500). The PM indicator is based on the principle that genetic differences increase with geographic and/or environmental distance between populations, a pattern supported by a century of theoretical and empirical evidence (75). The Ne500 indicator is based on the principle that sufficiently large populations promote enduring maintenance of GD. Below an effective size of ∼500, a population starts to lose GD via inbreeding and genetic drift, which means that gene dynamics are driven more by random effects than by adaptation (76). Ne can be estimated from DNA or from census size (counts or estimates of number of adult individuals), via the rule-of-thumb that Ne is often ∼10–20% of census size (76).

Several papers provided information on the advantages and disadvantages of GD indicators from viewpoints of science and policy (e.g., 77), plans for testing and calculating indicators (e.g., 78), and tools to support implementation (i.e., guidance documents, data-collection tools) (10). Next, to show that the indicators could be deployed at large scale for reporting under the KMGBF, an assessment was undertaken in 919 species (and approximately 5,000 populations) from 9 countries (including megadiverse and Global South ones) representing all continents (10). Data were largely available for many species, with 83% of species having data for at least one indicator. This important study found that most populations of most species assessed were too small to maintain GD. The authors also found that most species had to that point maintained many of their populations, albeit much reduced in size. This means that many current populations are at increased risk of extirpation. The findings were robust, being reached even with moderate Ne/Nc ratios (e.g., 0.3), Ne50 instead of Ne500, and different definitions of populations.

KMGBF signatories are required to report on Headline Indicators, including Ne500. Although its reporting is feasible (10), countries whose biodiversity personnel lack sufficient time and support may be challenged. Still, we anticipate that many countries will at least attempt to calculate this indicator for the 2026 reporting. Usefully, the same protocol, data-collection tools, and framework can be used to collect both the Ne500 and PM indicators (see Related Resources). Genetic indicators could be reported alongside DNA-based assessments, which are already mentioned in some NBSAPs and National Reports (e.g., 50, 79, 80). Ongoing work is further testing the indicators in more countries, at different scales, and in countries with very low resources.

Complementary indicator: an optional indicator for supplementary analysis of Headline Indicators, providing a thematic or in-depth analysis of KMGBF's goals and targets

The KMGBF also contains complementary indicators of GD (26). First is the scorecard (81), which qualitatively assesses genetic risks and the effectiveness of actions to mitigate genetic threats. This scorecard was deployed in Scotland for 26 species (81). One advantage of the scorecard is that it considers several dimensions of genetic health (e.g., hybridization, low recruitment), while one disadvantage is that it is only qualitative, not quantitative. Another indicator is the comprehensiveness metric, which measures the genetic representation of species in protected areas (in situ) or seed banks (ex situ). Its advantage is high scalability: It has been applied to thousands of plants in specific countries and globally and could also apply to animals (82). Tools are being developed to calculate such metrics in a highly automated way (83, 84). Other measures relating to agricultural breeds and ex situ, long-term storage of genetic resources are also complementary indicators.

5. ACTIONS TO HELP ACHIEVE THE KMGBF (CONSENSUS AND CONTROVERSY)

To help practitioners contribute to meeting the goals and targets of the KMGBF related to GD, we highlight guidance and decision-support tools for management based on several conservation genetic paradigms that have emerged from decades of research and applied conservation (85, 86) (**Figure 4**; see also the sidebar titled Better Integrating Evolutionary Principles into Conservation Management to Protect GD and **Supplemental Appendix 4**). We organize our guidance along a spectrum of intensity of genetic management, from ecosystems to individuals. Each intervention may contribute to achieving multiple KMGBF targets. The organization we use does not reflect the level of financial or other investment (e.g., effective governance and enforcement of protected areas may be expensive compared to some breeding programs).

