

INCLUSION OF GENETIC DIVERSITY IN THE POST-2020 GLOBAL BIODIVERSITY FRAMEWORK: SCIENTIFIC AND TECHNICAL KNOWLEDGE

Prepared by the Group on Earth Observations Biodiversity Observation Network (GEO BON)

I. INTRODUCTION

This information document¹ focuses on the evidence-based consideration, protection, and monitoring of genetic diversity in the post-2020 Global Biodiversity Framework (GBF), to prevent genetic diversity loss and improve its contributions to species, ecosystems, and society. “Genetic diversity” is the diversity in DNA sequences and traits within species which allows populations to adapt, evolve and survive over time. This document presents the current state of knowledge that genetic diversity within all species- not just agricultural species- contributes to (a) species’ survival, ecosystem resilience and productivity, and (b) nature’s contribution to people. Genetic diversity is the foundation of species and ecosystem diversity, though it has often been neglected. It is important to equally conserve “diversity within species, between species and of ecosystems” (as per the 1992 Convention text). **Drawing on previous CBD documents and the latest scientific literature, this document provides the scientific knowledge to better incorporate genetic diversity into the GBF, including via indicators.** Monitoring genetic erosion via a combination of DNA observations, Essential Biodiversity Variables and indicators based on proxies such as population size and geographic range is feasible and necessary.

II. WHY IS GENETIC DIVERSITY IMPORTANT AND WHAT IS GENETIC EROSION?

2.1 Why must we conserve genetic diversity within all species?

Genetic diversity is a critical resource for society and nature, as noted in every edition of the Global Biodiversity Outlook, the synthesis of scientific knowledge in CBD/SBSTTA/24/INF/9 prepared by a group of experts convened by the Earth Commission and Future Earth, and the IPBES report.

- There is abundant scientific evidence that genetic diversity is essential for the resilience and adaptability of species, communities and ecosystems. Genetic diversity enables adaptation to threats of climate change, habitat degradation, and pests and diseases. For example, genetic diversity in coral and seagrass ecosystems is needed for recovery after heat waves, and genetic diversity in trees allows forest restoration after pest and disease outbreaks².
- Genetic diversity helps to maintain ecosystem functions and services to people (e.g. carbon cycle, pollination, food, energy, culture, etc.). For example, genetic diversity within plant species supports more insect diversity, and maintains water quality and nutrient cycling in rivers and streams, and genetic diversity in cyanobacteria impacts carbon capture³.
- Likewise, there are many examples of catastrophic loss to societies and economies caused by narrow genetic stocks in agriculture, forestry and fisheries, especially through pests and disease. Genetic

¹ This document is submitted by the Group on Earth Observation Biodiversity Observation Network (GEO BON). The following groups contributed to and support this document: IUCN Conservation Genetics Specialist Group and Crop Wild Relative Specialist Group, Society for Conservation Biology (SCB) Conservation Genetic Working Group, and the European COST Action Genomic Biodiversity Knowledge for resilient Ecosystems (G-BiKE). Recommendations herein, including wording and quantitative elements, were determined through discussions among the groups listed

² Des Roches, S., Pendleton, L.H., Shapiro, B. and Palkovacs, E.P., 2021. Conserving intraspecific variation for nature’s contributions to people. *Nature ecology & evolution*

³ Stange, M., Barrett, R.D. and Hendry, A.P., 2020. The importance of genomic variation for biodiversity, ecosystems and people. *Nature Reviews Genetics*

diversity is the *foundation* of global food security, including for millions of people who harvest wild species. More examples can be found in a G-BiKE policy brief [here](#).

Key message: Genetic diversity is a solution to challenges such as invasive pests and diseases, food security, health and wellness, soil and water health, climate change, and the species extinction crisis.

