Biological Conservation 248 (2020) 108654

Contents lists available at ScienceDirect

Biological Conservation

journal homepage: www.elsevier.com/locate/biocon

Policy analysis

Genetic diversity targets and indicators in the CBD post-2020 Global Biodiversity Framework must be improved

Sean Hoban[a,*,1,2], Michael Bruford[b,1,2], Josephine D'Urban Jackson[b], Margarida Lopes-Fernandes[c,1], Myriam Heuertz[d], Paul A. Hohenlohe[e], Ivan Paz-Vinas[z,2], Per Sjögren-Gulve[f,1], Gernot Segelbacher[g,1,2], Cristiano Vernesi[h,1,2], Sally Aitken[i], Laura D. Bertola[j,1,2], Paulette Bloomer[k], Martin Breed[l], Hernando Rodríguez-Correa[m], W. Chris Funk[n,1,2], Catherine E. Grueber[o], Margaret E. Hunter[p,1,2], Rodolfo Jaffe[q], Libby Liggins[r], Joachim Mergeay[s,t,2], Farideh Moharrek[u,v], David O'Brien[w], Rob Ogden[x,1,2], Clarisse Palma-Silva[y], Jennifer Pierson[aa,2], Uma Ramakrishnan[ab], Murielle Simo-Droissart[ac], Naoki Tani[ad], Lisette Waits[ae,1,2], Linda Laikre[af,1]

[a] Center for Tree Science, The Morton Arboretum, 4100 Illinois Rt 53, Lisle 60532, USA
[b] School of Biosciences, Cardiff University, Cardiff CF10 3AX, UK
[c] Instituto da Conservação da Natureza e das Florestas, IP, Lisbon, Portugal
[d] INRAE, Univ. Bordeaux, Biogeco, 69 route d'Arcachon, F-33610 Cestas, France
[e] Institute for Bioinformatics and Evolutionary Studies, Department of Biological Sciences, University of Idaho, 875 Perimeter Drive MS 3051, Moscow, ID 83844-3051, USA
[f] The Wildlife Analysis Unit, The Swedish Environmental Protection Agency, SE-10648 Stockholm, Sweden
[g] Chair of Wildlife Ecology and Management, University Freiburg, Tennenbacher Str. 4, D-79106 Freiburg, Germany
[h] Dept. of Sustainable Agroecosystems and Bioresources, Research and Innovation Centre - Fondazione Edmund Mach, via E. Mach 1, S. Michele all'Adige, TN 38010, Italy
[i] Department of Forest and Conservation Sciences, Faculty of Forestry, University of British Columbia, 3041-2424 Main Mall, Vancouver, BC V6T 1Z4, Canada
[j] City College of New York, 160 Convent Ave., New York, NY 10031, USA
[k] University of Pretoria, Pretoria, South Africa
[l] College of Science and Engineering, Flinders University, Bedford Park, SA 5042, Australia
[m] Escuela Nacional de Estudios Superiores Unidad Morelia, Universidad Nacional Autónoma de México, Antigua Carretera a Pátzcuaro 8701 Ex Hacienda de San José de la Huerta, 58190, Mexico
[n] Department of Biology, Graduate Degree Program in Ecology, Colorado State University, Fort Collins, CO, USA
[o] School of Life and Environmental Sciences, Faculty of Science, The University of Sydney, NSW 2006, Australia
[p] U.S. Geological Survey, Wetland and Aquatic Research Center, 7920 NW 71st St, Gainesville, FL 32653, USA
[q] Instituto Tecnológico Vale, 66055–090 Belém-PA, Brazil & Department of Ecology, University of São Paulo, 05508–090 São Paulo, SP, Brazil
[r] School of Natural and Computational Sciences, Massey University, Auckland, Aotearoa, New Zealand
[s] Research Institute for Nature and Forest, Havenlaan 88, 1000 Brussels, Belgium
[t] Aquatic Ecology, Evolution and Conservation, KULeuven, Charles Deberiotstraat 32, box 2439, 3000 Leuven, Belgium
[u] Department of Life Sciences, Natural History Museum, London SW7 5BD, UK
[v] Faculty of Biological Sciences, Tarbiat Modares University, Tehran, 14115-154, Iran
[w] Scottish Natural Heritage, Leachkin Road, Inverness IV3 8NW, UK
[x] Royal (Dick) School of Veterinary Studies and the Roslin Institute, University of Edinburgh, Easter Bush Campus, EH25 9RG, UK
[y] Department of Plant Science, Institute of Biology, University of Campinas, Campinas, São Paulo 13083-862, Brazil
[z] Laboratoire Ecologie Fonctionnelle et Environnement, Université de Toulouse, UPS, CNRS, INP, UMR-5245 ECOLAB, 118 route de Narbonne, Toulouse 31062, France
[aa] ACT Parks and Conservation Science, Australian Capital Territory 2901, Australia
[ab] Ecology and Evolution, National Centre for Biological Sciences, TIFR, Bangalore 560065, India

[*] Corresponding author.
E-mail addresses: shoban@mortonarb.org (S. Hoban), BrufordMW@cardiff.ac.uk (M. Bruford), josiedjackson@gmail.com (J. D'Urban Jackson), Margarida.Fernandes@icnf.pt (M. Lopes-Fernandes), myriam.heuertz@inrae.fr (M. Heuertz), hohenlohe@uidaho.edu (P.A. Hohenlohe), per.sjogren-gulve@swedishepa.se (P. Sjögren-Gulve), gernot.segelbacher@wildlife.uni-freiburg.de (G. Segelbacher), cristiano.vernesi@fmach.it (C. Vernesi), paulette.bloomer@up.ac.za (P. Bloomer), martin.breed@flinders.edu.au (M. Breed), hrodriguez@enesmorelia.unam.mx (H. Rodríguez-Correa), Chris.Funk@colostate.edu (W.C. Funk), catherine.grueber@sydney.edu.au (C.E. Grueber), mhunter@usgs.gov (M.E. Hunter), r.jaffe@ib.usp.br (R. Jaffe), L.Liggins@massey.ac.nz (L. Liggins), joachim.mergeay@inbo.be (J. Mergeay), f.moharrek@nhm.ac.uk (F. Moharrek), david.obrien@nature.scot (D. O'Brien), rob.ogden@ed.ac.uk (R. Ogden), cpalma@unicanp.br (C. Palma-Silva), Jennifer.Pierson@act.gov.au (J. Pierson), uramakri@ncbs.res.in (U. Ramakrishnan), ntani@affrc.go.jp (N. Tani), lwaits@uidaho.edu (L. Waits), linda.laikre@popgen.su.se (L. Laikre).
[1] Conservation Genetics Specialist Group, International Union for Conservation of Nature (IUCN), 1196 Gland, Switzerland.
[2] Group on Earth Observation Biodiversity Observation Network.

https://doi.org/10.1016/j.biocon.2020.108654

0006-3207/ © 2020 The Authors. Published by Elsevier Ltd. This is an open access article under the CC BY license (http://creativecommons.org/licenses/BY/4.0/).

