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PERSPECTIVE

Monitoring status and trends in genetic diversity for the Convention on Biological Diversity: An ongoing assessment of genetic indicators in nine countries

Sean Hoban[1,2] | **Jessica M. da Silva**[3,4] | **Alicia Mastretta-Yanes**[5,6] | **Catherine E. Grueber**[7] | **Myriam Heuertz**[8] | **Margaret E. Hunter**[9] | **Joachim Mergeay**[10,11] | **Ivan Paz-Vinas**[12] | **Keiichi Fukaya**[13] | **Fumiko Ishihama**[13] | **Rebecca Jordan**[14] | **Viktoria Köppä**[15] | **María Camilla Latorre-Cárdenas**[16] | **Anna J. MacDonald**[17] | **Victor Rincon-Parra**[18] | **Per Sjögren-Gulve**[19] | **Naoki Tani**[20,21] | **Henrik Thurfjell**[22] | **Linda Laikre**[15]

[1]The Morton Arboretum, Center for Tree Science, Lisle, Illinois

[2]The University of Chicago, Chicago, Illinois

[3]Foundational Biodiversity Sciences Division, South African National Biodiversity Institute, Pretoria, South Africa

[4]Department of Zoology, Centre for Ecological Genomics and Wildlife Conservation, University of Johannesburg, Johannesburg, South Africa

[5]Comisión Nacional para el Conocimiento y Uso de la Biodiversidad, Ciudad de Mexico, Mexico

[6]Consejo Nacional de Ciencia y Tecnología, Ciudad de Mexico, Mexico

[7]Faculty of Science School of Life and Environmental Sciences, The University of Sydney, NSW, Australia

[8]INRAE, University of Bordeaux, Biogeco, Cestas, France

[9]U.S. Geological Survey, Wetland and Aquatic Research Center, Gainesville, Florida

[10]Research Institute for Nature and Forest, Geraardsbergen, Belgium

[11]KU Leuven, Ecology, Evolution and Biodiversity Conservation, Leuven, Belgium

[12]Department of Biology, Colorado State University, Fort Collins, Colorado

[13]National Institute for Environmental Studies, Tsukuba, Ibaraki, Japan

[14]CSIRO, Sandy Bay, Tasmania, Australia

[15]Division of Population Genetics, Department of Zoology, Stockholm University, Stockholm, Sweden

[16]Instituto de Investigaciones en Ecosistemas y Sustentabilidad, Universidad Nacional Autónoma de México, Morelia, México

[17]Australian Antarctic Division, Department of Climate Change, Energy, the Environment and Water, Kingston, Tasmania, Australia

[18]Instituto de Investigación de Recursos Biológicos Alexander von Humboldt, Programa de evaluación y monitoreo, Bogotá, Colombia

[19]Nordic Chapter of the Society for Conservation Biology, Uppsala, Sweden

[20]Forestry Division, Japan International Research Center for Agricultural Sciences, Tsukuba, Ibaraki, Japan

[21]Faculty of Life and Environmental Sciences, University of Tsukuba, Tsukuba, Ibaraki, Japan

[22]Swedish Species Information Centre, Swedish University of Agricultural Sciences, Uppsala, Sweden

Jessica M. da Silva and Alicia Mastretta-Yanes contributed equally.

Correspondence
Sean Hoban, The Morton Arboretum, Center for Tree Science, Lisle, Illinois; The University of Chicago, Chicago, Illinois
Email: shoban@mortonarb.org

Linda Laikre, Division of Population Genetics, Department of Zoology, Stockholm University, SE10691 Stockholm, Sweden.
Email: linda.laikre@popgen.su.se

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Abstract

Recent scientific evidence shows that genetic diversity must be maintained, managed, and monitored to protect biodiversity and nature's contributions to people. Three genetic diversity indicators, two of which do not require DNA-based assessment, have been proposed for reporting to the Convention on Biological Diversity and other conservation and policy initiatives. These indicators allow an approximation of the status and trends of genetic diversity to inform policy, using existing demographic and geographic information. Application of these indicators has been initiated and here we describe ongoing efforts in calculating these indicators with examples. We specifically describe a project underway to apply these indicators in nine countries, provide example calculations, address concerns of policy makers and implementation challenges, and describe a roadmap for further development and deployment, incorporating feedback from the broader community. We also present guidance documents and data collection tools for calculating indicators. We demonstrate that Parties can successfully and cost-effectively report these genetic diversity indicators with existing biodiversity observation data, and, in doing so, better conserve the Earth's biodiversity.