2.2 What is genetic diversity and how is it eroding?

“Genetic diversity” is the diversity within species which allows species to adapt, evolve and survive over time. It is usually defined as within-species (i.e. intraspecific) diversity, including DNA sequence diversity, alleles, haplotypes, breeds, landraces, varieties, distinct populations, and traits. This definition distinguishes genetic diversity from species diversity or higher levels of biodiversity. It is sometimes called evolutionary potential or adaptive capacity. It exists within all species, and without it, species will be lost. “Genetic erosion” is loss of genetic diversity, in the wild (in situ) or in controlled conditions (ex situ). Genetic erosion could also result from the disruption of processes that normally maintain genetic resilience, such as fragmentation, high levels of hybridization, and/or high inbreeding levels⁴. Recovery of genetic diversity is a slow and difficult process.

Available data from hundreds of studies show that genetic diversity within species is eroding as a result of habitat and population loss, direct harvest, disease, intensive agriculture and extreme climate events. One recent study⁵ documented 6% loss of genetic diversity over the past 100 years for 91 wild species, and 28% loss for island species, while another⁶ showed 12% lower genetic diversity in harvested fish than non-harvested fish species. Innovative approaches are helping to identify global trends, document responses of genetic diversity to over-exploitation and human disturbance, and combine genetic data with models of drivers⁷, all of which can support indicators. In addition, progress is being made on tools and best practices for genetic monitoring⁸ ⁹. However, raising awareness of the importance of genetic diversity remains a challenge. Genetic erosion occurs via similar processes in wild and domesticated species [e.g. inbreeding, genetically small effective population size, loss of habitat connections allowing movement among populations, and loss of distinct variants, breeds or populations]. **Conservation actions can help preserve genetic diversity both in situ and ex situ: protecting and restoring large populations, genetic exchange between populations or breeds, identification and conservation of distinct populations or breeds, and translocations or genetic rescue.**

2.3 How can we measure and report on genetic diversity?

Abundant genetic data exists which can already inform biodiversity targets. Scientists have assessed genetic diversity in thousands of species since the 1970s. Knowledge gaps in geographic regions, ecosystem realms, and under-represented taxa do exist, but the gaps are being filled due to continually decreasing genotyping costs, better data stewardship, and global capacity building. Affordable, frequent genetic monitoring can support ambitious targets on genetic erosion. Nonetheless, the amount of genetic data

⁴ Hoban, S., Bruford, M., Jackson, J.D.U., Lopes-Fernandes, M., Heuertz, M., et al, 2020. Genetic diversity targets and indicators in the CBD post-2020 Global Biodiversity Framework must be improved. Biological Conservation

⁵ Leigh, D.M., Hendry, A.P., Vázquez-Domínguez, E. and Friesen, V.L., 2019. Estimated six per cent loss of genetic variation in wild populations since the industrial revolution. Evolutionary Applications

⁶ Pinsky, M.L., Palumbi, S.R., 2014. Meta-analysis reveals lower genetic diversity in overfished populations. Molecular ecology

⁷ Millette, K.L., Fugère, V., Debyser, C., Greiner, A., Chain, F.J.J., Gonzalez, A. No consistent effects of humans on animal genetic diversity worldwide. Ecology Letters 23: 55-67.

⁸ Posledovic D, Ekblom R, Laikre L. 2021. Mapping and monitoring of genetic diversity in Sweden – a proposal for a program to start 2020. Swedish Environmental Protection Agency.

⁹ Walters, M. and Scholes, R.J., 2017. The GEO handbook on biodiversity observation networks. Springer Nature.

existing in many countries is not known, because it has rarely been systematically collated.

Genetic proxies, appropriately interpreted, can be used to represent genetic diversity within species. Proxies of genetic diversity may include the size and geographic distribution of a population, and the level of environmental variation within and among populations (see indicators below). Temporal trends in these proxies can be used to monitor changes in genetic diversity over time. Loss of populations directly equates to loss of genetic diversity, and reduction in geographic range or population size correlates with loss of genetic diversity. For example, geographic area has been used as a proxy¹⁰ to suggest that genetic diversity is inadequately safeguarded in situ and ex situ for thousands of important plant species. Other studies^{11 12} have used ecogeographic methods as proxies for planning to protect genetic diversity. In summary, many countries are working to implement genetic monitoring, while those that are not yet able to do so can apply proxies instead.