[ac] Plant Systematics and Ecology Laboratory, Higher Teachers' Training College, University of Yaoundé I, P.O.Box 047, Yaoundé, Cameroon
[ad] Forestry Division, Japan International Research Center for Agricultural Sciences, Tsukuba, Ibaraki 305-8686, Japan
[ae] Department of Fish and Wildlife Sciences, University of Idaho, Moscow, ID 83844, USA
[af] Department of Zoology, Division of Population Genetics, Stockholm University, SE10691 Stockholm, Sweden

ARTICLE INFO

Keywords:
Convention on Biological Diversity
International conservation policy
Biodiversity monitoring
Genetic resources
Target 13
Genetic erosion
Ne/Nc

ABSTRACT

The 196 parties to the Convention on Biological Diversity (CBD) will soon agree to a post-2020 global framework for conserving the three elements of biodiversity (genetic, species, and ecosystem diversity) while ensuring sustainable development and benefit sharing. As the most significant global conservation policy mechanism, the new CBD framework has far-reaching consequences- it will guide conservation actions and reporting for each member country until 2050. In previous CBD strategies, as well as other major conservation policy mechanisms, targets and indicators for genetic diversity (variation at the DNA level within species, which facilitates species adaptation and ecosystem function) were undeveloped and focused on species of agricultural relevance. We assert that, to meet global conservation goals, genetic diversity within *all* species, not just domesticated species and their wild relatives, must be conserved and monitored *using appropriate metrics*. Building on suggestions in a recent Letter in *Science* (Laikre et al., 2020) we expand argumentation for three new, pragmatic genetic indicators and modifications to two current indicators for maintaining genetic diversity and adaptive capacity of all species, and provide guidance on their practical use. The indicators are: 1) the number of populations with effective population size above versus below 500, 2) the proportion of populations maintained within species, 3) the number of species and populations in which genetic diversity is monitored using DNA-based methods. We also present and discuss Goals and Action Targets for post-2020 biodiversity conservation which are connected to these indicators and underlying data. These pragmatic indicators and goals have utility beyond the CBD; they should benefit conservation and monitoring of genetic diversity via national and global policy for decades to come.

Glossary

Adaptation Evolution via natural selection as environmental conditions change.
Allele A variant in DNA sequence at a given gene; a common way to measure "genetic diversity"
Census size (Nc) Usually, a count of the number of adult or mature individuals in a population.
Effective population size (Ne) An estimate of the genetic population size that is inversely proportional to the rate of genetic erosion; smaller *Ne* causes greater inbreeding and loss of genetic diversity. This relationship is non-linear: genetic diversity loss accelerates as *Ne* declines, and is especially rapid in very small populations. *Ne* is influenced by many demographic factors (see Box 2).
Genetic connectivity Movement of individuals or gametes (e.g., via pollen) betwen populations i.e. "gene flow".
Heterozygosity A measure of evenness; another common way to measure "genetic diversity".
Hybridization Mating between individuals of different species; "introgression" is the movement of genes or alleles from one species into another through repeated backcrossing of hybrids to a parent species.
Inbreeding Mating among relatives, e.g., siblings.
Inbreeding depression Loss of fitness (growth rate, lifespan, reproductive output) due to inbreeding and accumulation of genetic load, primarily recessive deleterious alleles.
Population A group of interbreeding individuals in a defined area, genetically distinct from other such groups. Note this is not equivalent to "population" used by the IUCN, who define "population size" as the total adult census of a taxon at the global level. Most species have multiple populations. Population genomic analyses or phenotypic/functional trait variation can be used to delineate populations (Funk et al., 2012).

1. Introduction

Genetic diversity is the basis for evolutionary change, and is critical for species to adapt to changing climate, habitats, and biotic interactions including novel diseases. Low genetic diversity will increase extinction risk (Spielman et al. 2004). There is also abundant evidence for the substantial role of genetic diversity in ecosystem resilience, and for maintaining species diversity (Clark, 2010; Morikawa and Palumbi, 2019; Prieto et al., 2015; Reusch et al., 2005). Genetic diversity helps to maintain ecosystem functions, stability and services, and has similar impacts on community structure and ecosystem processes as species diversity (Blanchet et al., 2020; Prieto et al., 2015, Raffard et al. 2019). Moreover, large social, economic and cultural losses can result from using narrow genetic stocks in forestry, fisheries, horticulture, and agriculture (Doyle, 2016; Ploetz, 2015; Wu, 2019). Genetic diversity has been assessed for thousands of species, and meta-analyses of hundreds of datasets show that genetic diversity is decreasing, especially since the industrial revolution, because of habitat degradation and population loss, unsustainable harvest, invasive species and increasing extreme climatic events (Aguilar et al., 2008; Leigh et al., 2019; Miraldo et al., 2016; Pinsky and Palumbi, 2014).

Genetic diversity is recognized as one of three basic elements of biodiversity under the Convention on Biological Diversity (CBD; www.cbd.int), an international treaty under the United Nations Environmental Programme (UNEP) opened at the Earth Summit in Rio de Janeiro in 1992 and currently ratified by 195 states, plus the European Union. In 2010, the CBD adopted a Strategic Plan (Convention on Biological Diversity, 2010a) for the period 2011–2020 that included 20 targets to be achieved by 2020 (i.e. the Aichi Targets), though few targets have been met (Erdelen, 2020; IPBES, 2019; Tittensor et al., 2014). At the 15th meeting of the Conference of the Parties (COP 15) currently planned for October 2020, the CBD will decide on a "post-2020" framework for biodiversity conservation and will set new conservation targets at a critical period for the planet and society. The strategy will have intermediate goals to halt loss of biodiversity and ecosystem integrity by 2030 and ensure ecosystem resilience with a vision for "living in harmony with nature" by 2050. Genetic diversity is also recognized under other international agreements including Target 2.5 of the Sustainable Development Goals (SDGs), Targets 5 and 9 of the Global Strategy for Plant Conservation (GSPC), USA and Canadian endangered species legislation, numerous EU policies including the Habitats Directive and EU Biodiversity Strategy and Action Plans, and other regional

environmental policies such as the Biodiversity Action Plans for Fisheries and Agriculture (Santamaria and Mendez 2012) and Baltic Sea Action Plan (HELCOM 2007).