5.1. Conserving Habitat Conserves Genetic Diversity

A broad-brush approach to protecting GD is habitat maintenance and restoration. Protected areas and other effective area-based conservation measures (OECMs, as defined at COP14 in 2018) should prioritize GD hot spots and areas important for conserving adaptive potential (e.g., 87) whenever possible. For example, researchers in California, USA, examined DNA data sets from 21 vertebrate and invertebrate taxa to identify hot spots of GD, connectivity, and population distinctiveness that could be considered as future protected areas (88). Similarly, a study of 22 vertebrate taxa in Italy identified areas of high GD that could be protected to meet the 30% land/sea commitment by 2030 under the KMGBF (89). Protected areas have also been assessed using the proportion of species' ecogeographic ranges protected—a proxy for GD protection. For example, only 40% of "useful" wild plant species had their GD adequately protected within their natural range (82). A large macrogenetic study of mammals and marine fishes across 2,500 geographic sites found similar levels of GD inside and outside protected areas and across taxa but found that mammal GD was higher nearer to multiple protected areas (90). Overall, the paradigm is that GD can and should be conserved via habitat retention and protection.

5.2. Managing Threats to Help Maintain Large Populations

The next approach to conserving GD is to address immediate threats causing small and/or declining populations (e.g., addressing diseases and invasive species, human–wildlife conflict, overexploitation, and habitat quality). The goal is management to prevent loss of GD in small populations. Recent global analyses of genetic data sets and nongenetic proxies have shown that many populations are below the critical size thresholds needed to maintain GD for future