KEYWORDS
adaptive capacity, conservation genetics, indicators, monitoring, policy, resilience

1 | REPORTING GENETIC DIVERSITY CHANGE IS VITAL AND IS FEASIBLE

Genetic diversity is variation at the DNA level, including differences among individuals and populations of each species. Because it contributes to the traits and survival of organisms, this intraspecific diversity is vital for helping species adapt to changing environments, including climate, pests, habitat changes, and disease. It also contributes to the stability and resilience of ecosystems including after extreme climate events (Raffard et al., 2019; Wernberg et al., 2018) and helps ensure successful ecological restoration (Breed et al., 2019), as has been documented in forest, grassland, streams, coral, and seagrass ecosystems (Booth & Grime, 2003; Des Roches et al., 2021; Ehlers et al., 2008). Unfortunately, genetic diversity has already declined substantially due mostly to habitat loss, habitat fragmentation, over-harvest, and other human activities (Exposito-Alonso et al., 2021; Leigh et al., 2019).

Although it is recognized as one of three basic levels of biodiversity (along with species and ecosystems), genetic diversity has been neglected in public policy and management (Hoban et al., 2020; Laikre et al., 2010; Laikre, 2010). Vague or imprecise wording in policy language, insufficient indicators to track progress, expensive technology, and metrics that are inaccessible to policy makers and conservationists have resulted in insufficient actions and minimal reporting on genetic diversity status and trends (Hoban et al., 2013; Laikre et al., 2020; Taylor et al., 2017; Vernesi et al., 2008). For instance, a recent analysis of 57 national biodiversity reports revealed that countries primarily use indicators which are not well connected to genetic erosion, primarily focus on breeds of economically important species or crop wild relatives, neglect genetic monitoring, and focus on ex situ rather than in situ gene conservation (Hoban et al., 2021). Clear policy on genetic diversity conservation is also hampered by complicated concepts and terminology, a disconnect between genetic statistics and practical conservation actions, and a need for more meaningful engagement between genetic scientists and decision makers.

It is a critical time to conserve genetic diversity, particularly through the United Nations Convention on Biological Diversity (CBD) post-2020 Kunming-Montreal Global Biodiversity Framework (GBF), which was approved in December 2022 at COP15 (15th Conference of the Parties). During the next decade, Parties to the CBD will be legally required to report on their GBF progress using the Kunming-Montreal indicators. Indicators calculated at national scales and disaggregated by taxonomic groups, habitats or other categories also help countries understand and mitigate biodiversity loss. Through in person

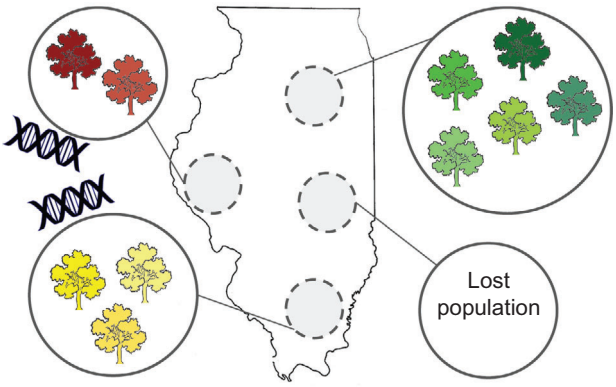
and virtual engagement with CBD negotiations over the past two years, geneticists worked to help improve GBF Goals and Targets to avoid confusing, unclear, or indecisive wording (Hoban et al., 2023). The final Goal A states "…genetic diversity within populations of wild and domesticated species, is maintained, safeguarding their adaptive potential," and Target 4 states "…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."

Safeguarding genetic diversity is feasible based on the finalized CBD Goals and Targets, but will depend on affordable, accessible, and relevant genetic diversity indicators (Frankham, 2022; Hoban et al., 2021). During COP-15 negotiations, many Parties mentioned they will need support in understanding and implementing indicators in practice, especially in developing countries.

Indicators of genetic diversity also provide useful measures of biodiversity for conservation and management efforts beyond the CBD. For instance, progress under national and international endangered species legislation (e.g., the U.S. Endangered Species Act and similar legislation in South Africa, Australia, and the European Union) is typically measured by numbers of species delisted. Indicators of genetic vulnerability within and among populations can provide finer assessment of changes in species' status, potentially improved allocation of resources, and targeted management. Similarly, simple indicators of genetic status may be useful for government and nongovernment organizations when communicating to the public about conservation threats to flagship species. Lastly, genetic diversity indicators highlight the importance of local populations for adaptive potential and resilience, which provides empowerment and leverage for local communities and indigenous peoples.

In this paper, we summarize significant advancements in indicators of genetic diversity that were ultimately recommended by the CBD at COP15 to assess status and trends in genetic diversity, and their application at national scales. Specifically, we

- reiterate the need for and purpose of three indicators, two of which do not require DNA-based analysis.
- summarize and address concerns from policy makers.
- describe ongoing deployment of indicators in 9 countries on 6 continents.
- describe indicator calculation, including with examples.
- address other challenges and describe a roadmap for uptake and use of genetic diversity indicators, including current and future support resources.