The first draft for the post-2020 strategy - the zero draft - was released in January (Convention on Biological Diversity, 2020). It calls for ambitious and transformative change. It suggests five Goals focusing on maintaining the three levels of biodiversity recognized in the CBD: (1) ecosystems, (2) species, (3) genetic diversity, and on ensuring (4) sustainable benefits to people, and (5) equitable sharing of benefits from use of biodiversity and traditional knowledge.

The inclusion of genetic diversity as a primary Goal (a higher level than the Action Targets) hopefully reflects increasing recognition of the role of genetic biodiversity for ecological and economic resilience. Moreover, the draft genetic diversity Goal does not focus specifically on domesticated and socio-economically or culturally important species, as the previous 2010 and 2020 CBD targets did (see below). This is an important and positive development. Genetic erosion occurs via similar processes in wild and domesticated species [e.g. inbreeding, genetically small effective population size (*Ne*), and loss of distinct variants, breeds or populations]. This shift could promote monitoring and conservation actions to preserve genetic diversity within many wild species in situ and ex situ, help close the gap between conservation actions directed at ecosystems and species with those at the genetic level, and increase the focus on genetic diversity in national and subnational policies.

However, the zero draft's Goal for genetic diversity is weak and unclear (Laikre et al., 2020). *There is no 2030 Action Target for genetic diversity. The suggested elements for monitoring, including proposed indicators of genetic change (number of threatened breeds, size of seed banks, and conservation of crop wild relatives), remain restricted to the genetic diversity of agricultural species and their wild relatives, as in the current Aichi Target 13 on genetic diversity.* The SDGs and the GSPC also have a strong focus on agriculture. Domesticated species make up a fraction of 1% of all species (Gaut et al., 2018). Such focus neglects non-domesticated species that underpin functional ecosystems and provide ecosystem services, especially under climate and environmental change (Prieto et al., 2015). Indicators only for domesticated species are also contrary to the vision of the CBD "to ensure that this diversity continues to maintain the life support systems of the biosphere" (Convention on Biological Diversity, 2001).

In the context of the important biodiversity policy development that the CBD post-2020 framework represents, and recognizing that timely provision of expertise can inform and guide policy and management, this article contains the following Sections:

2. Emphasis of the importance of maintaining genetic diversity within all species
3. A historical review genetic diversity within the context of the CBD
4. Discussion of shortcomings of genetic indicators proposed by the CBD

Box 1
Clarifying key genetic terms in global biodiversity policy.

Clear terminology is important for designing indicators, and for reporting on status and trends of biodiversity. Here and in the Glossary we suggest definitions for key phrases used by the CBD; we hope such suggestions can be included in a CBD "glossary of key terms and concepts" (e.g. CBD/COP/DEC/14/1).

"Genetic diversity" is the diversity within species which allows species to adapt. A similar term, "genetic resources," has been used to refer to "genetic material", usually from wild or semi-domesticated populations, with "actual or potential economic, environmental, scientific or societal value." This may include genes, genetic variants or genetic complexes controlling traits. It is used primarily in agriculture, medicine, horticulture, fisheries, and forestry (Food and Agriculture Organization of the United Nations, 2014; Harlan, 1975). However, all genetic diversity is a resource for ecosystems, species and populations, regardless of the direct or indirect benefit to humans. Sometimes "genetic resources" is used to refer to the number of wild relative species of domesticated plants and animals, although technically this would be a component of "species diversity". "Phylogenetic diversity" refers to measures of evolutionary distance, most often among species and higher levels (e.g. measuring the phylogenetic diversity of a seed bank, (Griffiths et al., 2015). Although all three concepts (genetic diversity, phylogenetic diversity and genetic resources) are important to biological conservation, the 2010 and 2020 targets for the CBD are most consistent with "genetic diversity *within* species".

In conservation literature "genetic erosion" usually refers to one or more of: loss of alleles (gene variants), decrease in heterozygosity; loss of distinct populations or significant conservation units; or altered gene flow, usually measured with genetic data (Hoban et al., 2014; Ouborg et al., 1991; Rubidge et al., 2012). In agricultural literature, genetic erosion often refers to loss or endangerment of varieties/landraces/breeds or traits/phenotypes (Hammer and Laghetti, 2005). In both wild and domesticated species, genetic erosion may also be presumed when high inbreeding or low effective population size (*Ne*) is observed. Note that the loss of entire species of wild relatives (species closely related to domesticated crops and livestock) is sometimes referred to as genetic erosion, but this is loss of species diversity, not genetic diversity. To help achieve clarity, we propose a comprehensive definition of genetic erosion applicable to both domesticated and wild species, which is connected to our proposed Action Target (Fig. 1). Genetic erosion is the:

- "*loss of genetic diversity (*e.g. *evolutionary potential), lineages, traits, populations or metapopulations, breeds, varieties, landraces or similar,* in situ *or* ex situ*; and/or*
- *the disruption of processes maintaining genetic resilience such as genetic connectivity; and/or*
- *high levels of hybridization; and/or*
- *other threats to genetic diversity such as high inbreeding".*

We propose that the phrase, "to prevent genetic erosion" is approximately synonymous with "genetic diversity is maintained."

"Safeguarding genetic diversity" may refer to in situ protection (e.g., via well-managed protected areas) or ex situ protection (e.g., seed, sperm, eggs, tissue, or living organisms taken from the wild and kept in large, well-documented, managed populations) of a sufficient, representative amount of genetic diversity from a species' geographic range including genetically distinct populations and the full range of environmental heterogeneity (Guerrant et al., 2014). Safeguarding may also include other complementary, non-mutually exclusive actions essential for conserving genetic diversity, such as genetic diversity assessments, supporting genetic exchange among populations, breeding programs, research, etc. We therefore propose to define safeguarding genetic diversity as "*actions performed in situ or ex situ which are designed to characterize, slow, halt or reverse genetic erosion (see above), and promote the processes ensuring adaptive potential*". To accomplish effective safeguarding will require increased knowledge on best care and curation of ex situ collections; and integration of genetic diversity concepts into the management of protected areas in situ. For example, recently updated guidance for Key Biodiversity Areas (IUCN, 2016) and Favourable Reference Populations (DG Environment 2017) under the European Union Habitats Directive (Council Directive 92/43/EEC) includes recommendations on "genetic viability", while the EUFORGEN program tracks detailed data on in situ protected gene conservation units in forest trees (euforgen.org).