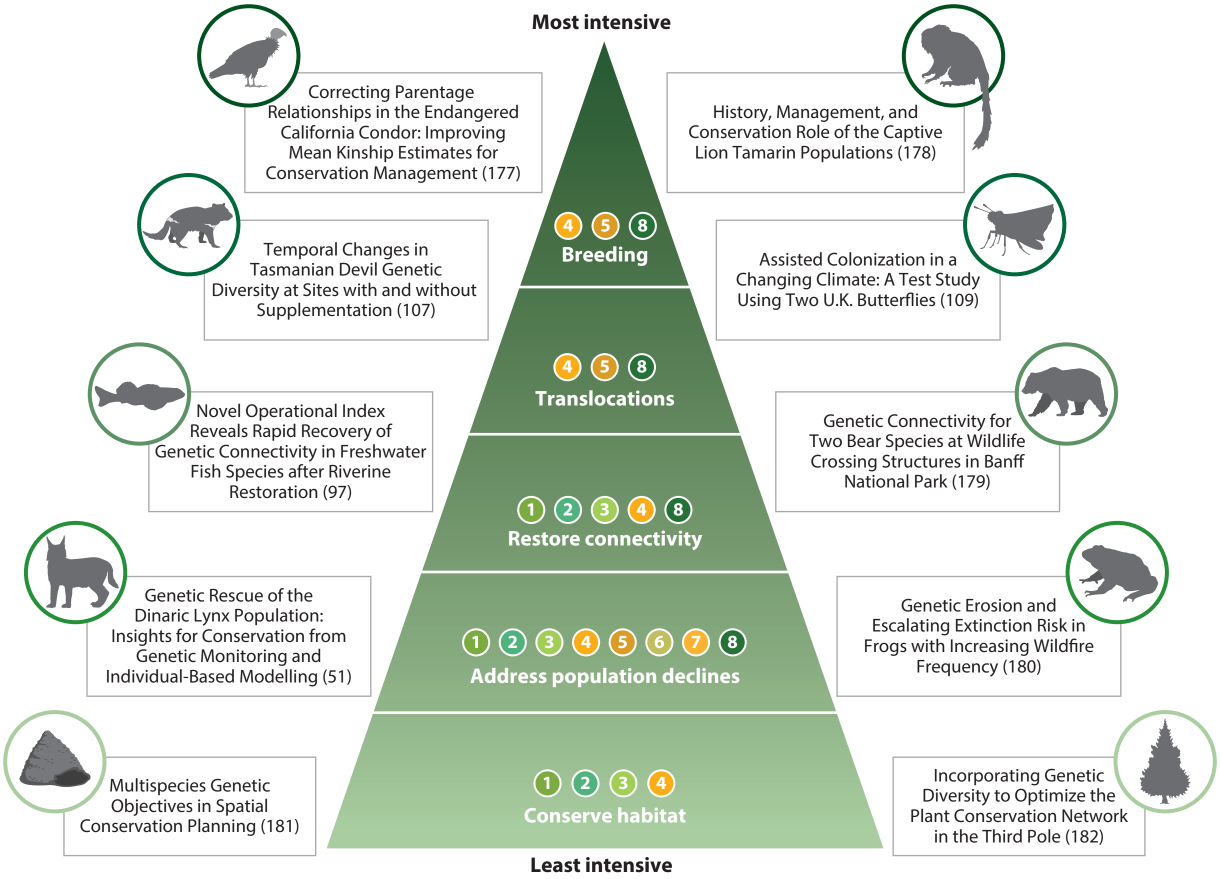


Figure 4

Management actions vary in intensity and impact. In general, the actions that are most impactful on the largest scale (bottom of the triangle) are the least intensive. Circled numbers refer to the most applicable Kunming–Montreal Global Biodiversity Framework targets; color scheme corresponds to **https://cbd.int/gbf/targets/**.

adaptation (9, 10). Species-focused threat management may, in some cases, help a species recover on its own once the threat is removed (91). Although demographic recovery does not necessarily entail full genetic recovery [e.g., *Nesoenas mayeri* (pink pigeon; 92), *Urocyon littoralis* (Channel Island fox; 93)], demographic recovery can halt or slow inbreeding and other genetic problems.

The paradigm is that GD is lost when populations are reduced in size, and this loss typically accelerates each generation that populations remain small due to genetic drift, inbreeding, and declines in fitness (94, 95). Populations whose decline can be reversed typically will experience less inbreeding, slower accumulation of harmful mutations, and fewer negative consequences (e.g., reduced fertility and increased vulnerability to disease) (39, 85, 86).

5.3. Implementing Measures to Maintain or Restore Connectivity

A more intensive intervention is to address habitat fragmentation where populations are surrounded by inhospitable habitat, or where barriers such as urbanization (e.g., fences and highways) have severed a once-continuous population. Restoring genetic connectivity can ameliorate some negative consequences of habitat fragmentation (96), a concept also recognized in the recent

BETTER INTEGRATING EVOLUTIONARY PRINCIPLES INTO CONSERVATION MANAGEMENT TO PROTECT GD

Globally, the integration of genetic/genomic diversity and evolutionary principles into conservation management remains limited (31, 167–169). For example, only half of 318 animal and plant species recovery plans across three continents considered genetic factors, and plans rarely addressed critical issues including fitness, inbreeding (7%), and effective population size (10%) (170). Barriers include limited understanding of evolutionary concepts and limited resources (e.g., funds, personnel) available (56, 171, 172). Training in genetics, including the paradigms in Section 4, and sharing of decision-support tools could improve integration. Managers also appreciate case studies demonstrating, in practical terms, how evolutionarily informed management enhances conservation outcomes (85, 173). Strengthening collaboration between scientists and managers—through projects that are codesigned from the beginning, recognition of the expertise of managers, shared decision-making, and adaptive management frameworks (urgent management is undertaken while filling knowledge gaps)—is another critical approach (31, 174, 175; see the sidebar titled Co-Creation of GD Research with IPLCs). Cross-agency partnerships and genetic scientists embedded in management agencies—increasingly common (176)—also offer opportunities for knowledge sharing and more effective conservation action. For further details, see **Supplemental Appendix 4**.

