Too simple, too complex, or just right? Advantages, challenges and resolutions for indicators of genetic diversity

Summary: describe criticisms of the genetic diversity indicators from Parties and scientists, and address them clearly; acknowledge things to work on. Only summarize indicators briefly before *focusing the bulk of the article on critiques and resolutions*. **Outcome… policy people can be more conversant on genetic diversity indicators at upcoming meetings.** Especially AHTEG, Parties can be prepared to talk about the indicators.

Proposal/ cover letter: preprop_genetic

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Key Words: Conservation genetics, international policy, Convention on Biological Diversity, effective population size, Global Biodiversity Framework

ABSTRACT

Measuring genetic diversity of wild species using DNA-based data remains resource intensive and time-consuming for nearly all species. Yet, genetic assessments are needed for global conservation commitments including the Convention on Biological Diversity (CBD) and for governments and managers to evaluate conservation progress as well as prioritize species and populations to preserve and recover genetic diversity (e.g., genetic rescue). Recently, indicators were developed for tracking and reporting genetic diversity status and trends for hundreds of species. The indicators quantify two simple proxies of within-population and among-population genetic diversity and adaptive potential: small effective size (Ne<500) and loss of genetically distinct populations. Indicators must balance scientific credibility, practicality, and simplicity. Here, we summarize the advantages of these pragmatic indicators; address critiques by scientists for simplifying assumptions and by policymakers for complexity; and propose potential solutions and next steps. We aim to support practitioners putting indicators into policy, action, legislation and reporting.

MAIN TEXT

"Inclusion of genetics and evolution is central to conservation planning and critical to the persistence of species." Michael Bruford et al 1998, Animal Conservation Genetics

The global biodiversity context

The Convention on Biological Diversity (CBD), an international treaty on nature conservation, sustainable use, and the fair and equitable sharing of benefits arising from genetic resources between 195 countries and the European Union, has been in force for thirty years. Yet losses of biodiversity and degradation of ecosystem services continue, including a 69% decline in monitored vertebrate populations in the last five decades (WWF 2022), alongside alarming losses in genetic diversity (Leigh et al. 2019, Hoban et al. 2021a, Exposito-Alonso et al. 2022)

At a key CBD meeting in December 2022, COP15, countries overcame major disagreements and signed the landmark Kunming-Montreal Global Biodiversity Framework (KMGBF) to set global ambition to reverse biodiversity loss (Díaz et al. 2020). The KMGBF was developed over four years through negotiations of CBD delegations, scientific deliberations, thousands of stakeholder and peer review comments, and collection of metadata by the United Nations Environment Program World Conservation Monitoring Centre (UNEP WCMC) (CBD 2022a,b, Hughes 2023, Obura et al. 2023). This agreement along with others, such as the recently signed High Seas Treaty and the Paris Climate Accords, could lead to a global turning point for biodiversity conservation.

Thus, the state of nature is at a critical point, necessitating unprecedented attention, capacity, and transformational societal change to ensure a livable planet (Diaz et al. 2020, Obura et al. 2023). Actions must be initiated immediately to achieve the KMGBF twenty-three 2030 targets and four 2050 outcome-oriented goals. Success or failure will depend on political will and action, *and on accurately monitoring progress* towards or away from conservation endpoints.

In this article we focus on *monitoring using indicators for genetic biodiversity,* a neglected but vital element of nature (Hoban et al. 2021). Genetic diversity is a foundational level of biodiversity, underlying species' ability to adapt to new environments, changing climates, and new diseases. Genetic diversity also supports ecosystem resilience after disturbance and increases the success of ecological restoration (Des Roches et al. 2021). The CBD mandates countries to monitor, manage and report on the genetic status of species. This focus extends beyond the CBD- other policies such as the European Union Biodiversity Policy, IUCN Key Biodiversity Areas, and national legislation protecting endangered species in numerous countries increasingly recognize and protect genetic diversity (Cook and Sgrò 2017, Hoban et al. 2021b).

To effectively monitor genetic diversity, in an affordable and rapid manner, it was proposed (Hoban et al. 2020, Laikre et al. 2020) to focus on processes that cause genetic erosion: the loss of genetically distinct populations and small effective population sizes (Ne) which relates to the number of individuals that contribute genetic diversity to the next generation. Ne is smaller than census size (Nc) because not all individuals of a population reproduce, among other factors. These indicators can be compiled even without DNA based studies, e.g. using demographic data. They were adopted by the KMGBF in 2022. During CBD negotiations, the scientific and policy communities pointed to some challenges of the genetic indicators. Here, we respond to those concerns by first defining indicators and their role in policy. We then elaborate the advantages, critiques, and feasible near-term solutions for genetic indicators, using real-world examples. We close by reviewing other critical elements for monitoring using genetic diversity indicators and steps for global implementation.

We aim to support policymakers in upcoming discussions at national and regional levels regarding putting indicators into policy, practice, legislation, and reporting, for example, through the recently appointed Ad Hoc Technical Expert Group (AHTEG) of the CBD on indicators SCBD/IMS/NP/JC/KM/90718, and other fora established by the CBD Executive Secretary (https://www.cbd.int/gbf/monitoring/ind/forum/). We also aim to support national and subnational governments and NGOs working to deploy indicators. Many are striving to conserve genetic diversity for the adaptive potential it provides to populations of species, its intrinsic biodiversity value, and its contributions to ecosystems and people (Des Roches et al. 2018, 2021).

What are indicators?

Multinational commitments like the CBD, and others such as the Montreal Process on sustainable forest management (https://montreal-process.org/), use indicators to assess progress on implementation of conservation measures and guide further conservation actions. Indicators are metrics capable of detecting a change in a system, and should be simple (not requiring specialized training or equipment, easy to measure consistently), feasible, relevant, responsive, accurate, scalable, and legitimate (Heink & Kowarik 2010). For example, ecological indicators help assess the health and function of ecosystems, how humans are perturbing them, necessary actions for improving the system, or the outcome of an intervention (Rapport and Hildén 2013, CBD 2022c). In contrast to the previous CBD 2010-2020 Aichi targets, KMGBF targets are designed to be "SMART" (Specific, Measurable, Ambitious, Realistic, Timebound) and to have quantifiable indicators (CBD 2019).

The KMGBF monitoring framework consists of three types of indicators: “headline indicators” (which capture the scope of a goal or target), and “complementary” and “component” indicators (which focus on elements within the goals and targets, but are optional) (Hughes 2023). All countries are mandated to report headline indicators. Countries are also required to update their National Biodiversity Strategic Action Plans in line with the KMGBF and produce National Reports in 2026 and 2029 (CBD/COP/15/L.27). Although 26 headline indicators were agreed at COP15, much work remains for indicator development and deployment, and to build monitoring and reporting capacity within many countries.