5. Expanded details on recently suggested genetic indicators (Laikre et al., 2020) to assess progress towards global conservation targets, along with data sources
6. Suggested post-2020 Goal and Action Target for genetic diversity, connected to indicators and data sources
7. Closing recommendations including suggested next steps for implementation, and future indicators

We also provide clarification of key genetic terms used in global conservation policy (Box 1 and Glossary). We hope to promote science-based discussion during the revision of the framework, and provide a reference for future testing and implementing indicators, and reporting on progress. We also aim to motivate and provide entry points for scientists and policy makers to engage each other for science-driven policy on the conservation of genetic diversity.

2. Emphasis of the importance of genetic diversity within *all* species

Although Aichi Target 13, and Target 9 of the GSPC, state "*and other socio-economically important species*," and the Technical Rationale (https://www.cbd.int/sp/targets/rationale/target-13/) for Target 13 recommends including "*selected wild species of plants and animals*", genetic indicators have long focused on domesticated species, which can limit the types of species and actions that countries include in CBD National Reports (Hoban et al. unpublished data). Many species that are not domesticated have high economic, ecosystem function, or cultural relevance. Economically important species include wild harvested plants that provide timber, non-timber forest products, herbs and medicines; hunted or gathered animals; and horticultural species (Hollingsworth et al., 2020). While >28,000 plant species have documented uses by humans (Royal Botanic Gardens, 2016), many others could yet prove useful, especially in a changing world. Other species are important for tourism or as icons for raising conservation funds (e.g., pandas, tigers, whales). Furthermore, many non-agricultural species are culturally valued for arts and folklore, emblems, culturally significant entities, or religious symbols (e.g., elephants, oak trees). The genetic diversity of ecosystem engineers or keystone species (e.g., trees, seagrasses, predators, pollinators, filter feeders, decomposers) supports larger numbers of species (Clark, 2010) facilitates ecosystem stability, or supports ecosystem functions including primary productivity, nutrients and energy flows. Such functions are crucial for nature in addition to ultimately impacting human health and livelihoods (Hughes and Stachowicz, 2009). Therefore, a sizable fraction of all species have demonstrable social, cultural, economic, or ecological importance. Note that ecosystem services are performed by co-evolved and interacting, interdependent species, whose relationships vary over time as traits and genes change. Recognizing these co-adaptations, and in the light of climate change, it is wise to adopt a holistic biocentric approach relying on resilience which ultimately depends on a broad base of genetic variation. In summary, genetic diversity within species supports not only species' persistence but also ecosystem integrity, adaptability and risk reduction.

Furthermore, monitoring a species subset based on socio-economic importance is unlikely to be representative of most other species (cf. Outhwaite et al., 2020). Therefore a post-2020 Goal should explicitly state "genetic diversity within *all* species", as recommended by the IUCN, Society for Conservation Biology, GEO BON, G-BiKE and others (see Table 1), in order to truly achieve conservation of genetic biodiversity (Laikre et al., 2020; Society for Conservation Biology, 2020; IUCN, 2020). Of course, actual monitoring of genetic diversity (as with monitoring of species and ecosystems) will encompass a science-based subset of taxa, including (but not solely) ecologically, socioeconomically and culturally important species across taxonomic groups. As one example, Hollingsworth et al. (2020) demonstrate a pragmatic process for reporting on genetic diversity for a subset of species.

3. A historical review of genetic diversity in the context of the CBD

In 1992, the Convention on Biological Diversity stated that biological diversity consists of diversity "*within species, between species and of ecosystems*". An ambitious target to halt biodiversity loss was set for 2010, with a subtarget on genetic diversity (Convention on Biological Diversity, 2001): "Genetic diversity of crops, livestock, and harvested species of trees, fish and wildlife and other valuable species conserved, and associated indigenous and local knowledge [is] maintained". The Global Biodiversity Outlook 2 (Convention on Biological Diversity, 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." This document also highlighted threats to genetic diversity including overharvesting of wild species, anthropogenically-induced hybridization, habitat fragmentation, selective hunting, and declines in abundance- which are still among the major threats recognized in conservation genetics. The Outlook also noted that genetic diversity was declining, that genetic diversity monitoring lagged behind species monitoring, and that genetic diversity indicators were weak and needed

Table 1
Examples of knowledge sharing initiatives for conservation genetics. These activities emphasize the substantial ongoing work to link genetic diversity research, policy and action.

Initiative	Duration	Webpage
Conserving Genetic Resources for Effective Species Survival	2010–2013	www.ConGRESSgenetics.eu
IUCN Conservation Planning Specialist Group (previously Conservation Breeding Specialist Group)	1979-current	https://www.cpsg.org/
IUCN Conservation Genetics Specialist Group	2015-current	www.cgsg.uni-freiburg.de/
G-BiKE-Genetic Biodiversity Knowledge for Ecosystem Resilience COST Action	2019-current	sites.google.com/fmach.it/g-bike-genetics-eu/news
GEOBON (Group on Earth Observation Biodiversity Observation Network) Genetic Composition Working Group	2018-current	https://geobon.org/ebvs/working-groups/genetic-composition/
Association of Zoos and Aquaria working group "Molecular Data for Population Advisory Group"	2016-current	https://www.aza.org/molecular-data-for-population-management-scientific-advisory-group
NCEAS/NESCent Working Group on Genetic Monitoring	2008–2009	https://www.nceas.ucsb.edu/projects/12140
Global Genome Biodiversity Network (GGBN)	2011-current	www.ggbn.org/ggbn_portal/
Wildlife Society Molecular Ecology Working Group	2016-current	https://wildlife.org/mewg/
Baltic Sea Genetic Biodiversity (BaltGene) & Baltic Sea Marine Biodiversity (BONUS Bambi)	2009–2017	https://bambi.gu.se/baltgene
Society for Conservation Biology Conservation Genetics Working Group	2016-current	https://conbio.org/groups/working-groups/conservation-genetics-working-group/
CONGENOMICS - European Science Foundation - Research Network Program	2011–2016	http://archives.esf.org/coordinating-research/research-networking-programmes/life-earth-and-environmental-sciences-lee/current-esf-research-networking-programmes-in-life-earth-and-environmental-sciences/conservation-genomics-amalgamation-of-conservation-genetics-and-ecological-and-evolutionary-genomics-congenomics.html

development - concerns also noted elsewhere (Bruford et al., 2017; Convention on Biological Diversity, 2010b; Laikre, 2010).

