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POLICY DIRECTION

Bringing together approaches to reporting on within species genetic diversity

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Abstract

1. Genetic diversity is one of the three main levels of biodiversity recognised in the Convention on Biological Diversity (CBD). Fundamental for species adaptation to environmental change, genetic diversity is nonetheless under-reported within global and national indicators. When it is reported, the focus is often narrow and confined to domesticated or other commercial species.
2. Several approaches have recently been developed to address this shortfall in reporting on genetic diversity of wild species. While multiplicity of approaches is helpful in any development process, it can also lead to confusion among policy makers and heighten a perception that conservation genetics is too abstract to be of use to organisations and governments.
3. As the developers of five of the different approaches, we have come together to explain how various approaches relate to each other and propose a scorecard, as a unifying reporting mechanism for genetic diversity.
4. *Policy implications*. We believe the proposed combined approach captures the strengths of its components and is practical for all nations and subnational governments. It is scalable and can be used to evaluate species conservation projects as well as genetic conservation projects.

KEYWORDS
biodiversity, conservation, convention on biological diversity, indicators, monitoring, policy, scorecard, wild species

1 | BACKGROUND

The Convention on Biological Diversity (CBD, 1992) recognises three main levels of biodiversity: 'diversity within species, between species and of ecosystems'. Genetic diversity within species (heritable variation) underpins their ability to react, adapt and be resilient, which is particularly crucial at this time of climate change, and biodiversity loss. Reporting is a key aspect of the CBD—all Parties must report progress approximately every 4 years. Reporting on changes over time allows policy makers to assess progress, evaluate policy effectiveness and learn from the outcomes. However, despite its importance, genetic diversity did not achieve similar levels of recognition to the other two levels of biodiversity in the 2020 Aichi targets (e.g. Hoban et al., 2020; Laikre et al., 2020) and where reported upon, reports were largely limited to species of agricultural or forestry importance (Hoban et al., 2021), which are largely unrepresentative of global biodiversity.

Concerns about neglect of wild species' genetic diversity over the past three decades have led to several potential monitoring and reporting approaches being proposed. While we welcome this burgeoning interest, we are concerned that a choice of multiple reporting approaches may lead to confusion among policy makers, conservation practitioners and other stakeholders. Such confusion may lead to continued lack of reporting on genetic diversity of wild species, as the issue may be perceived to be too complex to resolve. Having different approaches also limits opportunities to make comparisons among countries, within countries and regions, and across time, and thus may mask genetic diversity loss. Given genetic diversity's vital role, we believe that a consolidated approach to reporting is essential if all countries are to maximise opportunities to protect biodiversity. This paper presents a simple framework to bring together several proposed reporting methods, and shows how they are related.

In our proposals, genetic monitoring refers to 'monitoring of genetic diversity within and between populations of species across contemporary time frames covering at least two different time points' (Hvilsom et al., 2022). The examples below will show that such monitoring can make use of DNA data or proxies (Table 1), and results may be expressed as single indicators or grouped. Our focus is on monitoring genetic diversity within species, and does not include more general use of genetic data to study biodiversity (e.g. the use of molecular markers to track individual organisms, or the use of DNA barcoding to identify species). Indicators measure pressures on biodiversity, the state of biodiversity, conservation responses and benefits from ecosystem services (Butchart et al., 2010).

2 | APPROACHES IN USE OR IN DEVELOPMENT

The Group on Earth Observations Biodiversity Observation Network (GEO BON) Genetic Composition Working Group has used a collaborative international approach to develop genetic Essential Biodiversity Variables (EBVs; Hoban et al., 2022), designed for monitoring and understanding biodiversity change. These EBVs measure: (a) genetic diversity; (b) genetic differentiation; (c) inbreeding; and (d) effective population size (N_e). The first two require genetic sampling, but can usually be calculated from a single time point sample dataset. Furthermore, they can be calculated using different genetic markers (e.g. whole genome sequencing data, SNPs, DNA sequences, microsatellites), allowing cost to be reduced by using existing datasets (Kriesner et al., 2020), rather than requiring de novo sample analysis. Inbreeding and effective population size can be calculated using genetic data or inferred from proxies (Hoban et al., 2020, 2022). EBVs are summary measures of biodiversity rather than indicators.

Hoban et al. (2020) and Laikre et al. (2020) have also developed three complementary indicators for reporting on genetic diversity change, including 'genetic erosion'.