Key message: genetic monitoring and reporting are feasible using either DNA data or proxies.

III. WHAT HAS THE CBD SAID ABOUT GENETIC DIVERSITY?

- Genetic diversity is one of three central elements of biodiversity in the 1992 CBD text (biological diversity consists of diversity “*within species, between species and of ecosystems*”)
- CBD notes the importance of “ecosystems, species and genetic diversity within species, *each of them receiving the same level of importance.*” (CBD/SBSTTA/24/INF/9) and that “Genetic diversity is critical for the long-term stability, adaptability and resilience of biodiversity.” (CBD/SBSTTA/24/3/Add.2).
- CBD Targets for 2010 and 2020 aimed to maintain genetic diversity within numerous categories of agricultural and non-agricultural species, as well as associated traditional knowledge, and strategies for maintaining genetic diversity.
- The Global Biodiversity Outlook 2 (CBD, 2006), reflecting on target progress, stated that “Genetic variation is important for maintaining fitness and adaptability of species, and of direct importance for people through the maintenance of goods and services.”
- The GBO has stated numerous times that genetic diversity is declining, genetic diversity monitoring and reporting lags behind species monitoring, and that “*genetic diversity indicators are weak and need development*” (CBD, 2010). The GBO has highlighted threats to genetic diversity including overharvest of wild species, anthropogenically-induced hybridization, habitat fragmentation, selective hunting, and declines in abundance.
- As stated in the CBD, “where there is a threat of significant reduction or loss of biological diversity, lack of full scientific certainty should not be used as a reason for postponing measures to avoid or minimize such a threat”.
- A review of the failure to achieve Aichi Targets (CBD/SBI/3/2/Add.2) observed “*the issue of conserving the genetic diversity... and the development of strategies to minimize genetic erosion are not generally reflected in the targets set by Parties*”.

¹⁰ Khoury, C.K., Amariles, D., Soto, J.S., Diaz, M.V., Sotelo, S., et al., 2019. Comprehensiveness of conservation of useful wild plants: An operational indicator for biodiversity and sustainable development targets. *Ecological Indicators*

¹¹ Hanson, J.O., Rhodes, J.R., Riginos, C. and Fuller, R.A., 2017. Environmental and geographic variables are effective surrogates for genetic variation in conservation planning. *Proceedings of the National Academy of Sciences*

¹² Beckman, E., Meyer, A., Denvir, A., Gill, D., Man, G., Pivorunas, D., Shaw, K., & Westwood, M. (2019). *Conservation Gap Analysis of Native U.S. Oaks*. Lisle, IL: The Morton Arboretum.

IV. INDICATORS FOR GENETIC DIVERSITY: SCIENTIFIC BASIS FOR INCLUSION

4.1 Scientific basis for new indicators

A brief overview of past indicators used for reporting on genetic diversity is in Appendix A. **Based on the weaknesses and insufficiency of past indicators, Hoban et al (2020) and Laikre et al (2020) suggested the following measurable indicators which more closely reflect genetic change, and can be applied to wild or domesticated species.** These indicators are in development, but have been calculated on several case studies. They are aligned with the goal and targets, have data available, are suitable at national and global scales and can be aggregated/ disaggregated, have a responsible institution, are scientifically robust, have some data for all regions of the world, are very nearly ready for use, can be updated yearly or decadal, have a methodology, and are easily understandable (the requirements listed in the document on “Indicators for global and national biodiversity targets..” Aug 2020). **Several of these have already been included in CBD/SBSTTA/24/3Add.1.** The first is also based on an Essential Biodiversity Variable from GEO BON, effective population size.