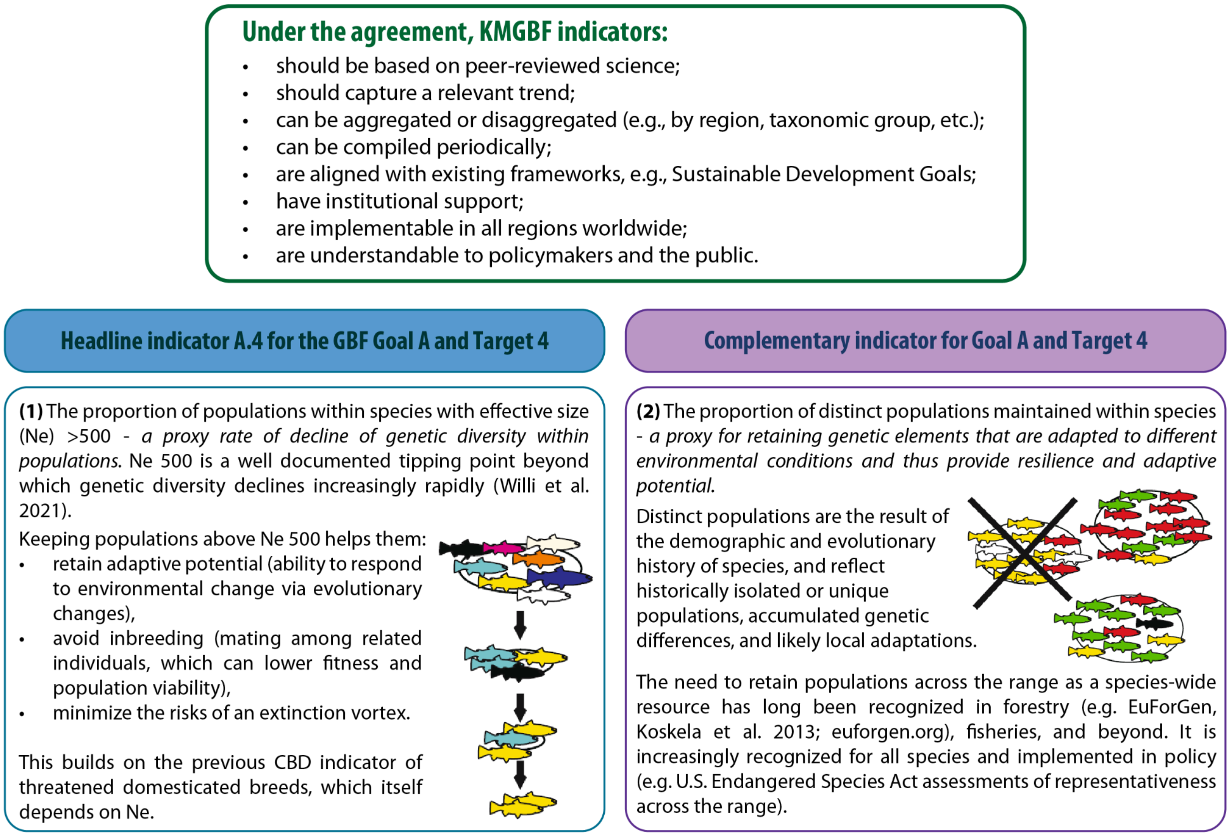
Several indicators for species and ecosystems are developed, though with recognized significant weaknesses and biases (Fraixedas et al. 2022). Prior to the KMGBF, indicators for genetic diversity - the most foundational level of biodiversity - were largely restricted to proxies of genetic diversity of domesticated animals and plants, such as the number of threatened local breeds and the number of accessions in genebanks. In other words, indicators for consistent and meaningful measurements of genetic diversity of wild species were entirely lacking. Fortunately, indicators are being developed and deployed.

Genetic diversity indicators

Concerns about neglect of genetic diversity in policy had been voiced since 2010 (Laikre et al. 2010). Genetic diversity indicators were proposed at a side event at CBD COP10 (Linda Laikre, Stockholm University, personal observation), but were not adopted in the 2010-2020 CBD targets. A decade later, following a call from the Biodiversity Indicators Partnership that noted a lack of genetic diversity indicators, genetic diversity indicators applicable to all species were proposed, which measured how much of species’ geographic ranges (a proxy for among population genetic diversity) were safeguarded in situ by protected areas and ex situ by germplasm (e.g., seeds) sampled for gene bank storage (Khoury et al. 2019). The following year, Laikre, Hoban, and colleagues introduced indicators relating to (1) rapid loss of genetic diversity in small populations, specifically those with an effective size (Ne) less than 500 (*Ne 500 indicator* hereafter); (2) loss of genetic diversity when distinct populations are lost (*populations maintained indicator* hereafter); and (3) development of knowledge of genetic diversity through DNA-based methods focused on conservation and genetic management (Hoban et al. 2020, Laikre et al. 2020). Meanwhile, Scotland introduced a methodology termed the genetic scorecard, which documents threats and actions relating to genetic status, and gives each species a green, yellow or red score (Hollingsworth et al. 2020).

These genetic diversity indicators were discussed by Parties to the CBD over the past three years. Expert consultation and political discussion will continue throughout 2023 and beyond to further develop and improve indicators for CBD COP16. In this article, we focus on the **Ne 500** and **populations maintained indicators** (Figure 1), which were adopted under the KMGBF. *They are quantitative, proxy-based, indicative of a species’ overall genetic status or health, deployable in all countries, and connected to conservation genetic theory and practice.* Discussion and advances to these indicators were made prior to COP15 (Frankham 2021, Hoban et al. 2021b, 2021c, Laikre et al. 2021, O’Brien et al. 2022, Thurfjell et al. 2022). Following their adoption, work related to their operationalization has accelerated (Hoban et al. 2022).

These indicators build on concepts such as measuring total species census size relative to a minimum viable threshold of 5000 (SAFE index, which recognized exponentially increasing risk as populations become smaller) (Clements et al. 2011); measuring the proportion of the species' range lost as representing a loss of adaptive potential (Ceballos et al. 2017); and assessing populations using IUCN Red List criteria (e.g., for salmon; Rand et al. 2012). As explained previously (Hoban et al. 2020), the two indicators can be calculated for 100 or more species per country (which should be taxonomically and ecologically representative, if possible), can be calculated and reported on starting now, can be reported every three to five years thereafter, and do not utilize Digital Sequence Information, or DSI (Scholz et al. 2022).



Under the agreement, KMGBF indicators:

- should be based on peer-reviewed science;
- should capture a relevant trend;
- can be aggregated or disaggregated (e.g., by region, taxonomic group, etc.);
- can be compiled periodically;
- are aligned with existing frameworks, e.g., Sustainable Development Goals;
- have institutional support;
- are implementable in all regions worldwide;
- are understandable to policymakers and the public.

Headline indicator A.4 for the GBF Goal A and Target 4

(1) The proportion of populations within species with effective size (Ne) >500 - *a proxy rate of decline of genetic diversity within populations.* Ne 500 is a well documented tipping point beyond which genetic diversity declines increasingly rapidly (Willi et al. 2021).

Keeping populations above Ne 500 helps them:

- retain adaptive potential (ability to respond to environmental change via evolutionary changes),
- avoid inbreeding (mating among related individuals, which can lower fitness and population viability),
- minimize the risks of an extinction vortex.

This builds on the previous CBD indicator of threatened domesticated breeds, which itself depends on Ne.