Recognizing the failure to achieve the 2010 targets, the CBD set 20 Aichi Targets for 2010–2020 (Convention on Biological Diversity, 2010a), including Aichi Target 13: "By 2020, the genetic diversity of cultivated plants and farmed and domesticated animals and of wild relatives, including other socio-economically as well as culturally valuable species, is maintained, and strategies have been developed and implemented for minimizing genetic erosion and safeguarding their genetic diversity." Meanwhile, the conservation genetics field blossomed with thousands of studies (Pérez-Espona et al., 2017); technical and theoretical developments (Allendorf et al., 2010); and numerous case studies where genetic information was fundamental to guide conservation assessments, planning, actions, and legal protections (cf. Ogden et al., 2020; Van der Walt et al., 2017). Important networking and knowledge sharing actions helped improve the support of conservation decisions with genetic scientific knowledge (Table 1). Unfortunately, despite these advancements, indicators and technical guidance for genetic diversity at the CBD still remain insufficient (Laikre et al., 2020).

4. Discussion of shortcomings of genetic indicators proposed by the CBD

An indicator is a simple "measure or metric based on verifiable data that conveys information about more than itself" (BIP et al. 2011). The paucity of currently used CBD genetic indicators and their weak correlation to genetic change has repeatedly been noted in CBD documents (Convention on Biological Diversity, 2010b, 2006). We discuss the relevance and shortcomings of four genetic diversity indicators (Table 2) recommended by the CBD in the zero draft (CBD/WG2020/2/3/Add.1, CBD, 2020), the first of which is also an indicator for the SDG and GSPC.

The first indicator is the "Number of plant genetic resources for food and agriculture secured in medium or long-term conservation facilities" (animal genetic resources were included in 2016 but not in 2020). In practice this means the number of seed collections (i.e., accessions) kept in seed banks. In theory, preserving more individuals or seeds ex situ should preserve more genetic diversity. However, seed banks often do not sufficiently safeguard genetic diversity because they often represent offspring of only one population or a few individuals of an entire species (Beckman et al., 2019; Maunder et al., 2001). As such, this indicator is only loosely connected to genetic diversity preservation and may more closely relate to conservation of number of species. In addition 10–20% of all plant species (therefore about 35,000 species) cannot be kept in conventional seed banks, many of them tropical (Walters et al., 2013). An improvement would be to modify the current indicator with a clause specifying that collections must be genetically representative (i.e. sampled across the geographic range, typically at least 5 populations), resilient (i.e. large samples, e.g. seeds from >50 plants per population), and replicated (i.e. backed up in multiple locations (Hoban, 2019). This information is available for many botanic gardens and seed banks.

Another CBD genetic diversity indicator is the "Proportion of local breeds classified as being at risk, not at risk, or at unknown level of risk of extinction" (threatened plant genetic resources was included in 2016 but not in 2020). While this indicator is not applicable to wild populations, endangered breeds of domestic species are comparable to endangered distinct wild populations; populations are the wild equivalent of breeds or plant varieties. The definition of threatened animal breeds includes discussion of the effective population size needed to avoid loss of genetic diversity (Hodges, 1992). Therefore, this indicator could be subsumed within our proposed indicator number of populations whose effective population size *Ne* is below 500 (i.e. at high genetic risk) as compared to the number with *Ne* larger than 500 (thus genetically "safe"; see Glossary and below for definition of *Ne)*.

A third indicator is the "Comprehensiveness of conservation of socioeconomically as well as culturally valuable species" (Khoury et al., 2019). It quantifies a proportion of a species range that is represented ex situ (held in seed banks) or in situ (within protected areas). (Additional indicators representing habitat quality and quantity were recommended in 2016 but not in 2020.) It is described as an indicator for crop wild relatives but its methodology is equally applicable to any species. In the absence of any knowledge of a species other than its geographic occurrences, this is an effective indicator of genetic erosion because on average, as geographic occurrence declines, populations and their diversity are lost (Alsos et al., 2012; Wasserman et al., 2012). It could be expanded to all species, with the caveats above regarding seed bank effectiveness and the caveat that protected areas must have high quality habitat, connectivity, and legal enforcement.

The final CBD genetic diversity indicator is the "Red List Index (species used for food and medicine and wild relatives of domesticated animals)", which reflects changes in the number of species in Red List (RL) categories (e.g. Endangered, Critically Endangered) based on updated assessments and new knowledge. The IUCN evaluates criteria such as total species census size, reductions in population size and/or geographic range, each of which should theoretically correlate with losses of genetic diversity. However, although genetic diversity is lower on average in threatened species, RL categories are poor predictors of genetic erosion and a metric based on effective population size and its influence on genetic erosion was subsequently recommended (Willoughby et al., 2015). Additionally, RL terminology considers "population size" as the total number of adults of the taxon (globally), and does not address genetically distinct populations within taxa, where genetic erosion primarily occurs. Moreover, for many taxa, RL thresholds will not meet the census size, or *Nc,* required for a genetic effective size of $Ne > 500$, even at the species level (see Glossary and below for definitions of *Nc* and *Ne*). For example, to be listed under the RL criterion D (very small or restricted population), the total *Nc* must be <1000 for Vulnerable, <250 for Endangered, <50 for Critically Endangered (IUCN, 2019). While in some cases the original data used for the assessments of the Red List (e.g. number of populations, size of populations) could help calculate the genetic indicators we propose below, the Red List Index itself does not suffice as a genetic indicator.

Table 2
Summary of weaknesses of zero draft indicators (from CBD document "Preliminary draft monitoring framework" CBD/WG2020/2/3/Add.1) and proposed changes.