Indicator 1. Proportion of populations large enough to maintain genetic diversity	Indicator 2. Proportion of populations still exist (not lost)	Indicator 3. Species monitored with DNA data (y/n)?
0.33	0.75	1

FIGURE 1 Example of genetic diversity indicators, for four hypothetical populations in Illinois, USA. Colors (red, green, yellow) indicate genetic differences among populations while shades within each color indicate genetic variations within each population. One tree = 1000 plants (five trees = 5000 plants). In 2020, 2 of 3 extant populations' census size is < 5000 (Ne < 500 considering an effective to census size ratio of Ne/Nc = 0.1) and thus too small to maintain genetic diversity (indicator 1). Three of four historic populations are maintained (indicator 2). DNA-based methods have been used to monitor genetic diversity in two populations (indicator 3—a value of 1 means that the species is monitored with DNA-based methods). DNA and tree images used are in public domain from clker.com.

We are confident that nations and subnational actors can successfully report these genetic diversity indicators, and in doing so, better conserve the world's biodiversity.

Game et al. (2015) emphasize that policy-relevant science should clearly identify "actors who could take policy or management action." Our audience for this article is policy makers at international and national levels, agency personnel, and scientists or practitioners engaged in determining relative vulnerability of species—stakeholders who work toward allocating resources among such species, determining baselines for restoration, and outlining action plans for recovery.

2 | NEED AND PURPOSE FOR EACH INDICATOR

In 2020, three genetic diversity indicators were proposed and discussed (Figure 1) (Frankham, 2022; Hoban et al., 2020; Laikre et al., 2020). The indicators have several motivations: to assess or approximate genetic diversity status

without requiring new DNA data; to be affordable and feasible with existing data and with limited time investment; to use simple calculations; to allow for easy translation into policy and management of species; and to be applicable and relevant in all countries, taxonomic groups, and ecosystems. It is also desirable to use concepts that are intuitive or accessible to nongeneticists (e.g., genetic losses due to small populations and loss of populations). Assessing genetic status without DNA-based genetic data is vital since relatively few species have DNA-based research, especially in biodiversity hotspots. With these attributes, the indicators meet the first of three criteria for policy relevance outlined by Game et al. (2015)—salience or relevancy.

The proposed indicators of genetic diversity relate to central conservation genetics concepts:

1. conserving genetic diversity within large populations for rapid response to changing environmental conditions,
2. conserving genetic diversity among populations to provide diverse "options" for the future adaptation of the species,
3. assessing genetic data directly to guide conservation actions and sustainable use.

Indicator 1 (adopted as a Headline indicator A.4 for Goal A and Target 4 of the monitoring framework for the CBD Kunming-Montreal GBF) is "the proportion of populations within species with a genetically effective size Ne > 500." Effective population size (Ne) is a concept that quantifies the rate of genetic erosion within a population; genetic erosion is the loss of genetic diversity, increase of inbreeding, and reduction of population ability to adapt. Past CBD indicators do not reflect genetic erosion within populations—though they did reflect genetic erosion in agricultural breeds (Hoban et al., 2020). Large Ne can help avoid population's and species' extinction, and supports high genetic diversity. (Genetic diversity statistics, such as "nucleotide diversity," are directly calculable from Ne and from how often changes in the DNA are known to occur ["mutation rate"].) Specifically, contemporary effective size of 500 is well regarded as a minimum threshold for populations to maintain genetic diversity (Frankham et al., 2013; Franklin, 1980) (though see Frankham et al., 2013). Using a ratio of effective to census size, Ne/Nc (0.1 to 0.3 for most species; Hoban et al., 2021) translates to comparing census population size (Nc) to a threshold of about 5000. In this way, demographic information—census size—is translated to information on genetic status. For example, *Cupressus abramsiana*, a USA endemic gymnosperm, has five populations, and two exceed a census of 5000. Indicator 1 for this species is 0.4 (2 of 5). We caution that past population size changes can impact Ne and Ne is not always correlated to Nc; past demographic changes, as well as population connectivity, should be considered when interpreting genetic-based Ne.

Indicator 2 (adopted as complementary indicator for Goal A and Target 4 of the monitoring framework for the CBD Kunming-Montreal GBF) is "the proportion of populations maintained within species." This indicator is needed because past CBD indicators do not reflect loss of genetic distinctiveness of each population. Each population may hold unique traits and genetic adaptations supporting species' survival (Karell et al., 2011; Palumbi et al., 2014). This concept is already recognized in distinct agricultural breeds, which are analogous to populations, each with unique traits or characters. Genetic, geographic and ecological variation allows future options for adaptation. Losses of species' populations and geographic range change are often quantifiable (Ceballos et al., 2017; Jetz et al., 2012). For example, *Capensibufo rosei* (Rose's mountain toadlet), endemic to the Cape Peninsula of South Africa, is known from five historical populations; only one of which exists today, along with a newly discovered population. Indicator 2 for this species is 0.33 (2 of 6 populations maintained). A caution with this indicator is that determining the baseline of historic range can be difficult and/or contentious. Where good information exists or can be estimated, this indicator estimates how much unique genetic diversity, available for adaptation, has been maintained or lost.