Complementary indicator for Goal A and Target 4

(2) The proportion of distinct populations maintained within species - *a proxy for retaining genetic elements that are adapted to different environmental conditions and thus provide resilience and adaptive potential.*

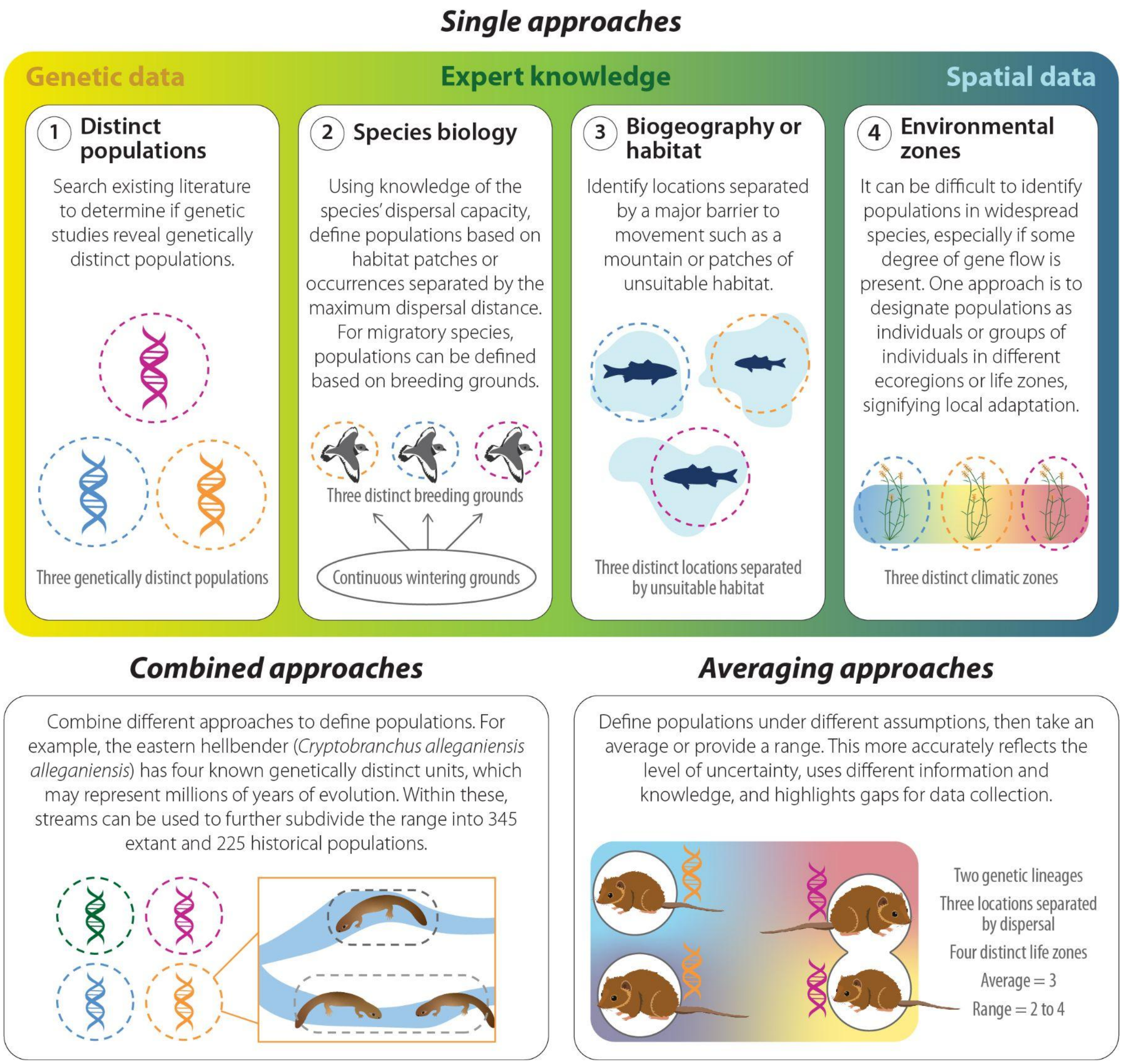
Distinct populations are the result of the demographic and evolutionary history of species, and reflect historically isolated or unique populations, accumulated genetic differences, and likely local adaptations.

The need to retain populations across the range as a species-wide resource has long been recognized in forestry (e.g. EuForGen, Koskela et al. 2013; euforgen.org), fisheries, and beyond. It is increasingly recognized for all species and implemented in policy (e.g. U.S. Endangered Species Act assessments of representativeness across the range).

Figure 1. Criteria of indicators in the Monitoring Framework of the Kunming-Montreal Global Biodiversity Framework (KMGBF). Headline indicator A.4 and complementary indicator for genetic diversity can support monitoring progress on Goal A and Target 4 on species populations in the KMGBF. CBD, Convention on Biological Diversity.

Box 1. How do we define a population?

Defining populations can be a challenging task that requires careful consideration. Sometimes populations can be easily defined based on clear boundaries, while in other cases, additional information drawn from the scientific literature, expert knowledge or geospatial data is required. Using a variety of approaches, it is feasible to define distinct populations that are biologically meaningful.



Single approaches

Genetic data — **Expert knowledge** — **Spatial data**

1 Distinct populations

Search existing literature to determine if genetic studies reveal genetically distinct populations.

2 Species biology

Using knowledge of the species' dispersal capacity, define populations based on habitat patches or occurrences separated by the maximum dispersal distance. For migratory species, populations can be defined based on breeding grounds.

3 Biogeography or habitat

Identify locations separated by a major barrier to movement such as a mountain or patches of unsuitable habitat.

4 Environmental zones

It can be difficult to identify populations in widespread species, especially if some degree of gene flow is present. One approach is to designate populations as individuals or groups of individuals in different ecoregions or life zones, signifying local adaptation.

Combined approaches

Combine different approaches to define populations. For example, the eastern hellbender (*Cryptobranchus alleganiensis alleganiensis*) has four known genetically distinct units, which may represent millions of years of evolution. Within these, streams can be used to further subdivide the range into 345 extant and 225 historical populations.

Averaging approaches

Define populations under different assumptions, then take an average or provide a range. This more accurately reflects the level of uncertainty, uses different information and knowledge, and highlights gaps for data collection.

Box 1: Defining distinct populations can be done through a combination of genetic data, expert opinion and spatial data. Information can be averaged across multiple data sources to incorporate uncertainty. Other approaches may be possible, including trait/ behavior/ morphology differences and management units.

Why these indicators are appropriate and advantageous

The list of advantages below is summarized in Figure 3.

Advantage 1: ***Can be implemented in all countries for many species*** *because they can be inferred from diverse data sources including quantitative and qualitative non-genetic data.* Ideally, indicators provide accurate information for tracking targets, in a standardized methodology, with minimal needs for additional capacity or funds. The *Ne 500* and *populations maintained* indicators aim to leverage all available biodiversity knowledge on local populations including knowledge that may not be quantitative enough for traditional ecological and evolutionary models. Specifically, their flexible methodology allows many types of data to be employed- including existing national or regional databases or monitoring networks, traditional knowledge from Indigenous People and Local Communities (IPs and LCs) and other right-holders, scientific expert consultation, scientific literature, government or NGO reports, citizen science platforms, range maps, and GIS based analysis of habitat and organism density (Hoban et al. 2023). As such, these indicators are accessible and it is likely that all countries could report on them for at least dozens of representative species.