CBD Indicator	Rationale	Limitation	Proposed changes
"Number of plant genetic resources … secured…"	Larger number of seed collections in storage facilities might conserve more genetic diversity	More seeds does not necessarily mean more genetic diversity	Include specification for "resilient, representative and redundant"[a]
"Proportion of local breeds… at risk..."	Breeds below a given *Ne* are likely losing genetic diversity	Ignores wild species	Subsume into our indicator 2 "Proportion of distinct populations maintained within species"
"Comprehensiveness of conservation for socioeconomically and culturally valuable species"	Percent of geographic range protected in situ and ex situ should conserve genetic diversity especially local adaptations	Ignores most wild species	Must apply to "all species". Complements our indicator "Proportion of populations maintained within species"
"Red List (RL) Index..."	Change in RL categories may reflect demographic and thus genetic change	Not well connected to genetic diversity	Do not use as a genetic diversity indicator (but RL assessment data can be useful)

[a] Definitions for resilient, representative and redundant are provided in Section 3.

5. New genetic indicators to assess progress towards global conservation targets

The Biodiversity Indicators Partnership, which supports CBD indicator development, recently stated, “it is still possible to identify datasets and indicators of which we were previously unaware, and there is often ongoing work that, with minimal support, could provide a new and innovative indicator for use” (http://www.bipindicators.net). We explain here three genetic diversity indicators (elaborating from Laikre et al., 2020), all of which are essentially counts of populations or species meeting a criteria and can be applied to wild or domesticated species, in situ or ex situ (Fig. 1).

(1) *Number of populations within species with effective population size (Ne) above 500* versus *those with Ne below 500:* A principal component of genetic diversity change is the genetic effective size (*Ne*) of populations, which determines rates of inbreeding, loss of genetic variation, and loss of adaptive potential. *Ne* is a theoretical concept with important practical value; *Ne* has well established thresholds regarding genetic erosion: Effective population sizes lower than 500 (Jamieson and Allendorf, 2012) will result in reduced ability to adapt to environmental change (some advocate a *Ne* threshold of 1000; Frankham et al., 2014). This threshold of *Ne* for preventing genetic erosion applies to all organisms' populations regardless of species' commonness, organism size, and life history characteristics; below this threshold adaptive genetic diversity cannot be maintained and random fluctuations in gene variants may overwhelm normal levels of natural selection. However we acknowledge that some species' populations have historically maintained *Ne* in the hundreds of thousands (e.g. tree species, Brown et al. 2004) and that higher *Ne* helps maintain more alleles and higher genetic diversity.

We suggest applying the *Ne* > 500 threshold to genetically distinct populations or to distinct, functional metapopulations (a set of local populations which exchange multiple migrant(s) each generation) to identify risk of genetic erosion. For continuously distributed species, populations may be defined by ecoregions, genetic data, seed zones or other delineations, depending on the species. Unless populations are nearly isolated (very low migration) or the metapopulation structure is well known, *Ne* estimates from molecular data can be hard to interpret. This indicator monitors the number of distinct (meta)populations whose current known or estimated *Ne* is below vs. above 500, representing loss of adaptive potential. We also note that *Ne* lower than 50 is a more extreme situation requiring immediate action to prevent rapid, harmful increases in inbreeding, decline in fitness and reproductive output, and very rapid loss of diversity. Note that these thresholds are minimum guidelines for risk assessment; *Ne* above a threshold doesn't necessarily mean that conservation intervention is no longer required nor does *Ne* below a threshold signify lost hope for recovery.

Ne can be assessed in several ways (details in Box 2). *Ne* can be calculated using freely available software if a pedigree is available, as with captively bred, closely monitored or domesticated species (Lacy et al., 2012). *Ne* can also be calculated from demographic data e.g. life history characters and demography for the focal or a related species

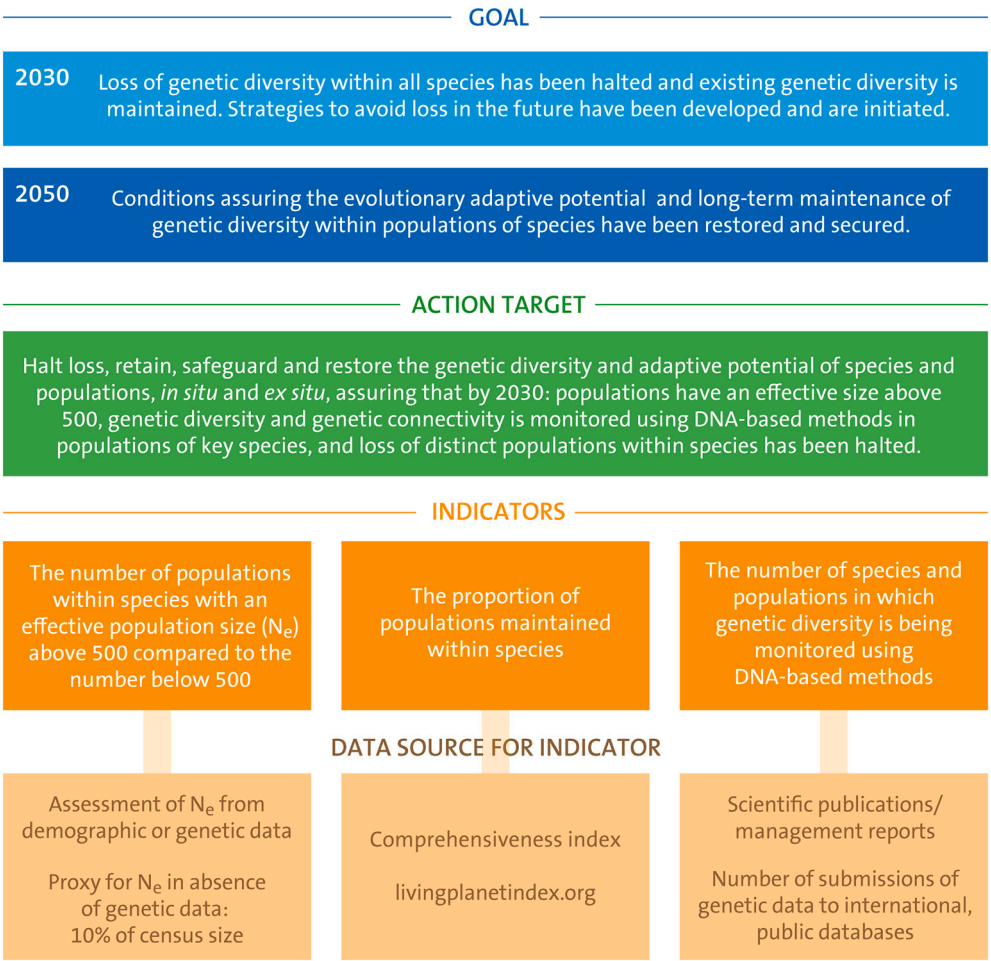

Fig. 1. New Goal, Action Target and indicators (including sources of data for those indicators) proposed for the CBD post-2020 biodiversity framework for efficient conservation of genetic diversity of all species.