1. Indicator 1 describes the relative status of genetic diversity and inbreeding within populations by comparing the effective population size to the size needed for conserving genetic diversity, by calculating the proportion of populations with an effective size over 500. This indicator can usually be calculated from population census data using a well-accepted ratio of 1:10, effective to census size (Hoban et al., 2020, 2022).
2. Indicator 2 calculates the proportion of distinct extant populations (e.g. Evolutionary Significant Units, Distinct Population Segment or similar) relative to historic levels and hence the percentage of populations that have been lost, to reflect likely loss of local adaptations. Khoury et al. (2019) developed a similar indicator that measures the proportion of a species' geographic range that (a) has been conserved ex situ or (b) is encompassed within protected areas.
3. Indicator 3 measures DNA monitoring and research within a given country by reporting the number of populations and species studied.

As with all indicators, these are imperfect measures of genetic change and careful interpretation and application of indicators is needed, including thoughtfully considering historic and recent population fragmentation (see Hoban et al., 2020, Hoban et al., 2022 for a more complete discussion). On average, although, they should provide relative assessment of genetic erosion, in an affordable manner, without requiring genetic data.

Several countries are developing national programmes for monitoring genetic diversity. The Swedish Agency for Marine and Water Management (SwAM) has proposed three indicators to integrate genetic diversity into the national aquatic monitoring programme (Andersson et al., 2021). These focus on monitoring genetic diversity within and between populations, and on assessing the genetically effective population size; they are being applied to several marine and freshwater species using different types of DNA data. Furthermore, the Swedish Environmental Protection Agency (SEPA) has recently prioritised species for monitoring genetic diversity, and initiated monitoring using different DNA methods depending on

TABLE 1 Comparison and congruence among different existing approaches for reporting on genetic diversity in wild species. Existing approaches are shown within the framework of proposed headlines—these describe different approaches to achieve the same end points. Accommodating different estimators of each headline issue is important to allow deployment across different resource settings and other operational constraints: End users are encouraged to use all indicators for which data are available, ideally including all categories. ✓ denotes where an indicator/approach is used or recommended, (✓) denotes where an indicator/approach may be relevant in some circumstances. [a]Proposed headlines for reporting on genetic diversity. [b]Data types that can be used for each approach: G = genetic data, N = non-genetic data. [c–h]A summary of approaches currently used or recommended, as reported by: [c]Hoban et al., 2022, [d]Hollingsworth et al., 2020, [e]Johannesson & Laikre, 2020; Andersson et al., 2021; traditional genetic markers and/or genomics are used depending on species, thus genomic measures are monitored in some cases, [f]Fischer et al., 2020, [g]Hoban et al., 2020, [h]Laikre et al., 2020

	Proposed headlines[a]	Indicators and/or approaches to monitor genetic diversity	Data types[b]	EBVs (GEO BON)[c]	Scotland[d]	Sweden[e]	Switzerland[f]	Hoban et al.[g], Laikre et al.[h]
Threats	1a. Diversity loss: loss of within-population genetic diversity	N_e (Effective population size)	G, N	✓	✓	✓	✓	
		Proportion of populations >N_e 500 threshold	G, N			✓		✓
		Range contraction or fragmentation	N		✓			
		Genetic diversity	G	✓		✓	✓	
		Change in genetic diversity	G		✓	✓	✓	
		≥ 95% variation within populations retained over 100 years	G			✓		
		Inbreeding	G	✓	✓	(✓)	✓	
		Genetic load	G			(✓)	✓	
	1b. Diversity loss: loss of between-population genetic diversity and divergent lineages	Genetic differentiation	G	✓		✓	✓	
		Change in genetic differentiation (F_{ST})	G	✓		✓	✓	
		≥95% variation between populations retained over 100 years	G			✓		
		Genetic connectivity	G	✓		(✓)	✓	
		Proportion of distinct populations maintained within species	G, N			✓		✓
		Loss of lineages known or thought to be genetically distinct	G, N	✓	✓	✓	✓	
	1c. Diversity loss: loss of important functional genetic diversity	Adaptive potential	G			(✓)	✓	
		Loss of local populations in distinct environments or with distinct phenotypes	N		✓			
		Loss of genetic variants known to encode important adaptations or phenotypes	G		✓		✓	
	2. Hybridisation resulting in genetic swamping	Hybridisation	G, N				✓	
		Morphological/demographic evidence for unwanted genetic swamping	N		✓			
		Genetic evidence for introgression/ unwanted genetic swamping	G		✓	✓	✓	
	3. Low turnover/ constraints on adaptive opportunities	Evidence for clonality or limited sexual reproduction/recruitment from field or genetic data	G, N		✓			
Conservation Actions	4. In situ conservation	Proportion of genetic diversity within and between populations maintained (by in situ conservation actions)	G			✓	(✓)	
		Number and/or proportion of populations maintained	G, N			✓	(✓)	✓
		Summary of types of conservation actions underway	N		✓			
		Management through Gene Conservation Units	G		✓			
		Existence of genetic conservation projects	G		✓		✓	