Advantage 2: Emphasizing the local population level ***may facilitate local empowerment, ownership, pride and action by local communities****.* Due to accepting a wide variety of data types, including knowledge outside of traditional scientific studies and biodiversity monitoring, the indicators allow local knowledge holders including IPs and LCs to lead or contribute to monitoring. Such participation can broaden the base of biodiversity observations, especially in areas where other data are sparse (example in Figure 2). This also encourages scientists to collaborate with IPs and LCs and local managers (in compliance with the CARE guiding principles (Carroll et al. 2020, Cook et al. 2021), and combine and compare data from different ways of knowing. The indicators have the potential for leveraging citizen science data if combined with observation models (Van Strien et al. 2013), and providing a powerful means of tracking change across space and time at a higher resolution than data collected by scientists alone. The indicators can also provide empowerment and pride; a focus on genetic diversity among and within populations emphasizes the importance of local populations for community-based protection. The active role of IPs and LCs is vital for successful conservation, as IPs and LCs safeguard and often sustainably manage most of the world’s biodiversity (Fa et al. 2020).

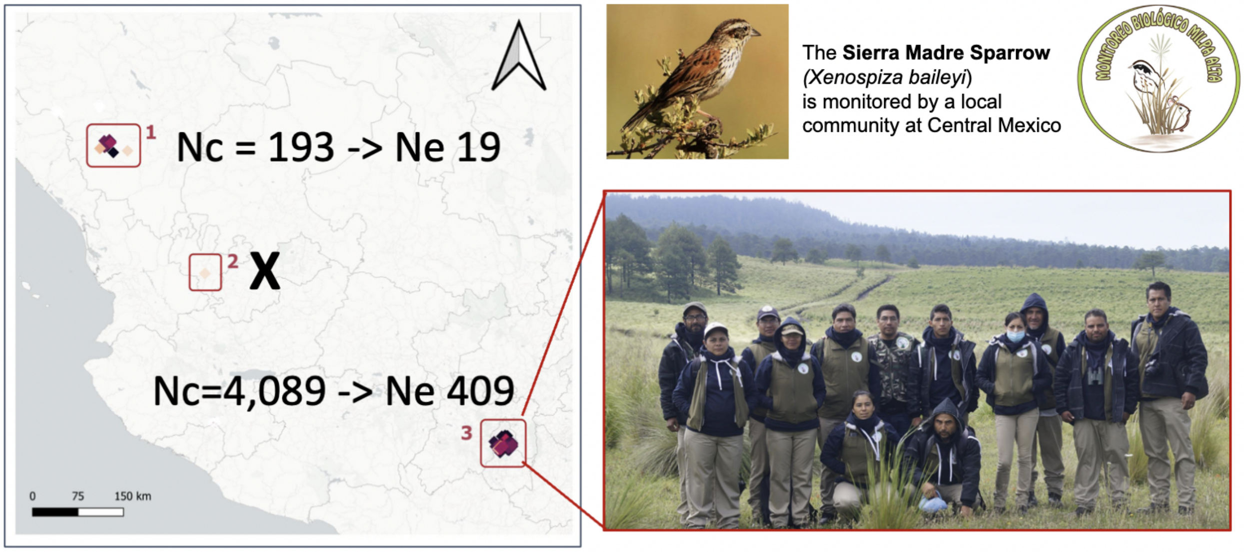


Figure 2: *Xenospiza baileyi* is a sparrow known from three geographically isolated populations in Mexico. The *population maintained* indicator is ⅔=0.66 because one population is extinct. Census data from local monitoring initiatives can be used to estimate Ne for the remaining populations, showing that neither of them is above Ne 500 (using the conservative Ne:Nc ratio of 0.1), but the southern most population census is increasing. This population experiences conservation and monitoring actions by a community organization ("Brigada de Monitoreo Biológico Milpa Alta") run by local inhabitants of San Pablo Oztotepec.

Advantage 3: Data supporting these indicators ***can be gathered for many species relatively quickly****- orders of magnitude faster than traditional DNA based genetic assessments.* Although DNA based studies are preferred to estimate indicators, they remain slow and expensive. A genetic study estimating Ne in five populations might take one to three years from planning to DNA analysis, and cost 10 to 30K USD for supplies and 50-200K for personnel. Staff must have technical training in molecular techniques, population genetics, and bioinformatics. Consequently, most countries lack population genetic data for most species. For example, Brazil has ~60,000 plants and vertebrate species but only 257 have genetic studies (Torres-Florez et al. 2018), less than 0.5%. Across the Americas, only about 350 vertebrate species had genetic data from multiple populations (Lawrence et al. 2019). Documenting genetic diversity lost from populations using historic DNA is often spatially and temporally biased (Jensen and Leigh 2022). Thus, an indicator based on molecular DNA data is unfeasible. In contrast, data for the *Ne 500* and *populations maintained* indicators can be rapidly gathered using existing reports, scientific and citizen science databases, and by consulting experts and IPs and LCs (in our experience, on average 3.5 hours/ species). For 100 species, this is 350 hours, or about 10 weeks of one person full time. The individual does not need to be a geneticist, but some help or collaboration from a geneticist is useful, and such collaborations are increasing (Taft et al. 2020, Pärli et al. 2021, Kershaw et al. 2022).

Advantage 4: The indicators are ***'forward compatible', meaning they can incorporate new methods that arise*** *due to technological advances; data collected now will be comparable* *to data collecting using future approaches.* Currently the primary data types used for approximating Ne and populations (Hoban et al. 2023) is geographic and demographic (maps, census population size [Nc], narrative text, natural history texts, texts of national flora; qualitative or quantitative), but as genetic data collection accelerates, information from DNA-based studies can be the basis of the indicators (see Andersson et al. 2022). There are thousands of populations globally with conservation-relevant DNA data. Temporal DNA monitoring is increasing, which can document indicator-relevant data, such as occurrence and loss of distinct populations, levels of genetic variation, effective size, and inbreeding (Hoban et al. 2022) and genetic swamping through hybridization (O'Brien et al. 2022). Forward compatibility also encourages future collection of genetic data and capacity building for countries to develop more genetic monitoring infrastructure (including genotypes inferred using remote sensing technology; Meireles et al. 2020).

Advantage 5: The indicators ***can utilise data from and align with other ongoing biodiversity assessments where they exist****.* Biodiversity assessments such as Red Listing, work by NGOs monitoring priority species, and Key Biodiversity Areas (KBAs) typically document species biology, demography, maps,and consult experts- the same knowledge underlying the genetic diversity indicators. Spatial planning and environmental impact assessment, also a part of the KMGBF, may also incidentally produce the necessary data. For example, Red List workshops and/or other detailed in-country assessments convene species experts with knowledge of literature and first-hand experience, to assess species threats using demography and data on geographic ranges. With little extra effort, in some cases a few minutes, experts can translate this to Nc or Ne (again, qualitatively or quantitatively) and populations maintained (Thurfjell et al. 2022), assuming that training, clear guidance and data storage infrastructure are in place to ensure standardized observation collection. Though we acknowledge that Red List assessments need improvements including more frequent updates (Fraixedas et al. 2022), we conclude that this synergy can save time and funds.