Indicator 3 (not currently an indicator of the monitoring framework) is "the number of species (and populations) monitored using DNA-based methods." Although not common in all countries, DNA-based genetic monitoring, when available, can guide conservation actions and policy (Posledovich et al., 2021; Schwartz et al., 2007). For example, DNA-based monitoring of mountain pygmy possums (*Burramys parvus*) revealed inbreeding, very low Ne of ~10 and loss of over 80% of the population's genetic diversity. Based on this knowledge, a genetic rescue program introduced six genetically healthy males from a nearby population. This binary indicator counts any monitoring program using DNA data to help managers assess genetic status and choose appropriate actions, including studies of genetic connectivity, hybridization, adaptation, etc. Indicator 3 for this species is 1. By emphasizing the importance of conservation genetic studies, and quantifying them, as a complement to the proxy-based indicators, this indicator could incentivize more countries to start implementing DNA-based monitoring; conservation genetic studies should work with stakeholders to ensure the data can inform management.

These indicators more directly assess genetic erosion than the Red List Index or Living Planet Index. Neither

Index focuses on the threshold of Ne 500 within populations; below Ne 500, genetic erosion is exponentially faster. Also, the Red List Index typically assesses the entire species, which may be safe from extinction but still suffer important losses of genetic diversity; wide-ranging species may lose entire populations, and their unique genetic diversity, without affecting Red List status. Meanwhile the Living Planet Index primarily focuses on vertebrate species and does not consider losses before the 1970s, though many populations were lost or declined prior to this time.

3 | ADDRESSING CONCERNS FROM POLICY MAKERS

The Coalition for Conservation Genetics (Kershaw et al., 2022) presented these indicators to policy and management personnel globally through 10+ webinars and attendance at CBD meetings such as the Subsidiary Body on Science Technology and Technical Advice, SBSTTA (Supplemental Material). Five concerns about indicator uptake were common (Table 1): (1) necessity of DNA data, (2) feasibility of obtaining sufficient amounts of data, (3) realistic limitations on time, (4) limitations on skills or knowledge, and (5) concerns over data sharing, particularly Digital Sequence Information (DSI) (Scholz et al., 2022).

We address these concerns in Table 1, highlighting that: no new DNA collection is needed, most countries have sufficient data for reporting on these indicators, a small team can complete analysis in a fraction of one year without specialized expertise, and no DSI is shared in indicator reporting. Preliminary results of this assessment were presented to Parties in a side-event of the COP-15. By addressing these concerns through a dialogue with stakeholders, the indicators better meet the legitimacy criteria outlined by Game et al. (2015).

In the remainder of this article, we describe the transparent process of further developing the indicators, and address another of Game et al. (2015) credibility criteria.

4 | TOWARD INDICATOR DEPLOYMENT

While the indicators were being discussed by the CBD (CBD/WG2020/3/5, CBD/ID/OM/2022/1/2), a trial was initiated by the Swedish Environmental Protection Agency. Examining Swedish National Red List assessments, this trial (1) assessed data quality/ availability for 22,000 species and (2) calculated indicator values for 79 species (Thurfjell et al., 2022). Approximately 33% of species had census size estimates and 20% of species had historic and modern population information—data which are the basis for indicators 1 and 2. The trial also found that 70% of herptile and 49% of mammal populations likely had Ne > 500 while 32% of herptiles and 84% of mammals are maintaining their geographic range. This study concluded that

- Data for the indicators are likely available for thousands of species.
- A large proportion of species are already experiencing genetic erosion within and among populations.

A new pilot project described here is implementing the indicators in nine countries across six continents, in order to:

1. create and refine a standard workflow, definitions, methodology, and data collection device, and
2. evaluate > 100 species for each country to:
3. determine how many species have necessary data to calculate indicators,
4. when possible, extract data and perform indicator calculations, and
5. identify challenges so guidance and calculations can be improved for use by more countries.

We describe the approach to demonstrate that data are available to calculate the indicators in countries around the world, and to show that data collation is practical, achievable and adaptable.

Gathering data on populations of species can be challenging because there is no global, standard database of population census size or changes in populations. However, population level data of many species are available in different reports, atlases, and databases, and with local and expert knowledge holders.

We identified three approaches to gathering data, which suit different countries' needs and can be used in combination (Figure 2).