4.2 List of genetic diversity indicators

1. **The proportion of populations within species sufficiently large to maintain genetic diversity, which is a genetically effective population size > 500.** The genetic effective size (N_e) of populations determines rates of inbreeding, loss of genetic variation, and loss of adaptive potential. This indicator is needed to allow for maintaining genetic diversity for populations to evolve and adapt. N_e has well established thresholds regarding genetic erosion. Effective population sizes lower than 500 will result in reduced ability to adapt to environmental change¹³. N_e can be assessed in several ways: with a pedigree, from demographic data e.g. life history characters and demography, or with molecular genetic data. Such data is available for at least hundreds of populations. Furthermore, in the absence of such knowledge, N_e can be roughly approximated as 1/10th the estimated census size of a population (N_c , the number of reproductive adult individuals). In other words in absence of particular knowledge an N_c threshold of 5000 can be used to indicate genetic erosion. We note that large declines in N_e , even if N_e remains far above 500, will also result in genetic erosion, are cause for alarm, and should be reported as well.
2. **The proportion of populations, or geographic range, maintained within species to prevent the loss of unique adaptations.** The loss of distinct wild populations, or the agricultural equivalent - breeds, landraces, or varieties - will result in large losses of genetic diversity within species, especially loss of local adaptations. The loss of distinct populations could be calculated by repurposing data underlying the GEO BON [Species Habitat Index](#) (SHI) which is a headline indicator¹⁴. It provides a decrease in habitat-suitable range and the populations it might support per year. Other possible data sources include IUCN Red List data, historic Global Biodiversity Information Facility (GBIF) occurrences, or data underlying the Living Planet Index, as well as national and local databases. This indicator complements and does not replace the BIP indicator “[comprehensiveness of conservation of plant species](#)”, a measure of protected area and seed bank coverage, which we also support.
3. **The number of populations in which genetic diversity is being monitored using DNA-based methods.** Knowledge on genetic diversity within and among populations (in situ and ex situ), environmental drivers of that diversity, and degree of genetic connectivity between populations is

¹³ Jamieson, I.G. and Allendorf, F.W., 2012. How does the 50/500 rule apply to MVPs?. *Trends in ecology & evolution*

¹⁴ See also UNEP/CBD/SBSTTA/24/3/INF/XX “Scalable data, observation systems and indicators to support effective monitoring of goals and targets for the post-2020 global biodiversity framework: GEO BON support for implementation”

critical to directly guide management for safeguarding genetic diversity. This indicator measures the extent to which countries are tracking genetic diversity. The number of countries with genetic diversity assessments will continue to increase with more affordable genotyping and more capacity building.

4. **Genetic scorecard for wild species.** This indicator focuses on compiling knowledge on ex situ and in situ genetic status, and threats for species. It encompasses a simple scorecard method for assessing risks to genetic diversity in species using structured expert opinion assessments of likely loss of genetic diversity, hybridisation and undesirable replacement of genetic diversity, or restrictions to regeneration. For plant species where seed-banking is a viable mechanism, the scorecard also assesses these ex situ collections.

V. SUMMARY OF RECENT LITERATURE ON GENETIC DIVERSITY AND THE GBF

5.1 What degree of genetic conservation is realistic and feasible?

Several recent scientific articles have reviewed the state of knowledge on genetic erosion and the feasibility of commitments regarding genetic diversity for the GBF. Hoban et al (2020) suggested that the current genetic goal of “maintain genetic diversity” is vague and lacks ambition, a conclusion also reached by Diaz et al (2020). These authors emphasize that populations must be maintained in order to prevent genetic erosion. **In some cases, 100% of populations that currently exist can be maintained, and populations can be restored, thus maintaining genetic diversity among populations.** Populations are the unit of adaptation and evolution. Some species only have one population but many species have multiple or many populations. Genetic diversity among and within populations provides the basis for sustaining species and ecosystems.