EU Nature Restoration Law (48). Restored habitat and highway overpasses or underpasses can help some organisms traverse barriers and restore genetic connectivity, as evidenced by DNA studies [e.g., genetic connectivity reestablished in fish species following dam removal (97)]. The paradigm is that restoration of genetic connectivity typically leads to positive outcomes, such as enhanced individual and population fitness, increased evolutionary potential, and reduced probability of population extirpation or extinction (98, 99). Enhancing genetic connectivity will ultimately help maintain populations (as reflected by the PM indicator). Note that genetic drift can cause strong differentiation—especially in small and isolated populations—that may not indicate evolutionary divergence but rather a distorted subset of the historical gene pool. It is imperative to distinguish these two situations (100, 101). Importantly, small patches of habitat, even single trees, can help improve connectivity (102).

The pro-connectivity paradigm contrasts with an older conservation paradigm to keep populations separate (i.e., maintain local gene pools), and many managers remain reluctant to connect populations even to help avoid population extinction (101). The long-held assumption that local genetic lineages are more suited to local conditions is increasingly countered by evidence. This is particularly true as populations and habitats shrink and fragment, while environments change rapidly (100, 103). Occasionally, crossing populations can have negative consequences [e.g., outbreeding depression from crossing *Capra ibex* (Alpine ibex) and *Capra nubiana* (Nubian ibex) (104)], but often distinct populations can be crossed with great benefit. Fortunately, there are risk-assessment approaches for anticipating when problems could arise (98, 105). In contrast, inbreeding and loss of GD are almost always harmful (1).

5.4. Conservation Translocations

Translocations are an intensive, hands-on approach to enhancing connectivity. The potential genetic benefits of moving individuals include increased GD, fitness, and adaptive capacity (106). For example, three out of four immigration-supplemented sites of *Sarcophilus harrisii* (Tasmanian devils) showed positive impacts in GD; the fourth showed declines, underscoring the need to understand levels of gene flow and population sizes (107). Translocation decisions should also be guided by knowledge of historical and evolutionary differences and practical constraints (108).

Additionally, modeling of future conditions is increasingly being used in decision-making, such as predicting suitable sites for two United Kingdom butterfly species, *Melanargia galathea* (marbled white) and *Thymelicus sylvestris* (small skipper). The translocated populations grew and expanded their ranges over six years (109). In another example, reinforcement of *L. lynx* in the Dinaric Alps between 2019 and 2023 was guided by stochastic modeling of the long-term viability of the post-translocation population's genetic health (51). The paradigm is that good candidates for translocation come from populations with similar environments, no major chromosomal differences, and recent connectivity (less than 500 years ago) (110). A corollary is that inbreeding depression is usually worse than outbreeding depression, and that population managers should be liberal when considering source populations (101, 111).

A related paradigm is that long-term monitoring ($\geq$3 generations) is important for assessing the outcome of genetic rescue to help ensure the positive impact is lasting (112, 113). If insufficient, genetic rescue attempts may result in short-term positive impacts followed by a decline due to inbreeding, which may be exacerbated if populations do not grow sufficiently or if reproductive success is highly skewed (114). Scientists have developed empirical and simulation-based tools to determine suitable candidate individuals, and the frequency and number of individuals, for supplementations. For example, past gene flow has been estimated as a recommended target of four effective migrants per generation in genetic rescue of *Lichenostomus melanops cassidix* (helmeted honeyeater), which also set a target of reducing population inbreeding to $F < 0.1$ and maintaining 95% of GD (58). Lastly, translocations should not be guided by gene-targeted conservation for several reasons: Gene-by-environment effects cause genetic variants to have very different consequences in different environments, potentially resulting in unintended outcomes; different mutations or changes in very different pathways can lead to the same adaptation; and many fitness traits are controlled by many genes, subtle shifts in allele frequencies, and regulatory variation more than changes in proteins (115, 116).