Advantage 6: These indicators are ***useful for directing action and policy*** *towards those populations and species most needing it, and prioritization under limited resources, not just for reporting.* Indicator 1 highlights which and how many populations within a species need rapid action to elevate them above the Ne 500 threshold (e.g., by reintroducing captive bred individuals, gene flow/ connectivity, genetic rescue). Ranking species by indicator 1 values can prioritize species with many small populations which need intervention now- including wide-ranging species not threatened at the species level but suffering population extinctions. Both indicators, but especially indicator 2, based on losses of populations, could highlight species needing greater legal protection. We also suggest that the indicators could be used with a traffic light system of risk, for easy explanation to decision makers (at the population level, green: Ne >> 500, yellow: Ne ~ 500, red: Ne < 500, alarm: Ne < 50. Similar thresholds could apply to proportions of populations lost (Exposito-Alonso et al. 2022).

Advantage 7: *The indicators* ***are scientifically valid****, whilst meeting all other criteria and being practical.* They are connected to core concepts in population and evolutionary genetics: genetic erosion, adaptive potential, and resilience to environmental change. Specifically, they leverage two established concepts: a threshold change at Ne 500 and the existence of local adaptation. Other indicators do consider genetic concepts but more tangentially. Khoury et al. (2019) uses geographic area as a genetic diversity proxy, leveraging the genetic concepts of Isolation by Environment and Isolation by Distance. Hollingsworth et al. (2020) also considers them, but more qualitatively (good/ bad condition). The Living Planet Index is complementary to, but insufficient as a genetic diversity indicator, because it calculates percent change in Nc, rather than the critical Ne 500 threshold. Percent decline depends on initial Nc (and when it was calculated) and results in variable impacts on genetic diversity (Hoban et al. 2021). We emphasize that a genetic diversity indicator must connect to core concepts of genetic diversity.

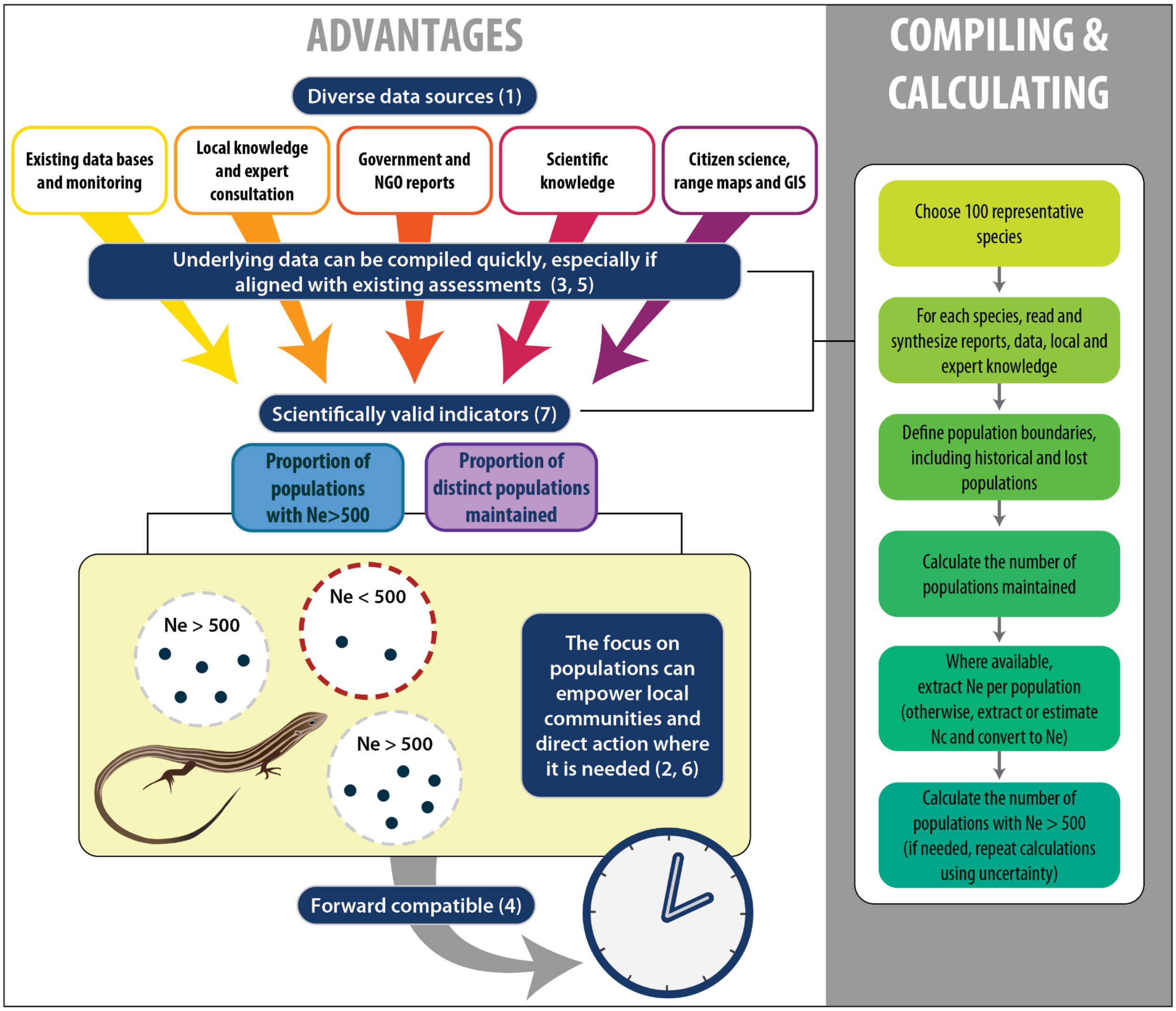


Figure 3: Advantages of diverse data sources to inform the two scientifically validated genetic diversity indicators. The right panel describes the process for each country to select ~100 species, gather data and calculate the values for the two indicators. The numbers in parenthesis refer to the numbered Advantages in the section, “Why these indicators are appropriate and advantageous.”

Section 2. Challenges and solutions

We divide challenges into two rough categories, scientific and policy, though some are common to both. Suggested solutions are presented after each, with a summary in Table 2.

Policy challenge: Gathering data on the indicators still requires personnel, time, and funds. When first starting, assessing species for these indicators may necessitate training by or collaboration with geneticists. However, support materials (guidance documents, case studies, webinars, etc.) exist, critical metadata is being defined, workflows to automate gathering and curating data and metadata are in development, and scripts for automatically calculating indicators from data are being piloted (Hoban et al. 2023). Moreover, the advantages outlined above, especially regarding flexible data collection and information provided by IPs and LCs, support inclusivity, as well as fairly rapid data collection. As noted in Advantage 5, the indicators can also be assessed as part of other species assessments in progress, like Red Listing or national priority taxa surveys.