In addition, as much genetic diversity within populations should be maintained. A threshold of 90% (often used in zoos and captive breeding) to 95% (often used in botanic gardens, seed banks, and plant reintroductions) of within population genetic diversity has been used as a scientifically based guiding rule in conservation biology and agronomics for several decades¹⁵. It is feasible ¹⁶, yet ambitious, and is measurable directly with genetic data and indirectly via acceptable proxies (see indicators). These authors emphasize that ex situ *and* in situ conservation is vital. Wild and domesticated species’ genetic diversity should be maintained because: the relatives of domesticated species provide genetic material to ensure resilience to environmental change, pests and disease; many thousands of other species are of known direct use to humans (food, timber, medicine, pollinators, cultural symbols, etc); and those species not of known use contribute to ecosystem services and have potential future value to society. In summary, current knowledge shows that preventing genetic erosion means to maintain 100% of populations and at least 90 to 95% of genetic diversity within populations of all wild and domesticated species, in situ and ex situ, and restore conditions ensuring evolutionary adaptive potential.

¹⁵ Brown, A.H.D. and Marshall, D.R., 1995. A basic sampling strategy: theory and practice. Collecting plant genetic diversity: technical guidelines. CAB International, Wallingford

Brown, A.H.D. and Hardner, C.M., 2000. Sampling the gene pools of forest trees for ex situ conservation. Forest conservation genetics: principles and practice

Hoban, S. and Strand, A., 2015. Ex situ seed collections will benefit from considering spatial sampling design and species’ reproductive biology. *Biological Conservation*

¹⁶ Hoban, S., 2019. New guidance for ex situ gene conservation: Sampling realistic population systems and accounting for collection attrition. *Biological Conservation*

Paz-Vinas, I., Loot, G., Hermoso, V., Veyssiere, C., Poulet, N., et al., 2018. Systematic conservation planning for intraspecific genetic diversity. *Proceedings of the Royal Society B: Biological Sciences*

5.2 What actions are needed? Hoban et al (2020) also point out that the current list of targets do not include actions to stop the drivers of genetic diversity loss. Current scientific and technical knowledge shows that the drivers of genetic diversity loss must be addressed to achieve Goal A- maintain all levels of biodiversity. **It is critical to recognize that actions which preserve ecosystems and prevent species' extinctions will not necessarily conserve genetic diversity.** "While population abundance is a key factor in the maintenance of genetic diversity, it is not a sufficient indicator since it does not account for within-population genetic diversity, *hence the need for genetic diversity to be explicitly included.*" (CBD/SBSTTA/24/3/Add.2). Although "healthy and resilient populations" should encompass genetically healthy populations, genetic concerns are very frequently not considered in species' population management and must be made more explicit.

Maintaining genetic diversity and adaptive potential requires several factors (a) sufficiently large population sizes; (b) baseline numbers of populations and geographic range, with natural levels of connectivity among populations; and (c) management actions specific to genetic diversity. Principally, sufficiently large populations are needed across a species' ecological breadth, connected by gene flow to enable exchange of adaptations (e.g. by protecting habitat connectivity). Next, knowledge on how genetic diversity is partitioned in space and how distinct genetic groups are is important for guiding management. Supportive actions include reintroduction/ restoration, conservation and use of genetic diversity on farms and by indigenous people, active management of small populations e.g. through translocations, and in some cases management of hybridization. Lastly, legislation committing to safeguarding genetic diversity, and investment in systematic genetic monitoring are needed (e.g. the Endangered Species Act in the USA and the Species At Risk Act in Canada). **Although these actions support species' survival, the converse is not true- conserving species does not necessarily conserve within species' genetic diversity.** Much genetic diversity is lost before species near extinction (like trees hollowed before they fall), while lost populations result in lost genetic diversity but not necessarily threatening extinction. Thus action to conserve genetic diversity can be taken before species are threatened with extinction. In summary, key elements to consider going forward:

- Genetic diversity must be valued and *protected*, ideally through legislation, and integrated into planning across sectors.
- Genetic diversity must be *maintained*- not lost.
- Genetic diversity must be *managed* through scientifically informed direct action (see list above), such as restoring lost gene flow by migration corridors, which can help enhance variation in isolated populations where genetic diversity was reduced.
- Genetic diversity must be *monitored* to ensure these actions are effective.