- "Manual data extraction" involves reviewing national or subnational documents (management or recovery plans, status assessments, environmental impact reports), scientific literature, country flora or natural history descriptions, IUCN Red List assessment or NatureServe assessment text, etc.
- "Expert consultation" involves facilitated discussion and knowledge sharing among local experts and traditional knowledge holders with firsthand (but perhaps unpublished) information—similar to Red List assessment workshops which elicit quantitative information on species.
- "Automated data extraction" from existing databases on national surveys, where species' occurrences or pop-

TABLE 1 Resolving common concerns regarding genetic diversity indicators

Concerns	Solutions or clarifications
Data needed Is genetic data (DNA-based analysis) needed?	Indicators 1 and 2 do not need genetic data (DNA sequencing), genetic expertise, or laboratory facilities to generate data. Genetic data can be used to estimate Ne, but *in most cases existing census size data* (counts of individuals using camera traps, surveys, etc.) along with an Ne/Nc ratio can be applied to obtain a valid proxy of Ne, and similar records for measuring "populations maintained."
Achievable Is there enough census or geographic data?	Yes, many countries monitor priority species, maintain biodiversity databases or citizen science tools, and contribute Red List assessments which may have geographic and census data. Data collection can include local knowledge or expert consultation, or categorical or imperfect data. Genetic diversity indicator reporting is not necessary for all species; it would be for a relatively small, representative sample of species per country (we recommend ≥100) (Frankham, 2022; Hoban et al., 2021; Laikre et al., 2021). Representative = from a diversity of ecosystems, taxonomic groups, rarity, and lifespan
Realistic Is indicator calculation too time-consuming?	Collection of census sizes and number of populations is similar in scope to compiling other information for CBD National Reports. From pilot tests, 3–5 persons could complete analyses on a total of 100 species in 2–4 weeks, or 1 person could do it in 2–4 months per country.
Realistic Does indicator calculation require special skills or tools?	No. An undergraduate biology education, and short training sessions, should provide sufficient foundation for gathering data. Our guidance documents explain how to choose representative species, how to find and record data, and how to resolve challenges (Supplemental Material; see also Hvilsom et al., 2022). A data collection device allows for standard recording and storage of data, and analysis (Supplemental Material).
Data sharing Does reporting genetic indicators require reporting or sharing genetic data or Digital Sequence Information (DSI)?	Reporting on genetic indicators does not involve sharing or reporting any DSI. Indicators 1 and 2 will typically be based on demographic and geographic data (e.g., census sizes, population distributions), which do not use DNA data (DSI) at all. If DNA data were used to calculate Ne or define population boundaries, only the count of populations and estimates of effective size would be recorded; *no DSI is reported or shared*. Even raw census data and population data could be retained by the country, reporting only the proportions for the indicators Although indicator 3 does assess genetic studies in the country, it is only a count of studies. It does not assess DNA data or share DSI. Indicating DNA data availability is at the discretion of each country (Scholz et al., 2022).

ulation sizes are regularly assessed and stored, often in a gridded spatial database (common in some fish, plants, birds, and mammals), as with stock assessments, some National Red List databases, or forest inventories. Population presence can also be obtained from citizen science databases (e.g., iNaturalist). Automated analysis can compare census sizes per population to the Ne (or Nc) threshold, and compare historic data, atlases, or range maps to current population presence or projections of habitat change to assess "populations maintained."

Examples from different countries illustrate the diverse options available (Table 2). Recovery plans for dozens to thousands of threatened species are mandated by national legislation (e.g., Australia—the Environment Protection and Biodiversity Conservation Act 1999, https://www.dcceew.gov.au/environment/epbc; South Africa—Biodiversity Management Plans, https://www.dffe.gov.za/content/management_plans/biodiversity; USA—the Endangered Species Act, https://www.fws.gov/law/endangered-species-act). These documents typically detail species biology and demographic status. In Japan, many threatened vascular plants have been surveyed for census size for over two decades by the Japanese Society for Plant Taxonomy, while for common trees, statistical estimates for population size (Fukaya et al., 2020) were estimated from vegetation survey data. In Mexico, taxonomic experts who recently helped validate distribution models for crop wild relatives will be consulted for indicator values (Goettsch et al., 2021). In France, Belgium, and Sweden, much biodiversity data