Policy challenge: Genetic concepts and terminology are too technical. We acknowledge that “effective population size” is a challenging concept. However, the reasoning behind Ne can easily be communicated- that populations lose genetic diversity faster when they are smaller, and that loss accelerates when populations reach the tipping point captured by the Ne indicator. The concept of thresholds in conservation are common and easily explained (e.g., minimum viable population size). In addition, by engaging stakeholders, we have found that simple graphics can demonstrate how Ne is smaller than census size Nc, and how Ne influences change in genetic diversity. To overcome this challenge, clear communication is needed- a lesson for future COPs where indicators perceived as overly complex may be rejected. Improved communication techniques, infographics and briefs may help overcome hesitancy due to perceived complexity (Hoban et al. 2013, 2023, Taylor et al. 2017, Lundmark et al. 2019).

Policy and scientific challenge: Achieving Ne 500 may not always be practical. For example, sufficient supplementation or habitat restoration to meet this threshold may be infeasible for some populations of critically endangered species without huge investment of resources. An example is the Sumatran rhino which has fewer than 100 adult individuals and breeds slowly (Havmøller et al. 2016). Nonetheless, an indicator is still needed to highlight the critical situation for such populations and species, encourage monitoring, and inform strategies for reversing decline and aiming towards Ne 500, even if improving the census size will be slow and laborious (as with many Critically Endangered Red List species).

Scientific challenge: *Some species naturally occurring in small population sizes may persist below Ne 500 without negative consequences*. For example, micro-endemic species, or populations on islands or other highly restricted habitats, may have evolved to tolerate small populations and/ or persisted at small populations for hundreds of generations (e.g. the Devil’s hole pupfish *Cyprinodon diabolis*; Brown 2021). These species may have experienced purging or other genetic mechanisms (or life strategies like clonality) to help them persist at a small size for long periods. We suggest that a key knowledge gap to be addressed is enumerating how many and which species fall into these categories, and establish guidance for them. Additionally, knowledge of baseline Ne or Nc can help identify any change in Ne.

Policy challenge: Focusing on populations might divert resources from other activities needed to halt biodiversity loss at the ecosystem and species levels. This critique is misguided, because extinction first starts with loss of populations, and with it their genetic diversity. Moreover, loss of populations weakens local ecosystems by removing supportive biotic interactions and vital ecosystem services, and resilience to environmental change (Ceballos and Ehrlich 2002). Lastly, ensuring high values for the genetic diversity indicators can ensure species stay out of the costly and difficult conservation “emergency room” (recovery from critical situations) (DeWoody et al. 2021). Detecting and targeting interventions is critical to halt losses of populations.

Scientific challenge: A few scientists question the need to monitor and maintain neutral genetic diversity for conservation. Functional genetic diversity (i.e. diversity related to adaptation) may not always be represented by neutral genetic diversity (i.e. diversity assessed by most genetic markers) (Kardos et al. 2021, Teixeira and Huber 2021). However, this debate does not affect the genetic diversity indicators, because they are proxies for both functional and neutral genetic diversity. The *populations maintained* indicator accounts for functional genetic diversity- conserving distinct populations on average conserves functional (or locally adapted) genetic diversity, even if specific alleles or genes are not identified (Meek et al. 2022). The *Ne 500* indicator also accounts for functional diversity, because below the 500 threshold, adaptive alleles are lost faster due to genetic drift, and the efficacy of natural selection that drives adaptation is reduced (Willi et al. 2022). Thus, although functional genetic studies are desirable in some cases (e.g., breeding or translocating individuals better adapted to drought), the proposed indicators are a proxy for maintaining functional genetic diversity in sufficiently large distinct populations throughout the species range.

Scientific challenge: Populations are hard to define. We acknowledge that defining populations has generated debate among biologists for decades. However, often populations can be simply defined based on geography or habitat (distinct lakes or patches, mountain tops, discontinuous habitat; see Box 1). For numerous other species, defining populations without genetic data is feasible with careful guidance, including using ecoregions, expert defined ‘adaptive capacity units’, or life zones subdivided by biogeography, as proxies of genetic differentiation reflective of local adaptation and/or long-term evolutionary lineages (Tobón-Niedfeldt et al. 2022). Migratory species can be defined by focusing on breeding populations (e.g., piping plover, *Charadrius melodus* winter in a continuous region but breed in geographically distinct locations; Miller et al. 2010). Genetic knowledge from other species (including phylogeographic patterns) can also help. Any uncertainty about the scale of populations, or the degree of human-caused fragmentation on genetic distinctions, can be incorporated by calculating the indicator under different assumptions of population isolation (e.g., 4, 10, or 20 populations) and taking an average or propagating uncertainty such that the national indicator calculation displays confidence intervals. Showing uncertainty is advantageous- it more accurately reflects knowledge, allows the use of more data, and can highlight gaps and priorities for data collection.

Scientific challenge: The Ne/Nc ratio varies among species and the previously advised ratio of 0.1 should be refined because it is too broad. Approximating Ne from Nc depends on an Ne/Nc ratio. We acknowledge this ratio varies based on species' breeding strategy, sex ratio, and variance in reproductive success among parents (Frankham 1995, Waples 2002). We note that the methodology focusing on Ne 500 allows the use of different ratios if that information is available (Laikre et al. 2021). The 0.1 ratio (and the rule of thumb Nc 5000) is well supported as a conservative ratio (see Frankham et al. 2017, Frankham 2021, Hoban et al. 2021c for recent reviews on existing ratios across species). However, it is only a default when no other knowledge exists. For example, many birds and plants have a ratio of 0.3, which would be an Nc of 1500 (see Figure 4). Other scientists have advocated Ne 1000 instead of Ne 500, which can also be implemented. Work is needed to increase the list of populations/species/taxonomic groups with estimated Ne/Nc ratios.