We also note that a suggestion to include genetic diversity under existing Targets was mentioned in CBD/SBSTTA/24/3/Add.2 Item 33. Several Targets relate closely to genetic diversity: Target 1 (spatial planning and restoration) and Target 2 (connectivity of protected areas) because ensuring maintenance of or restoration of genetic exchange among populations is vital for retaining genetic diversity. Target 3 (active management of species) because genetic diversity is essential for species to survive environmental change. Target 4 (wild harvest) because wild harvest of fish, trees, and wild animal species is in some cases causing loss of genetic diversity. Target 5 (invasive species) because introduced and invasive species and populations can cause genetic erosion. Target 7 (climate mitigation) because genetic diversity and genetic rescue can help species survive changing climate and extreme weather. Target 9 because maintaining genetic diversity in domesticated species, their breeds and varieties, their wild relatives, and associated agricultural species (soil microbes, pollinators, insectivores) will support productivity and sustainability.

6. Additional important issues and enabling conditions

Several gaps must be closed to advance genetic diversity conservation and sustainable use post 2020.

- Greater investment in systematic genetic monitoring, using metrics closely correlated to genetic erosion to close the large data gap in temporal trends of genetic diversity, such as Essential Biodiversity Variables developed by GEO BON.
- National and intergovernmental commitments to fund CBD implementation should explicitly include reference to supporting activities that directly conserve genetic biodiversity as well as to support training and partnerships to enhance capacity
- Genetic diversity to be recognised as important for scientific discovery and conservation planning. We support capacity-building for documenting, curating, connecting and accessing regional and global databases on genetic diversity information. Biodiversity Observation Networks (BONs)- communities of practice that share methodologies- are a recognized approach to achieving this goal.
- Continued improvement in models connecting proxies to genetic erosion is required.
- Relating to societal knowledge of biodiversity, increased awareness and appreciation of genetic diversity is needed for society to commit appropriate resources towards genetic conservation. There must be more engagement between policy makers, scientists, and the public.

Appendix A: Scientific critique of previously used indicators

Four genetic diversity indicators were noted in the zero draft (CBD/WG2020/2/3/Add.1, CBD, 2020); Hoban et al. (2020) critically evaluated these and concluded that they are insufficient to protect genetic diversity. Similar weaknesses have also been noted in CBD documents (Convention on Biological Diversity, 2010b, Convention on Biological Diversity, 2006). (1) “*Number of plant genetic resources for food and agriculture secured in medium or long-term conservation facilities,*” i.e. the number of collections or accessions in seed banks. Often, these facilities conserve limited genetic diversity within species, except for a few crop species. If this indicator is kept it should be modified with a clause specifying that collections must be genetically representative (i.e. across the geographic range), resilient (i.e. from >50 plants per population), and replicated (i.e. in multiple locations), and to include all plant species, not just agricultural ones. This information is available for many botanic gardens and seed banks. (2) “*Proportion of local breeds classified as at risk.*” This indicator only applies to domesticated animal species, and could be subsumed within our proposed indicator on populations with sufficient effective population size N_e (thus genetically “safe”). (3) “*Comprehensiveness of conservation of socioeconomically as well as culturally valuable species.*” This quantifies a proportion of a species range that is represented ex situ (held in seed banks) or in situ (within protected areas), and may correlate to genetic diversity conservation, but has the drawback of not actually tracking in situ populations on the ground. However, it is the most suitable of the current set of indicators and can be quickly calculated, and is the most useful of these four. (4) “*Red List Index*”, which reflects changes in the number of species in Red List (RL) categories. Although the RL evaluates criteria such as total species census size, reductions in population size and/or geographic range, which should theoretically correlate with losses of genetic diversity, the RL has demographic thresholds that do not match thresholds for genetic erosion. Also it focuses on species, not populations. Studies¹⁷ show RL status is poorly correlated to maintenance of genetic diversity. **In summary, previously used indicators for genetic diversity Target 13 have little documented correlation to genetic erosion or safeguarding of genetic diversity and are thus not well suited for monitoring and reporting on genetic diversity status and trends.**