(Continues)

TABLE 1 (Continued)

	Proposed headlines[a]	Indicators and/or approaches to monitor genetic diversity	Data types[b]	EBVs (GEO BON)[c]	Scotland[d]	Sweden[e]	Switzerland[f]	Hoban et al.[g], Laikre et al.[h]
	5. Ex situ representation	Proportion of genetic diversity within and between populations maintained (by ex situ conservation actions)	G			✓		
		Number and/or proportion of populations represented	G, N		(✓)	✓		(✓)
		Number and coverage in biobanks, zoos, seed collections etc.	G, N		✓			
Monitoring	6. Monitoring effort	Number of species/populations being monitored with DNA-based studies	G			✓	✓	✓
		Genetic diversity within and between monitored populations	G			✓	✓	

target species and techniques available (Posledovich et al., 2021). SEPA is also using Swedish Red List data to apply the indicators proposed by Hoban et al., 2020, which use proxies for genetic diversity (Thurfjell et al., 2022).

Switzerland is also implementing a strategy for a national monitoring of genetic diversity and currently runs a pilot study (https://gendiv.ethz.ch) for a small number of high priority species based on an earlier feasibility study (Fischer et al., 2020) and stakeholder analysis (Pärli et al., 2021). This will monitor genetic diversity, N_e, population structure, gene flow, inbreeding, hybridisation, genetic load and, if possible, adaptive potential. Switzerland uses historical DNA (hDNA) from collections to directly explore the temporal dimension of genetic diversity and to infer baselines of past genetic diversity. It uses individual whole genome resequencing and de novo genome assemblies for all species, perhaps making it the most powerful of the methods considered, although at high cost and complexity. As technologies mature, cost typically declines, possibly making this approach more widely applicable.

Hollingsworth et al. (2020) developed a scorecard approach to assessing genetic diversity in wild species and published a report for Scotland. This was compiled using available data and expert knowledge across multiple disciplines including conservation, agriculture and forestry and statistics. The method was designed to be practical in all countries regardless of economic development, focuses on threats to genetic diversity, and is not dependent on prior genetic knowledge. It assesses: (a) demographic declines likely to lead to genetic diversity loss (genetic erosion—including declines in population size, loss of functional diversity and loss of divergent lineages), (b) hybridisation likely to lead to undesirable replacement of genetic diversity (note that not all hybridisation is unwanted—in some cases it is beneficial to adaptation or may be a natural process at contact zones—and genetic rescue can rely on crossing with allochthonous populations), (c) restrictions to regeneration/turnover likely to impede evolutionary change and (d) representativeness of ex situ collections, where applicable. The overall risk and mitigation are summarised into 'green', 'amber' or 'red' status for each species. The Scottish scorecard covered 26 terrestrial species with plans to expand to marine species. A version is being developed in Libya to test its application in a country facing severe resource constraints. Additionally, standard bibliographic methods are being developed to facilitate a basic inventory of genetic studies of wild and domestic species within any given country, which can then be reported, although this does not refer only to genetic monitoring but also genetic surveys (single time point studies).

3 | ISSUES

Despite recognition of the importance of wild species' genetic diversity, reporting under CBD was very limited (Hoban et al., 2021). This may be partly because broad-scale monitoring of genetic diversity is seen as difficult. For example, while effective population size can be measured for populations (Hoban et al., 2022), getting meaningful data across a whole country for tens of species is resource intensive and thus challenging for developing nations. DNA sequence data collection for dozens of species may cost hundreds of thousands to several million euros per reporting period: for example, Posledovich et al., 2021 and developing nations may need better access to training and equipment (Hvilsom et al., 2022). In contrast, where detailed data are available, it makes sense to use them. Differential access to data may restrict comparisons among nations or regions if some use DNA data while others use proxies. Comparable data are important for nations to share good practice, or to enable interpretation across a species' international range. Reporting requirements must be flexible enough to allow nations to participate using the best level of technology available in each country for their own requirements.