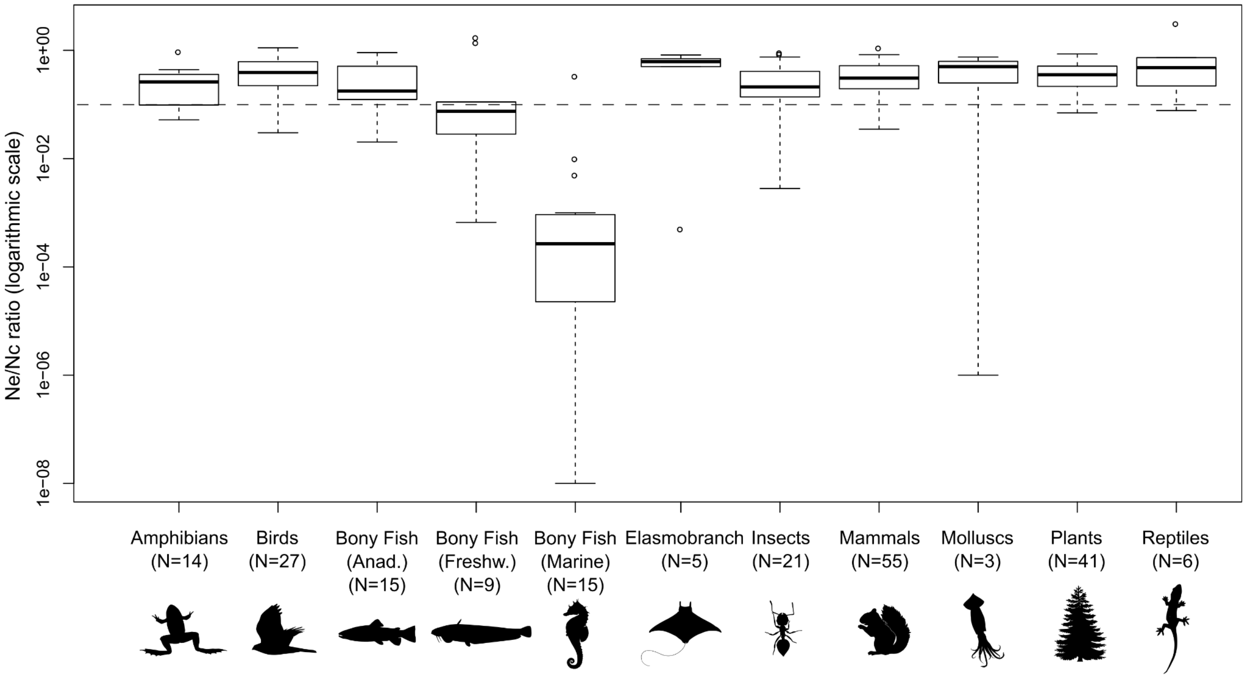


Figure 4: Boxplot of the mean Ne/Nc ratios (on a logarithmic scale) per taxonomic group calculated from values reported in 208 studies reviewed in Hoban et al. 2020, omitting a few taxonomic groups with low sample size. Thick lines represent median values. Up and lower hinges represent first and third quartiles, whiskers represent the range of data extending up to 1.5 times the interquartile range, and points represent data outside of this range (outliers). The horizontal dotted line corresponds to the recommended Ne/Nc ratio value of 0.1.

Scientific, and some policy-maker, challenge: These indicators do not use genetic data such as alleles, inbreeding, etc. from single or temporal monitoring. We applaud that an increasing number of species have genetic data, and that progress is being made in translating genetic data into metrics comparable across species. However, such knowledge is rare in most countries and species (Hogg and Belov 2022) and the gap in sufficient genetic data needs to be addressed. When available, genetic datasets can be used to calculate Ne and help define distinct populations. Collation of genetic data is also vital (Lawrence et al. 2019, Schmidt et al. 2020, Leigh et al. 2021). This could encourage more genetic studies to take place, and remind researchers already conducting genetic studies that clearly reporting Ne and population structure has conservation impact. However, such work is not on the timescale for the current framework and targets for all species given the scarcity of such data at present.

Table 2. Summary of challenges associated with the genetic diversity indicators presented by the scientific and/or policy communities, as well as suggested solutions to overcome them.

Challenge	**Community**	**Suggested Solution**
Gathering data is still time consuming (thus requiring money and capacity)	Policy	Time is required for all indicators. Practical guidelines and new protocols are making it faster
Genetic concepts and terms (including Ne) are hard to understand	Mostly policy	Clear science communication tools can help
Achieving Ne 500 is infeasible for some highly threatened organisms' populations	Policy	Actions to increase Ne as much as possible can still be enacted, to help genetic diversity
Ne 500 may not be needed for some organisms (e.g., island and small habitat endemics)	Policy and Scientific	In these cases, a more appropriate minimum Ne may be defined by ongoing research. Also the trend in Ne remains important
A focus on populations may divert funds from species' or ecosystem conservation	Policy	All levels of biodiversity are vital. Extinction starts with population losses
Neutral genetic diversity does not directly support adaptive potential	Scientific	The indicators are proxies of adaptive and neutral genetic diversity
Populations are hard to define	Policy and Scientific	In many situations defining populations is feasible (Box 1), and where difficult tools and guidance can help. In all situations, reporting uncertainty should take place.
The 0.1 assumption for Ne/Nc is too conservative and neglects taxon specific Ne/Nc knowledge	Scientific	Apply specific taxonomic group ratios when possible. Use DNA based Ne estimates if possible. Researchers need to compile Ne/Nc ratios for more species/taxonomic groups

Indicators are too basic because they don't use DNA based metrics	Mostly scientific	Most species do not have DNA data; using non-DNA data allows for assessing exponentially more species. Also, DNA data can be used when available.
Ne 500 is insufficient as Headline indicator (see Section 3)	Policy and Scientific	Must be reported with the Complementary indicator the proportion of *populations maintained* within species

Section 3. Final challenge and ways forward

The *Ne 500* indicator is a headline indicator under the KMGBF (mandatory for countries to report), while the *populations maintained* and other genetic diversity indicators are Complementary indicators, meaning they are optional and therefore will likely be implemented by a subset of countries, species and regions.

It would be problematic if Ne 500 *is the only genetic diversity indicator reported*, *because it was designed to directly complement the* populations maintained *indicator*, to maintain both among *and* within population genetic diversity. The two indicators are equally important. The *Ne 500* indicator (currently) does not have a calculation adjustment for when populations are lost. It is currently defined as the proportion of extant populations > 500. If populations are lost, they are no longer in the calculation and so population loss actually improves the indicator value- an extremely undesirable outcome.

We assert that the most ideal situation would be to have both indicators 1 and 2 as Headline indicators, along with, when feasible, other genetic indicators. Gathering data underlying the two indicators and calculating them can take place simultaneously.

If the Ne 500 indicator is used alone, it must be adjusted to incorporate local population loss. A simple discounting mechanism would assign an Ne value of 0 to recently (after a defined baseline year) extinct populations, thus keeping them in the calculation as populations with Ne<500. This would ensure the indicator value does not 'improve' following local population extinctions.

An alternative would be to present multiple genetic indicators in a single framework. In this way, indicators could be complemented with other knowledge on genetic diversity, including genetic statistics and threats to genetic diversity. These elements could all be reported simultaneously as a series of statistics, and/or as a synthetic single measure like the Ocean Health Index (Halpern 2020). This builds on the idea of the 'Scottish scorecard' which compiles information on aspects of species' genetic health and threats. Ideally, a platform that gathers and compiles all available genetic data, population data, and knowledge-based data, with clear open-source workflows, and an output index of health, with statements on data caveats and uncertainty, would be produced and updated in real-time (Walters and Scholes 2017).