¹⁷ Willoughby, J.R., Sundaram, M., Wijayawardena, B.K., Kimble, S.J., Ji, Y., et al., 2015. The reduction of genetic diversity in threatened vertebrates and new recommendations regarding IUCN conservation rankings. *Biological Conservation*

Appendix B. Further description of progress by key proponents

A large group of scientists (see list of proponents on page 1), is working to provide the capacity and enabling conditions for genetic diversity monitoring, including tools, databases, guidance documents, case studies, and resources to make genetic diversity data more accessible and usable. Prior work includes:

- [EUFORGEN](#) – the European Forest Genetic Resources Programme, started in 1994 – is an international program promoting conservation and sustainable use of forest genetic resources. Among other accomplishments, this program manages a database of information on 3657 gene conservation units (with minimum genetic requirements in terms of Ne) for 109 tree species in 35 countries, and provides input to European and global biodiversity assessments. Improving genetic criteria and indicators for monitoring is part of EUFORGEN's working group activities.
- [ECPGR](#) – the European Cooperative Programme for Plant Genetic Resources, started in 1979 - is a collaborative Programme aiming at ensuring the long-term conservation and utilization of plant genetic resources in Europe. The Programme has largely focused on *ex situ* conservation of crop landrace (LR) and crop wild relative (CWR) populations. There are >2 million accessions of LR and CWR preserved *ex situ* by almost 400 institutes in 43 countries. ECPGR is currently working to establish an *in situ* network for landrace and CWR conservation (see www.ecpgr.cgiar.org).
- Crop Wild Relative Specialist Group ([CWRSG](#)), started in 2000, aims at promoting effective conservation and use of CWR and their increased availability for crop improvement, for the benefit of the environment and society. The CWRSG is undertaking a Red List threat assessment of 1,400 global priority CWR taxa (500 new Red List assessments). It also is establishing networks of CWR *in situ* conservation at global (150 genetic reserves for populations); European and regional (25 genetic reserves); (3) and national scales.
- ConGRESS (<http://www.congressgenetics.eu/>), an EU funded project from 2010-2013, laid the foundation for improving genetic diversity in policy and action, and cross border collaborations. Its results include a genetic study database, informational documents, a tool to guide sampling, and advice and direct information for policy.
- Scientific articles on this topic and on improved indicators, Target and Goal wording have been published in leading scientific journals, continuing to build on a foundation of approximately 45 years of conservation genetic knowledge: Laikre et al 2020 ([Science](#)), Hoban et al 2020 ([Biological Conservation](#)), O'Brien et al 2020 ([Science](#)), Hoban et al 2021 (BioScience, in press).
- Policy briefs have been created and disseminated for [explaining the importance of genetic diversity](#) (4 pages, available in 20 languages), [introducing indicators, Goal and Target](#) (2 pages, available in 8 languages), and summarizing the [state of the art for genetic conservation](#) (3 pages).
- A recent study emphasizes limitations of CBD indicators and Targets, and how genetic diversity is reported on (Hoban et al. 2020 [bioRxiv](#), not yet peer reviewed). Analysis of CBD National Reports from 2014 and 2018 found that genetic diversity of non agricultural species (including wild species of conservation concern, forestry or fishery species, and even crop wild relatives) was neglected. Actions regarding genetic diversity were infrequent and focused primarily on ex situ facilities and research agencies. Aichi Target 13 may have influenced, and restricted, the actions taken and reported on. A policy brief on this is available [here](#) (1 page, 12+ languages)
- Webinars for CBD focal points, delegates and support staff, were held in late 2020 to introduce and discuss indicators, open dialogue and receive feedback and interest from different countries and contexts, reaching approx. 40 countries and 100 participants. We are using feedback to improve indicator explanation, design a manual, and establish collaborations to apply indicators at country level. A short video introducing indicators is [here](#). These GEO BON and G-BIKE led webinars are continuing in April 2021 and are open to all focal points, collaborating scientists and other actors.