Gene-targeted conservation: conservation strategies focusing on preserving or restoring specific genetic variants or alleles that are fitness related and deemed important for species survival

5.5. Captive Breeding and Reintroductions

A highly intensive intervention is ex situ breeding, in which individuals and their GD are managed outside their natural habitat (e.g., in a zoo, garden, or conservancy), ideally with the goal of reintroducing individuals as rapidly as possible. Ex situ breeding helps prevent extinction of species that cannot survive in the wild due to habitat deterioration or other threats. For example, the last 27 living *Gymnogyps californianus* (California condor) were captured in 1987 and bred in captivity to prevent extinction due to habitat loss, lead poisoning, and poaching (117). The population has since increased to more than 500 birds, with many reintroduced into the wild. Ex situ individuals or their offspring can supplement existing wild or captive populations or reestablish populations that become extinct in the wild [e.g., *Gallirallus owstoni* (Guam rail, or ko'ko') (118)]. Primary challenges of ex situ breeding include the economic expenses of zoos and botanic gardens but also genetic considerations (119, 120). Captive breeding programs typically are limited to the GD present in the original founders (and occasionally supplemented), which may be further compromised by genetic drift, inbreeding, and adaptation to captive conditions. Proactive management is required to prevent genetic deterioration (121) or genetic adaptation to captivity so future reintroductions can be successful (122). Ex situ populations traditionally were managed based on pedigree-based estimates of relatedness or direct monitoring of offspring fitness, but genomic estimates are more precise in estimating founder relatedness and correcting mistakes in pedigrees (e.g., misassigned parentage 123, 124). Carefully selecting breeding pairs to minimize kinship (based on pedigrees and DNA-based analysis) will slow the loss of GD relative to random mating or to breeding based on a single trait (125).

Prior to any management intervention, practitioners should set clear goals to clarify values; identify any potentially incompatible goals; and determine appropriate budgets, timelines, and approaches (126). Ideally, all interventions should be accompanied by long-term monitoring because some effects will emerge only after multiple generations (127). Monitoring and adaptive management help conservation actions to proceed despite uncertainty (128, 129). Baseline genetic data should be collected first to inform conservation decisions (e.g., genetic structure, inbreeding) and assist in monitoring change.

6. FRONTIERS

6.1. Standardized Assessment and Monitoring of Genetic Diversity

An important future direction for GD in the context of the KMGBF is to build on the foundations of GD indicators and work toward standardized, globally applicable genetic assessments that can incorporate DNA-based data or pragmatic proxy-based information. A standardized assessment would assist KMGBF constituents, such as NGOs seeking to focus their efforts, industries involved in reclamation/restoration, finance entities involved in biodiversity credits, and national or subnational entities charged with implementing the KMGBF. A standardized assessment might include population genetic/genomic and Ne metrics; metrics of effective reproduction (i.e., evolutionary fitness); metrics of fragmentation and hybridization; and conserving GD with protected areas, biobanks, or seed banks. Such a future assessment tool might consist of single integrative values, suites of metrics, or criteria-based approaches (like the IUCN Red List). Several initiatives using DNA and proxy data to assess genetic risk status of tens to thousands of species have been identified (50). Such work could be upscaled and made more tractable with satellite data assessing population sizes or fragmentation (e.g., 84), machine learning models to estimate threats, and engagement with community knowledge and local citizens who are interested in conservation science. Many aspects of GD (e.g., heterozygosity or genomic load) can be spatially interpolated into a GIS (Geographic Information System) framework via thematic mapping (130, 131).

Meanwhile, there are practical ways in which GD could be incorporated into IUCN's Red List or Green Status (e.g., 132–134). The Red List uses quantitative and qualitative criteria to rank populations and species according to current threat category (e.g., from Least Concern to Critically Endangered), whereas the Green Status measures the degree of recovery toward a desired state. Genetic or genomic data can provide key conservation insights, especially for species that are otherwise data deficient (125, 132). For instance, genetic knowledge and data could be used to estimate the extent of population size reduction, calculate the degree of fragmentation, or enhance quantitative models of extinction probability [e.g., IUCN criteria A (size reduction), B (fragmentation), C and D (number of individuals), and E (simulation model)].