Policy makers are a key audience who need access to clear, accurate information on the status of genetic diversity in order to make informed decisions affecting biodiversity (Hoban et al., 2013; Klütsch & Laikre, 2021; Vernesi et al., 2008). The multiplicity of methods may lead policy makers to conclude that reporting is too complex or impractical (Young et al., 2014). The healthy debate integral to scientific development may lead to mixed messages, even if most specialists agree on the key issues (Spierenburg, 2012).

Furthermore, monitoring and reporting should be valuable to practitioners. The disconnect between conservation geneticists and conservation practitioners ('conservation genetics gap'; Hoban et al., 2013) remains a problem (Klütsch & Laikre, 2021). These issues must be resolved for genetic diversity to be properly considered nationally and internationally, and for global species conservation plans. Standardised tools will allow practitioners to integrate genetic diversity into conservation efforts across the in situ and ex situ continuum, ensuring that this essential facet of biodiversity receives adequate attention and reporting to CBD can be achieved.

4 | OPPORTUNITIES

All the approaches to measure and report genetic change detailed above have strengths and are already being implemented, demonstrating that they are well aligned with policy-makers' needs. Hvilsom et al. (2022) have found that they have much in common, both in terms of policy goals and selection criteria (Figure 1).

As well as being essential for measuring change and informing policy, these approaches are relevant to species and habitat conservation. Existing and proposed genetic diversity conservation measures, such as gene conservation units (GCUs; Koskela et al., 2013; Minter et al., 2021) rely on monitoring to assess their efficacy. GCUs are designed to protect genetic diversity and evolutionary processes in situ, aiding adaptation to environmental change, and complementing existing approaches to species and habitat conservation. Effective population size is frequently used as an assessment criterion for GCUs.

The various teams developed ideas separately but are now in frequent communication, particularly through the Coalition for Conservation Genetics (Kershaw et al., 2022), providing an opportunity to collaborate on international standards. We also recognise the benefits of engaging with initiatives such as the Earth BioGenome Project, Africa BioGenome Project, International Barcode of Life and others around the world. We should embrace pragmatism. In order to serve all nations, we believe that we should cooperate to develop a practical and flexible approach that can encompass genetic (including genomic) data as well as proxies or expert opinion.