Appendix C: Plan and commitments for genetic diversity indicators, and example calculation

- The information to calculate these indicators exists in many national level databases (systems monitoring species and ecosystems) as well as expert knowledge, including local and traditional knowledge. Global databases can also be used. DNA data is not required to compute indicators 1, 2 or 4 (but may be quite efficient and helpful). *Populations of species can be monitored through genetic (i.e., DNA analysis) data or using proxies, deduced from observations.*
- Each indicator results in one measure per country. Below are 3 tables with a brief, very rough example for computation, using a few species with populations in Sweden to illustrate the basic principles.
- We intend to elaborate details on these computations and test the indicators with collaborating countries. We are working with the Swedish EPA and Swedish Species Information Centre to test feasibility of indicators for more than twenty thousand species.
- During 2021-2022 we will develop data infrastructure, computational/ online resources, and a detailed guidance manual for calculation and use of the genetic diversity indicators, simultaneous with webinars and case tests, in consultation with practitioners and focal points from as many countries as possible. We will provide guidelines regarding selection of organism groups and species/taxa, precision on the kinds of data needed, and examples of monitoring programs in different countries using different data.

Example calculation for four species in Sweden

Indicator 1: Genetic effective population size index

Selected species type*	Species	Population	Ne assessment method	Ne	Index per species (no above 500/no below 500)	Proportion of populations above 500
Top predator	Wolverine <i>Gulo gulo</i>	Metapopulation, northern Sweden	Simulations	346	0/1	0.00
Pollinating insect	Butterfly <i>Lopinga achine</i>	County Östergötland	10% of census size	610		
	Butterfly <i>Lopinga achine</i>	Island Gotland	10% of census size	700	2/0	1.00
Amphibian	Pool frog <i>Pelophylax lessonea</i>	Uppland county	10% of census size	490		
	Pool frog <i>Pelophylax lessonea</i>	Östergötland	10% of census size	10	0/2	0.00
Socio-economically valuable fish	Salmon <i>Salmo salar</i>	Torne River	molecular genetics	800		
		Kalix River	molecular genetics	1300		
		Byske River	molecular genetics	200		
		Rickle River	molecular genetics	30		
		Vindel River	molecular genetics	450		
		Ore River	molecular genetics	100		
		Ljungan River	molecular genetics	500		
		Morrum River	molecular genetics	300	3/5	0.38

* Note: here four example groups of species. We suggest more key species groups than these are selected per country

Indicator 1 value for Sweden

1.38/2 = 0.69

Indicator 2: Index populations maintained

Selected species type*	Species	No baseline populations	No populations maintained	maintained
Top predator	Wolverine <i>Gulo gulo</i>	1	1	1
Pollinating insect	Butterfly <i>Lopinga achine</i>	2	2	1
	Pool frog <i>Pelophylax lessonea</i>	2	2	1
Socio-economically valuable fish	Salmon <i>Salmo salar</i>	13	8	0.62

Indicator 2 value for Sweden**0.905****Indicator 3: Populations monitored with genetic methods**

Selected species type*	Species	Population	Populations monitored with molecular data	Proportion per species monitored with genetics
Top predator	Wolverine <i>Gulo gulo</i>	Metapopulation, northern Sweden	1	1
Pollinating insect	Butterfly <i>Lopinga achine</i>	County Östergötlan	0	
	Butterfly <i>Lopinga achine</i>	Island Gotland	0	0
Amphibian	Pool frog <i>Pelophylax lessonea</i>	Uppland county	0	
	Pool frog <i>Pelophylax lessonea</i>	Östergötland	0	0
Socio-economically valuable fish	Salmon <i>Salmo salar</i>	Torne River	1	
		Kalix River	1	
		Byske River	1	
		Rickle River	1	
		Vindel River	1	
		Ore River	1	
		Ljungan River	1	
Morrum River	1	1		

Indicator 3 value for Sweden**2/4 = 0.5**