The Green Status could be enhanced with a GD correction because relative GD is associated with population productivity and adaptability (132). This enhancement involved weighting a population's GD against the average GD among related Least Concern species (to correct for inherent differences across organismal groups). Effective size and expected heterozygosity loss over the next century were estimated using population genomic data sets from 80 mammalian species (132). We anticipate increasing use of genetic data in the IUCN Red List and Green Status assessments, and we encourage authorities to harness the conservation value of genetic data whenever available.

One challenge for genetic assessments and for reporting on KMGBF commitments is that genetic indicators are determined on a population level, but a single, standard approach for defining a population is lacking (see **Supplemental Appendix 5** for more detail). Difficulties may arise in defining populations where species have large and continuous distributions, migrate seasonally, or display hierarchical population structure (e.g., rivers within hydrologic basins) or where once-continuous distributions are now fragmented. Guidance and tools have been developed to aid in delimiting populations (10), and additional efforts are underway (e.g., 84).

6.2. Genomic Frontiers

We note three relevant topics for maintaining GD and achieving KMGBF commitments: (*a*) genomic offset, (*b*) genomic load, and (*c*) pangenomics. Genomic offset is a conceptual measure of how far the current genetic composition is from the optimal state predicted for a future population in the face of changing environmental conditions, especially climate change. Larger genomic offset is assumed to relate to decreased likelihood that the population will thrive in the future. Genomic offset has been calculated for dozens of plant and animal populations, facilitated by increasingly available genomic data sets, environmental niche modeling, climate forecasts, and easy-to-use software. For instance, genomic offset was examined in two rosewood tree species (*Dalbergia cochinchinensis* and *Dalbergia oliveri*) in southeast Asia; some populations of *D. cochinchinensis* were identified as having high genomic offset and may therefore benefit from genetically informed translocations or management (135). Gene flow from other species or populations may help reduce genomic offset and reduce vulnerability to projected climate [e.g., rainbowfish (*Melanotaenia* spp.) in Australia (136)]. However, genomic offset uses the unrealistic assumptions that the contemporary gene pool is perfectly adapted to the contemporary environment and perfectly reflected in allele frequencies (137). Accordingly, several studies advise against relying on genomic offset for practical implementation of actions due to its complex relationship with levels of adaptive variation (90), validation difficulties (138), or projected change in niche suitability (139). Nevertheless, those predictions may improve over time and could become important in KMGBF assessments.

Genomic load reflects the degree to which individual genomes contain alleles that may harm fitness. A deleterious allele may have little negative impact on individual fitness if recessive and in a heterozygote (potential or masked load), but in small, inbred populations, where homozygosity is elevated, load can become realized (140, 141). Understanding genomic load could help identify suitable source populations for translocations that are designed to reduce genomic load, as suggested for a quail, *Cyrtonyx montezumae*, in Texas, USA (142), or optimize pairings of mates in ex situ breeding programs, as with *Grus americana* (whooping crane) in the United States (143). There are numerous cautions regarding estimating genetic load, including technical issues (e.g., the choice of reference genome) and biological unknowns (e.g., the variance of load expression in different environments or the genomic architecture of fitness) (144, 145). However, as with genomic offset, many of these concerns may abate with further evidence and validation of predictions. If so, then load metrics (e.g., the change in load over time) may also inform KMGBF assessments.

Pangenomes are alignments of multiple whole-genome sequences that parse variants into those found in every individual (the core genome) and those found in only some individuals (the accessory genome) (146). Pangenomes quantify the spectrum of GD, such as SNPs, in coding and regulatory genes and structural variants such as inversions that often impact fitness [e.g., stress response in high-altitude populations of *Populus pseudoglauce* (Chinese white poplar) (147), *Haemorhous mexicanus* (house finch) disease resistance to a bacterial pathogen (148)]. Assessing pangenomes may benefit the discovery of adaptive traits linked to population resilience with future potential use in achieving CBD commitments.