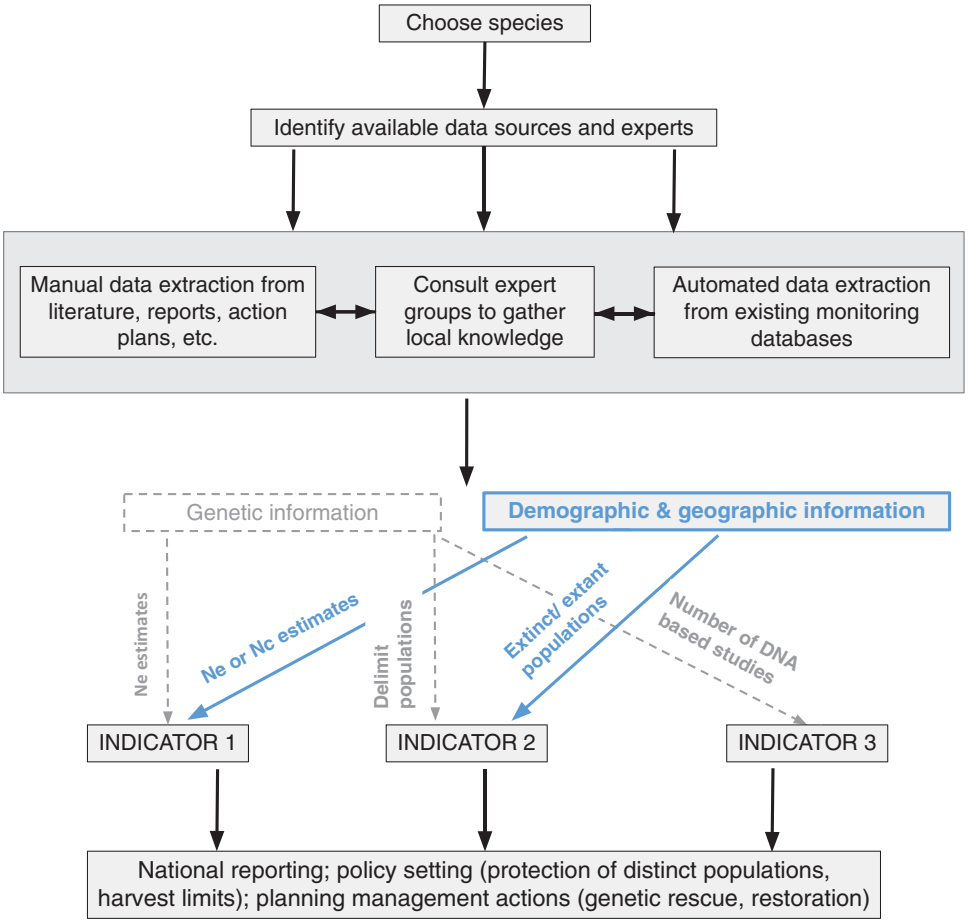


FIGURE 2 Process of assessing indicators for a set of species, using data from different sources (manual, expert, automated). Indicators 1 and 2 are primarily obtained from demographic and geographic information. Note that genetic information is optional for indicators 1 and 2 as shown in grey dashed lines. For indicator 1, census sizes (Nc) can be converted to effective sizes (Ne) by applying a species-specific effective to census size ratio, and/or a ratio of Ne/Nc = 0.1. Indicator assessment leads to reporting, policy outcomes, and management action.

from experts and diverse sources are collected in easy to access web-based portals (France—https://inpn.mnhn.fr/; Belgium—https://www.biodiversity.be/1767; Sweden—https://www.artdatabanken.se/en/). In Colombia, the Biodiversity Information System (SIB) repository compiles species surveys from throughout the country (https://biodiversidad.co/), which is mandated by many public and private organizations. These data are reviewed by national experts for validation and used to create freely available species distribution models (http://biomodelos.humboldt.org.co/) and for conservation prioritization.

5 | CALCULATING INDICATOR VALUES AT NATIONAL LEVELS

Genetic indicator calculation is straightforward. First, indicators are calculated for each species. When data are available as a range (e.g., Nc is 10,000 to 20,000), the mean is used. Qualitative data such as "a few hundred" or "at least 5000" are often sufficient for comparison to the Nc 5000 threshold. In the case of differing estimates from multiple sources, either the most recent source is used, or a mean of values based on the different sources is taken (see Table 3). We add that in most practical applications, indicator 1 will typically be based on an Nc estimate and an Ne/Nc ratio, but Ne can be calculated directly from DNA-based genetic studies. In such cases the contemporary Ne value should be used, and reported with confidence intervals.

While indicator 3 is a simple sum (species for which one or more populations are monitored using DNA), the country indicator value for indicators 1 and 2 is the mean of values across species (a median could be used for skewed distributions). If taxonomic groups are not represented evenly, the indicator value is the mean of each taxonomic group's means, which down-weighs overly represented taxonomic groups (e.g., mammals). Additionally, each species can be weighted by the proportion of its geographic

TABLE 2 Countries participating in testing of genetic diversity indicators, showcasing variation in overall approach

Country	Number of people	Taxonomic groups*	Approach	Sources**
South Africa	7 or 8	B, F, H, I, M, Ma, P	Manual + Expert	AH, EGI, NRL, GRL, SMP
USA	10	B, F, H, I, M, P	Manual	AH, GRL, SMP
Japan	4 or 5	P	Manual + Auto	AH, FG, ND, NRL
Mexico	10	B, CW, F, H, M, P	Expert + Auto	AH, EGI, ND, NRL
Australia	8	B, F, H, I, M, P	Manual	AH, GRL, ND, SMP
Sweden	2+	B, F, H, I, M, P	Manual + Expert	AH, ND, NRL, SMP
Belgium	2+	B, I, M, P	Manual + Expert	AH, ND, NRL, SMP
Colombia	3+	B, H, M, P	Manual + Expert	AH, EGI, GRL, ND, NRL
France	4	B, F, H, I, M, P	Manual	AH, ND, SMP, NRL

*B = Birds, CW = crop wild relatives, F = freshwater fish, H = herptiles, I = invertebrates, M = mammals, Ma = marine, P = plants.
**AH = ad hoc/ other (websites, email experts, scientific literature), EGI = expert group input, FG = field guide, GRL = Global Red List, ND = national data set or database of species information and/or occurrences, NRL = National Red List, SMP = species-specific management, action or recovery plan.