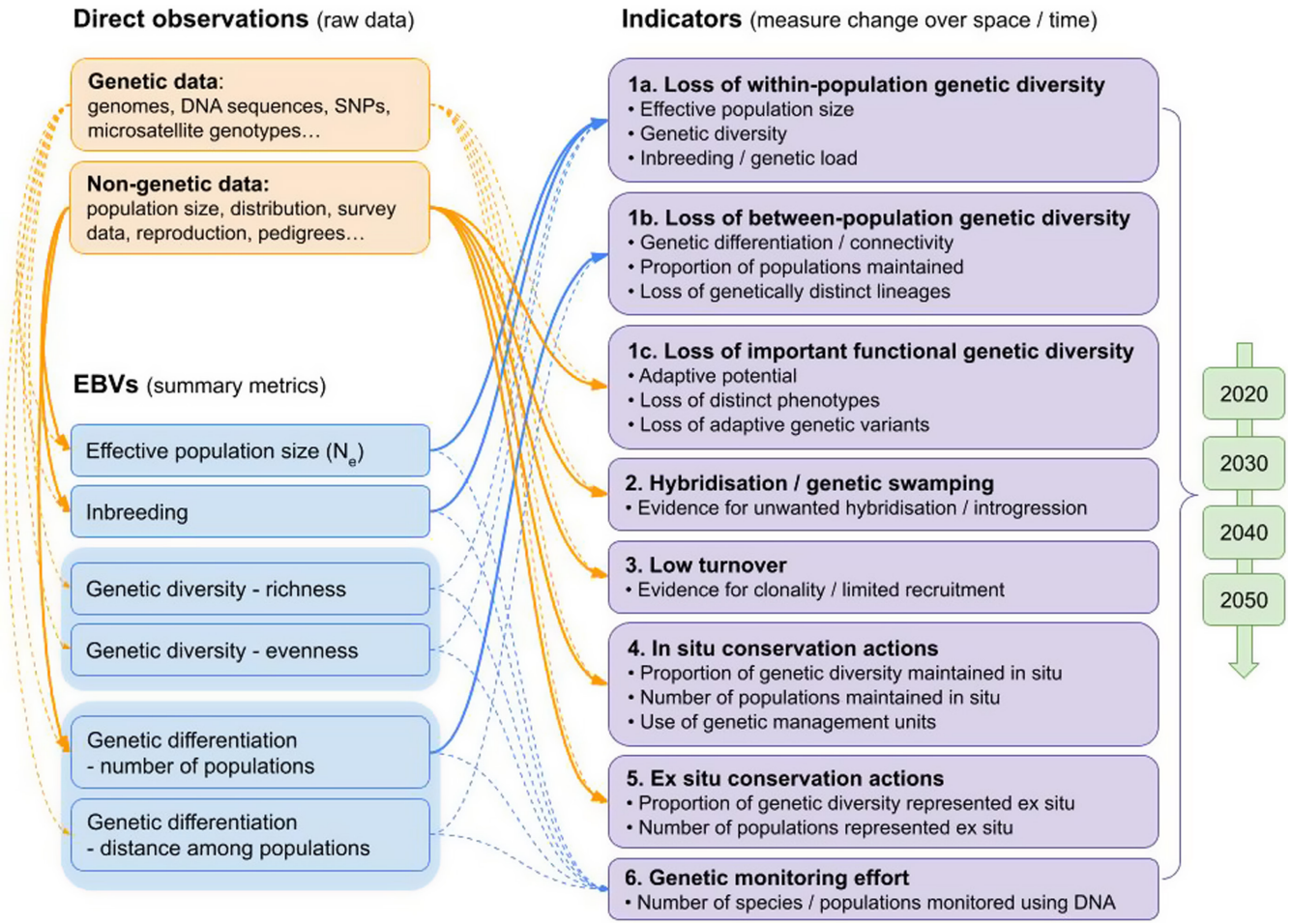

FIGURE 1 Relationships between data sources, genetic essential biodiversity variables and the different categories of genetic diversity indicators reviewed in Table 1. In this figure, for each category of headline, a range of existing indicators are summarised: These may be variously implemented in different countries through measurement of status, trend or threshold values. Dashed lines indicate molecular data are required, solid lines indicate that molecular or non-molecular data can be used.

5 | PROPOSAL

Given common themes within the various approaches to genetic diversity reporting, we propose bringing them together, using the categories outlined in the Scottish scorecard (Hollingsworth et al., 2020) as headlines, and nesting all approaches within this framework (Table 1). This categorisation would allow users (e.g. Parties to the CBD and other agreements) to select and report on those metrics most suitable for their needs and resources (using as many as possible), considering expertise, time and data availability. Equally importantly, it would provide an overview of potential steps for increasingly comprehensive reporting. The framework approach enables consideration of all main threats to genetic diversity. It can also monitor interventions, in situ and ex situ, which may incentivise active conservation of genetic diversity.

To support genetic diversity reporting, we propose creation of a centrally held database to hold both monitoring and underlying data. This would allow transparency and encourage contributions from nations that may not have the resources to set up local mechanisms. The database could be established and maintained by an intergovernmental organisation such as GEO BON or IUCN, potentially linking into and informing the Red List process. Embedding genetic diversity metrics into the Red List would give appropriate weight to this crucial aspect of biodiversity (Garner et al., 2020; Willoughby et al., 2015). Experience with EUFORGEN, which has a much broader scope albeit over a smaller geographic area, suggests that a collaboratively funded coordination mechanism need not be expensive (EUFORGEN's annual budget ≈€350,000; member states contribute €2500–€35,000 each; EUFORGEN, 2019). We suggest that funding is required for at least the whole CBD reporting cycle (i.e. to 2030) to ensure its benefits are realised. Our proposal would provide all nations, regardless of economic status, with the ability to report on the pressures, state, conservation interventions and ecosystem services provided by genetic diversity.

AUTHORS' CONTRIBUTIONS

D.O. conceived the paper; D.O., L.L., S.H. and A.J.M. managed the editing process and coordinated the paper's production; All authors contributed to the design of the component approaches, contributed critically to the drafts and gave final approval for publication. R.E.S. designed the graphical abstract.

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CONFLICT OF INTEREST

The authors declare that they have no conflict of interest.

DATA AVAILABILITY STATEMENT

This article does not contain data.

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