SUMMARY POINTS

1. It is crucial for researchers to develop a solid understanding of the international biodiversity policy landscape, including Kunming–Montreal Global Biodiversity Framework (KMGBF) goals and targets, to better contribute to global, national, and local legislative commitments.
2. Genomic diversity (GD) should be conserved because scientific knowledge strongly supports its role as a key determinant of individual fitness, population persistence, and ecosystem function, hence its inclusion in the KMGBF.
3. Standardized, globally applicable genetic assessments will assist numerous constituents of the KMGBF, including in industry and finance as well as national or subnational entities implementing the KMGBF.
4. GD under the KMGBF can be assessed with DNA-based metrics or with proxy indicators, both of which are increasingly inexpensive to assess and integrate into management.
5. Analysis of GD indicators and large-scale DNA studies show that genetic erosion is happening, and most species' populations are too small to maintain GD, indicating that intervention may be necessary to ensure their short- and long-term persistence.
6. Genetically informed management actions are impactful and useful, preventing further loss of GD, as illustrated by the examples in the text.
7. Paradigms, best practices, and support tools exist for guiding genetically informed management, such that action can proceed even in situations with uncertainty or limited data.
8. Emerging techniques in analyzing and interpreting population genomic data and emerging technologies, like earth observations and artificial intelligence, have potential for effectively assessing and conserving GD in the context of international commitments like the KMGBF.

FUTURE ISSUES

1. To prevent further genetic erosion, governments and civil society must prioritize the protection and restoration of GD, including through policy mandates, investment, legislation, and action plans.
2. Achieving fair and equitable sharing of the benefits of digital sequence information and genetic resources will require substantive commitment from the global conservation community, including the Cali Fund and FAIR and CARE data principles.
3. Genetic researchers must engage more with the Convention on Biological Diversity, Intergovernmental Science-Policy Platform on Biodiversity and Ecosystem Services, International Union for Conservation of Nature (IUCN), and civil society by working on applied problems, cocreating projects with partners, and translating their knowledge to policymakers and the public.

4. International organizations with global networks and infrastructure (e.g., IUCN, Group on Earth Observations Biodiversity Observation Network, Global Biodiversity Information Facility) are encouraged to take the lead on advancing the integration of GD in monitoring and ecosystem and species assessments to implement KMGBF targets.
5. Conserving and managing GD will require North–South capacity building and collaboration, with sustained and sufficient funding.
6. A more in-depth understanding of the genomic basis of population vulnerability is needed, especially for novel metrics like genomic offset and genomic load. On-the-ground validation is required to demonstrate their use in managing GD.
7. Tools for monitoring and taking action to realize KMGBF's and other commitments in 2030, including indicators, exist and must start being used immediately in all countries.
8. There is also a need for new, feasible, low-cost DNA-based monitoring tools, with associated easy-to-use data storage and retrieval systems.

DISCLOSURE STATEMENT

The authors are not aware of any affiliations, memberships, funding, or financial holdings that might be perceived as affecting the objectivity of this review.

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6. Global meta-analysis of temporal genetic data showing that biota are losing genetic variation and that action can halt and reverse genetic erosion.

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11. First paper highlighting that GD was overlooked in international policy, calling for standardized indicators and genetic monitoring to inform conservation.

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RELATED RESOURCES

CCG (Coalition for Conservation Genetics): **https://www.coalitionforconservationgenetics.org**. A website containing CCG's mission, initiatives, resources (policy briefs, news, etc.), and scientific publications.

Coalition for Conservation Genetics GitHub for genetic indicators: **https://github.com/CCGenetics/guidelines-genetic-diversity-indicators**. Guidelines and R code for quantifying PM and Ne 500 indicators.

CBD (Convention on Biological Diversity). 2024. *2030 Targets*. CBD. **https://www.cbd.int/gbf/targets**. Detailed descriptions and guidelines for each of the Kunming–Montreal Global Biodiversity Framework's 23 targets.

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