TABLE 3 Example indicator values for select species

Species	Taxonomic group	Country	Indicator 1 (Ne)	Indicator 2 (populations)	Indicator 3 (studies)*
Pelobates fuscus	Amphibian	Belgium	0	0.33	1
Rana arvalis	Amphibian	Belgium	0.18	0.84	1
Angelica heterocarpa	Angiosperm	France	0.5	1	1
Zingel asper	Fish	France	0.2	1	1
Tetrao urogallus	Bird	France	0.33**	0.6	1
Taraxacum yuparense	Angiosperm	Japan	0	0.5	0
Carex cinerascens	Angiosperm	Japan	0.5	0.8	0
Capensibufo rosei	Amphibian	South Africa	0.5	0.33	1
Clinus spatulatus	Fish	South Africa	N/A***	1	0
Syncerus caffer caffer	Mammal	South Africa	0.3	1	1
Alces alces	Mammal	Sweden	0.67	1	1
Silurus glanis	Fish	Sweden	0	0.5	1
Cupressus abramsiana	Gymnosperm	USA	0.4	1	0
Rana muscosa	Amphibian	USA	0	0.76**	1
Charadrius melodus	Bird	USA	0.39**	1	1
Erigeron maguirei	Angiosperm	USA	0.5	1	0

*Indicator 3 is binary for each species, 0 or 1 (1 = one or more populations of the species is monitored with DNA-based method; 0 = no DNA-based monitoring for the species).
**Different reports suggest different values or different interpretations of population boundaries; these values are means of the different interpretations.
***Indicator 1 could not be calculated because no Nc or Ne data are available.

range in the country, from 0 to 1, to reflect national responsibility, with full weight for endemic species (Domisch et al., 2016). Transboundary populations can be weighted similarly.

Equation (1): simple indicator value (IV) mean across species (s)

$$\frac{\sum_{s=1}^{s=100} IV_s}{s}$$

Equation (2): indicator value (IV) weighted by proportion of geographic range in country (W)

$$\frac{\sum_{s=1}^{s=100} IV_s W_s}{\sum_{s=1}^{s=100} W_s}$$

Equation (3): indicator value (IV) giving equal weight to birds ($b = 20$ species), plants ($p = 30$ species), and

mammals ($m = 50$ species)

$$\frac{\frac{\sum_{b=1}^{b=20} IV}{b} + \frac{\sum_{p=1}^{p=30} IV}{p} + \frac{\sum_{m=1}^{m=50} IV}{m}}{3}$$

6 | OVERCOMING CHALLENGES

In trials of the methodology outlined above we have resolved several challenges: biases, uncertainty in data, and difficulty in defining populations.

Biases

Ideally, the 100+ species assessed by a country reflect diverse ecosystems, taxonomic groups, rarity categories, and life history traits (e.g., lifespan). In reality, biases exist due to a country's habitat types, biogeography, latitude, and investment priorities in biodiversity monitoring and thus data availability. The Red List Index and Living Planet Index also have such biases (Bachman et al., 2019; Puurtinen et al., 2022). Weighting by taxonomy or ecosystem can help address bias (previous section). Additionally, biases should be noted by displaying counts per category in a matrix, as is common in Red List summary tables.

Uncertainty or qualitative information

Sometimes, census sizes are recorded as a range of values rather than point values; using vague wording such as "several hundred"; or census at the species but not population level. Our draft guidance (Supplemental Material) provides the assessor with advice on translating these into quantitative information, and recording uncertainty.

In addition, for indicator 1, if census size is not available, it may be possible to use known occupied area multiplied by mean density (number of individuals supported per unit area) to estimate the number of individuals. This allows evaluating whether an area is capable of housing a population Nc larger than the threshold; if the area is smaller, the Ne will likely be smaller than 500 (Mergeay et al., 2020). For indicator 2, if information on the number of historic populations is not known, the assessor may record overall decline in area, which will ultimately result in lost populations and genetic diversity (Exposito-Alonso et al., 2021).

Definition of population boundaries (required for indicators 1 and 2)

Ecologists and geneticists have worked for decades to understand population distinctions (Jost et al., 2018; Waples & Gaggiotti, 2006). For the indicators, available knowledge can be used to assess genetic distinction, typically less than one migrant per generation from other populations (Mills & Allendorf, 1996), such as using population designations from the report or experts consulted, which reflect knowledge of the species biology, history, and dispersal; discrete patches such as forest or lakes; ecoregions, geographic (and migration) barriers such as mountains/ valleys, or hydrological zones, which may promote local adaptation; phylogeographic studies (i.e., "proxies of genetic differentiation"; Tobón-Niedfeldt et al., 2022); or grid cells based on species' dispersal.