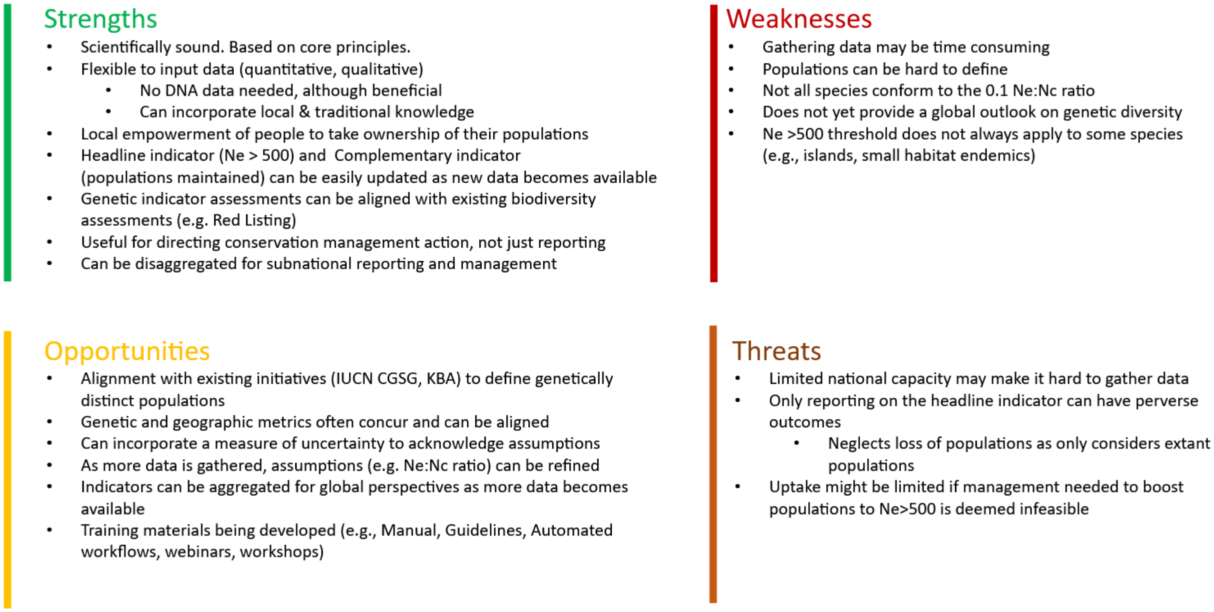
Elements that may be important to include for reporting genetic diversity status and trends include proportion of populations with Ne< 50 (e.g. populations at severe inbreeding risk, which may be entering an extinction vortex), a count of species in which genetic management is occurring or planned (e.g., translocations), a quantitative assessment of hybridization as a threat (e.g., genetic swamping, genetic ‘pollution’, extinction by hybridization), geographic range protected in situ and ex situ (Khoury et al. 2019), geographic range likely lost due to land use change (Powers and Jetz 2019), population trends based on local surveys (Loh et al. 2005), ex-situ conservation efforts including the number of maternal lines represented ex-situ (as a proxy for Ne ex-situ), and/or information on the genetic knowledge/ genetic studies available in country (Laikre et al 2020). Predictions of likely genetic diversity loss from simple simulation models could also be reported. Meanwhile, direct assessment of DNA data can complement these proxies, including likely genomic threats (Bertorelle et al. 2022), and observed loss of genetic variants (Andersson et al. 2022).

Conclusion and outlook

We summarize the mid to long term vision of the genetic diversity indicators using a Strengths-Weakness-Opportunities-Threats (SWOT) diagram (Figure 5). These two indicators are feasible for all countries, use diverse data, and can empower local monitoring and action (Advantages 1-3). We note the two indicators should be used in combination as both were designed to be complementary. Assessment can be repeated every five years as required by the CBD, for hundreds, if not thousands, of species per country. They can be efficiently completed along with Red Listing or other processes, are comparable across space and time even if new data arise, and can directly inform action (Advantages 4-6). They have national and global usefulness to highlight priority species and populations. They are scientifically valid (Advantage 7), yet also a communication tool to help policy makers and the public better visualize and recognize genetic diversity and evolutionary processes. They can systematically mobilize a wealth of currently under utilized knowledge and data, in a manner similar to the Red List, and would improve the resolution of species trends in species’ assessments.

Work remains to be done, including building capacity, working with species with naturally small ranges, connecting theoretical work (Exposito-Alonso et al. 2022, Tobón-Niedfeldt et al. 2022) to the indicators, and increasing the list of species with known Ne/Nc ratios. Informatic tools and GIS-based methods are also needed to make the indicators more standardized (e.g. for defining and delineating populations) and useful to more people. We foresee genetic diversity indicators following the trajectory of tools such as the IUCN Red List of Ecosystems and Green Status, towards standardized, accessible, widely implemented, and comparable indicators.

In the coming years, CBD Parties, national and subnational governments, and NGOs will discuss and begin to implement genetic diversity indicators. We hope this article helps ameliorate some concerns, provide solutions to challenges presented by these indicators, and provides a blueprint for successful operationalization.



Strengths

- Scientifically sound. Based on core principles.
- Flexible to input data (quantitative, qualitative)
  - No DNA data needed, although beneficial
  - Can incorporate local & traditional knowledge
- Local empowerment of people to take ownership of their populations
- Headline indicator (Ne > 500) and Complementary indicator (populations maintained) can be easily updated as new data becomes available
- Genetic indicator assessments can be aligned with existing biodiversity assessments (e.g. Red Listing)
- Useful for directing conservation management action, not just reporting
- Can be disaggregated for subnational reporting and management

Weaknesses

- Gathering data may be time consuming
- Populations can be hard to define
- Not all species conform to the 0.1 Ne:Nc ratio
- Does not yet provide a global outlook on genetic diversity
- Ne >500 threshold does not always apply to some species (e.g., islands, small habitat endemics)

Opportunities

- Alignment with existing initiatives (IUCN CGSG, KBA) to define genetically distinct populations
- Genetic and geographic metrics often concur and can be aligned
- Can incorporate a measure of uncertainty to acknowledge assumptions
- As more data is gathered, assumptions (e.g. Ne:Nc ratio) can be refined
- Indicators can be aggregated for global perspectives as more data becomes available
- Training materials being developed (e.g., Manual, Guidelines, Automated workflows, webinars, workshops)

Threats

- Limited national capacity may make it hard to gather data
- Only reporting on the headline indicator can have perverse outcomes
  - Neglects loss of populations as only considers extant populations
- Uptake might be limited if management needed to boost populations to Ne>500 is deemed infeasible

Figure 5, Strengths-Weakness-Opportunities-Threats (SWOT) analysis. Summarizing the key elements of the adopted indicators. The threats are primarily elements beyond this community's control. Ne, effective population size; Nc, census size; GI, genetic indicator; IUCN CGSG, International Union for Conservation of Nature Conservation Genetics Specialist Group; KBA, Key Biological Area.

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Supplemental: composite of photos from COP15 showing us discussing + our booth?, summary of webinars

Author contributions: SH conceived of the manuscript, contributed resources and project administration and acquisition, analysis, interpretation and synthesis of information, wrote the original draft and critically edited the manuscript.

JdS contributed to the concept, acquisition, analysis, interpretation and synthesis of information and assisted in writing and editing the manuscript.

AH, BKS,LR, KM assisted in validation and investigations and reviewed and edited drafts.

MH, AMY, IPV contributed to the methodology, resources, project administration and acquisition and interpretation of information and reviewed and edited drafts.

RS contributed to the methodology, visualization, resources and acquisition and interpretation of information and reviewed and edited drafts.

CCG provided critical feedback and input throughout the process, assisted with methodology and validation and reviewed and edited drafts.

LL, CV contributed to the concept, resources, and funding acquisition, and the acquisition, analysis, interpretation and synthesis of information and assisted in writing and editing the manuscript.

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