(Palstra and Fraser, 2012; Waples et al., 2011) or with molecular genetic data (Do et al., 2014; Wang et al., 2016). In the absence of such knowledge, *Ne* can be roughly approximated using the estimated census size of a population (*Nc*, census size, typically the number of adult individuals) multiplied by 0.1. The approximate value 0.1 has been observed as mean and/or median in scientific reviews of *Ne/Nc* ratios in animal and plant populations (Frankham, 1995; Ruzzante and Palstra, 2008), and implies that *Nc* of 5000, in the absence of other data, may be assumed to have an *Ne* of 500, on average.

Ne/Nc varies among species primarily due to their demographic and life history traits (Frankham, 1995; Palstra and Fraser, 2012; Palstra and Ruzzante, 2008; Wang et al., 2016), see Box 2. We include a compendium of *Ne/Nc* values from previous reviews plus 35 additional studies in Supplemental Tables 1 and 2 and Fig. S1. Clearly, variation is large, but for some populations and species robust estimates are available, and with increasing genetic monitoring efforts, knowledge is rapidly accumulating and estimation techniques are improving (Ryman et al., 2019).

We emphasize that use of the *Ne/Nc* ratio (e.g. 0.1) in the absence of robust genetic or demographic assessments, is for most species consistent with the precautionary principle. Box 2 illustrates caveats to the *Ne/Nc* approach, including how the ratio may be estimated at local population versus at metapopulation levels. Despite some caveats, *Ne* is one of the most important parameters for halting genetic erosion and maintaining adaptive potential and we recommend its use in most situations, particularly when each population is fairly discrete with low gene flow, when populations are continuous with high gene flow (one population), or when information on the metapopulation structure is available. When calculated across numerous species, this indicator should be a powerful assessment of genetic erosion in which bounds of uncertainty (see Box 2) emphasize optimistic and pessimistic scenarios (and acknowledge gaps in our knowledge).

(2) *The proportion of distinct populations maintained within species:* Another accessible indicator is the number of genetically distinct populations, relative to some baseline, preferably from historic records. The loss of distinct wild populations, or the agricultural equivalent - breeds, landraces, or varieties - will result in large losses of genetic diversity within species (Alsos et al., 2012), especially the loss of local adaptations. Conservation's historic focus on species extinctions has neglected the loss of diversity as species' ranges shrink and millions of populations disappear (Ceballos et al., 2017). The loss of distinct populations could be calculated from IUCN Red List data, historic Global Biodiversity Information Facility (GBIF) occurrences, or data underlying the Living Planet Index. The question arises, what is a population? While populations are often geographically distinct (e.g. a wetland, a forest patch), in many cases they are not (see caveat above for *Ne*). Genetic data can reveal population boundaries (Waples and Gaggiotti 2006), though observed genetic differences should be interpreted carefully to avoid misinterpretation. For example, recent population decline and/or cessation of gene flow can lead to observed population differentiation that is only very recent. Moreover, high resolution genomic datasets may detect very small population divergence with little conservation significance. Nonetheless, such low divergence can still reflect local adaptation (e.g., Hill et al., 2019). Alternatively, a percentage of the species' historic range which is maintained would suffice, which could be calculated in an automated procedure similar to the “comprehensiveness” indicator, e.g. using occurrence records.

Box 2

Challenges with *Ne* and the *Ne/N*c ratio, including an example for the pool frog (*Pelophylax lessonae*).

Several challenges to assessing *Ne* are worth enumerating. *Ne* is determined by fluctuation in population size, variance in number of offspring among individuals, unequal sex ratio, overlapping generations (Frankham, 1995; Waples, 2002). Further, several different effective population sizes have been defined relating to different types of genetic change including inbreeding effective size, variance effective size, and linkage disequilibrium effective size. In isolated populations these *Ne* are the same but in non-isolated populations they may differ considerably (Hössjer et al. 2016; Ryman et al., 2019). In addition, assessments in natural populations show that *Ne/Nc* ratios may vary greatly among and within taxonomic groups due to factors like gene flow, metapopulation structure and population turnover (Frankham, 1995; Palstra and Ruzzante, 2008; Palstra and Fraser, 2012). We have compiled *Ne/Nc* estimates from previous reviews and this study (Tables S1 and S2) and illustrate the variation in Fig. S1. In general, species characterized by type III survivorship curves (high juvenile mortality and high fecundity) and high variance in reproductive success such as many marine fish or planktonic copepods, displayed much lower *Ne/Nc* ratios than other groups [e.g., median ratio of 2.67×10^{-4} for bony marine fish species; Tables S1–2]. The ratio *Ne/Nc* is also much lower when interannual census population size (Nc) varies (Frankham, 1995). The ratio tends to be slightly higher than 0.1 in large mammals and birds, and lower in marine fish. Additional compilation of *Ne* values across many taxa will help refine the range of Ne/Nc by taxonomic group and allow better operationalisation of *Ne* in this indicator; this will be enabled by increasing affordability and accessibility of genetic data analysis (and clear reporting in publications).

Even within species, the *Ne/Nc* ratio may vary over geographic and spatial scales. For example, it is important to note whether *Ne/Nc* is of a local subpopulation or of the whole metapopulation. Sjögren (1991) quantified *Ne* for a generation of pool frogs using detailed demographic data of a local population, and also using Maruyama and Kimura's (1980) *Ne*-meta model to estimate long-term *Ne* per generation at the metapopulation level. Local *Ne* was either 59 (reproduction was normal all years) or 35 (reproduction was poor in 2 out of 5 years). The number of adults during the full generation was 327, and the annual estimates of the number of adults (*Nc*) ranged from 79 to 204 (Sjögren, 1991)). Therefore within this local population, *Ne/Nc* was from 0.107 to 0.180 if *Nc* is calculated over the entire generation, while according to annual *Nc*, it varied from 0.289 to 0.366 during years with normal reproduction and from 0.357 to 0.443 during years with poor reproduction.