Other challenges remain and will require capacity building across the biodiversity conservation sector, including from the CBD, national agencies, NGO partners, scientists, and local monitoring initiatives. These challenges include significant time (at least several person months per country, see Table 1), translation of guidance and infrastructure to non-English languages, and continued scientific work to make sure indicators are appropriate in challenging situations such as small countries, highly managed species or species with large ex situ populations, and species with naturally small populations. However, as detailed in Section 7, we believe these challenges can be overcome.

7 | ROADMAP

We have presented the purpose and straightforward methodology of each indicator, addressed concerns of policy makers, showed that data are available and usable, and described ongoing work in nine countries. We demonstrated that genetic diversity indicators are ready for use in biodiversity conservation and reporting, with existing data.

Increased uptake of these indicators by Parties to the CBD and other users (environmental agencies, wildlife managers, national legislation, etc.) will require further successful demonstrations, published step-by-step workflows, and training workshops, ideally in multiple languages (Kershaw et al., 2022). We have created an online data collection form using Kobotoolbox (www.kobotoolbox.org/) and a guidance document (Supplemental Material, and https://github.com/AliciaMstt/GeneticIndicators) for anyone to use. Kobotoolbox is a free open source tool for data collection in a standardized structured format, with connections to analysis in Excel, R, Python or GIS software. Our GitHub encourages interactive engagement with stakeholders who can offer suggestions or ask questions.

Future development of online resources can enhance data storage, managing, and sharing. An online portal could accept and store submitted data such as Ne or Nc values, population designations, and references over multiple reporting cycles at global, national and subnational levels,

which would make compilation of the indicators easier and increase transparency. Other cyber infrastructure would be connections to resources like species distribution models (Jetz et al., 2012), which could help with defining populations, calculating Ne based on area and density, loss of distinct populations etc. Finally, as noted by others (Garner et al., 2020; Thurfjell et al., 2022), it would be advantageous for Red List assessment workshops to include gathering raw data and information needed for calculation of the indicators, including population boundaries. Red List assessors scour literature and consult experts for demographic and geographic information, and indicators could be recorded systematically in the Red List database.

Lastly, we note that the indicators presented here complement other useful indicators for tracking genetic diversity which other authors have suggested. For example, the "genetic scorecard" assesses genetic diversity threats such as hybridization and low reproduction (Hollingsworth et al., 2020), while another indicator assesses the extent to which geographic ranges are protected in situ or ex situ (Khoury et al., 2019). Additionally, indicators using direct assessments of genomic health based on DNA data are available for some species, and collection of DNA data for species management remains important (van Oosterhout, 2020; Andersson et al., 2022; O'Brien et al., 2022). In the future, genetic indicators could be synthesized together for comprehensive genetic assessment (Frankham, 2022).

8 | CLOSING REMARKS

The indicators support and enable CBD Goal A and Target 4 wording (Frankham, 2022; Hoban et al., 2020; Laikre et al., 2021).

We note that many Parties (and non-Parties) will also set National Targets, which are typically in line with, but may be more ambitious, than the global targets, and the setting of these targets offers further opportunity for scientists to work with policy makers.

We close by reiterating that scientific evidence shows that genetic diversity is a basic pillar of all biodiversity that must be *maintained (not lost), protected (via legislation and policy), managed (through interventions such as restoring gene flow and genetic rescue), and monitored (with DNA-based and non-DNA-based metrics like the indicators*) (Des Roches et al., 2021; Hoban et al., 2021). This is necessary to enable all species to adapt to environmental change, ensure resilient ecosystems, and benefit humanity.

AUTHOR CONTRIBUTIONS

SH, JdS, AM-Y, and LL conceived the study. SH wrote the first draft and conceived Figure 1. All authors contributed to discussions and revisions. IP-V conceived Figure 2. MH and AM-Y conceived Table 1.

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DISCLAIMER

Any use of trade, firm, or product names is for descriptive purposes only and does not imply endorsement by the U.S. Government.

DATA AVAILABILITY STATEMENT

The only data for the article are in Table 2; no other data were used.

ORCID

Sean Hoban https://orcid.org/0000-0002-0348-8449
Catherine E. Grueber https://orcid.org/0000-0002-8179-1822
Myriam Heuertz https://orcid.org/0000-0002-6322-3645
Ivan Paz-Vinas https://orcid.org/0000-0002-0043-9289
Anna J. MacDonald https://orcid.org/0000-0003-2972-200X
Per Sjögren-Gulve https://orcid.org/0000-0001-6584-128X
Linda Laikre https://orcid.org/0000-0001-9286-3361

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SUPPORTING INFORMATION

Additional supporting information can be found online in the Supporting Information section at the end of this article.

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