When populations are substructured, the metapopulation effective size (Ne-meta) and local subpopulation effective sizes are of interest and can be assessed (Gomez-Uchida et al. 2013; Maruyama and Kimura, 1980). *Ne-meta* can be larger or smaller than the raw sum of the *Ne* per sub-population due to factors like gene flow and metapopulation structure (Palstra & Ruzzante 2011; Paz-Vinas et al. 2013; Hössjer et al. 2016; Marzo et al. 2020) and the type of *Ne* considered (Ryman et al., 2019). In the pool frog, at the metapopulation level, with 30 local populations in a metapopulation and using the Maruyama and Kimura (1980), *Ne/Nc* was 0.078. VORTEX modeling (Lacy and Pollak, 2017) of 16 of these 30 local populations with data from Sjögren (1988, 1991) indicated that observed heterozygosity during 100 years declined with a rate corresponding to a *Ne/Nc* = 0.086. *In conclusion, metapopulation dynamics and the method used to calculate Ne will influence the Ne/Nc estimate.* Few studies have this amount of detail or are conducted over sufficient time frames (full generations). In this pool frog case, *Ne/Nc* varied between 0.11 and 0.44 at the local population level, and was lower (0.08–0.09) at the metapopulation level. If no data had been available on this species, the conservative estimate of 0.1 for *Ne/Nc* seems reasonable. When employed as an indicator, reporting of *Ne* should detail the method(s) used (e.g. pedigree, genetic (and which estimator), demographic, “rule of thumb”, and any assumptions), and the range of values from different methods. *More Ne estimation in natural populations is needed, particularly in metapopulations. With increased monitoring of genetic diversity (Indicator 3) such information can be generated within the CBD post-2020 biodiversity framework.*

This indicator is challenged by the prospect of species' range shifts under climate change. It is possible in theory but unlikely in reality for populations to perfectly track climate (i.e. all populations shift with no gain or loss of populations and genetic composition is unchanged). The most likely scenario is loss of trailing-edge populations (i.e. loss of some populations) either with or without a leading-edge shift. Theory and data suggest that new leading-edge populations will be limited by competition, dispersal limits, and other ecological factors. Moreover, newly colonized leading-edge locations cannot make up for losses on the trailing-edge, likely resulting in overall genetic erosion. Another scenario is more complex- some populations shift, migration patterns change (with potential for genetic homogenisation), and populations are lost and gained in various locations. In this case some aspects of genetic diversity are maintained (possibly allelic richness), but other aspects (e.g. genetic differentiation, local adaptations) may not. This indicator would not fully capture such complex situations, nor would it capture hybridization between species. This challenge emphasizes the importance of monitoring genetic diversity and population boundaries (indicator 3); one indicator alone is insufficient for monitoring progress towards the CBD genetic diversity goal.

(3) *Number of species and populations in which genetic diversity is being monitored using DNA based methods:* A further important aspect of safeguarding genetic diversity, as noted above, is knowledge on genetic diversity within and among populations (in situ and ex situ), environmental drivers of that diversity, and degree of genetic connectivity between subpopulations. Such knowledge is often used to directly guide management for safeguarding genetic diversity, such as clarifying taxonomic distinctiveness of rare species, assessing current vs. historic genetic connectivity to inform translocations and restoration, optimal protected area design, informing captive breeding, and identifying genetic consequences of stocking or harvest (Bowman et al., 2016; Holliday et al., 2017; Koskela et al., 2013). We thus propose an indicator as the number of populations of extant species whose within-species genetic diversity (more than one individual and ideally multiple populations) has been assessed in a publication or published in online databases and/or where this data is used to inform conservation. An improvement upon this, as genetic data accumulates (see Conclusion), will be to focus on the number of species with routine monitoring of genetic diversity to facilitate conservation action.

We consider this to be an informative and practical indicator but recognise that it is a proxy for conservation genetic data observations and knowledge rather than conservation genetic action (e.g. the research-implementation gap, Taylor et al. 2017). This indicator could also reflect increased laboratory capacity, or an increase in imperiled species needing conservation efforts, and therefore cannot be relied on in isolation. Data sources for this indicator could include journal articles, reports (cf. Bowman et al., 2016) and the number of species' populations with genetic datasets submitted to major repositories including GenBank, EMBL-EBI, GEOME, Sequence Read Archive, Dryad, FishBank, and CartograTree. The submission of genetic information in such repositories in a coordinated, standardized fashion is still largely lacking, a clear task for the groups in Table 1.

Concluding remarks on the three proposed indicators: These indicators are applicable to all species, in situ and ex situ, and are available immediately. Indicators 1 and 2 do not require genetic data. They are each scalable- as essentially counts of populations meeting a criteria they can be calculated locally, regionally or globally, and can be aggregated across species and among different taxonomic groups. Transnational collaboration will be useful for species that cross borders. We identify examples of high-quality data sources for the indicators (Fig. 1), though of course other data may be available. These indicators are suitable for adoption in the post-2020 CBD framework.

6. Suggested post-2020 Goal and Action Target for genetic diversity, connected to indicators and data sources

We identify a post-2020 genetic biodiversity Goal and Action Target which is clearly connected to suitable indicators and to definitions of terminology in Box 1 (Fig. 1). The revised Goal is more specific and inclusive than that of the zero draft; clearly emphasizes all species; emphasizes the near term (2030) outcome of stability (minimizing loss, developing effective strategies and plans); and emphasizes the long term (2050) outcome of maintaining adaptive capacity and resilience, and restoring evolutionary processes in natural systems (e.g. large populations and migration). The timelines match other CBD Goals and reflect feasibility- stabilization and forming strategies are achievable by 2030, while ensuring and restoring adaptive capacity will require restoring population connectivity, increasing population size, and in some populations active management of adaptive potential, which will take longer (2050, though in some species, those with short generation times, the Goal can be achieved sooner).

Currently the zero draft has no Action Target leading to conserving genetic diversity. To support a genetic goal, at least one genetic Action Target is needed to emphasize the activities that must occur to achieve the goal; actions supporting genetic diversity differ from those supporting species, ecosystems, society etc. Our Target wording in Fig. 1 focuses on actions needed: assure large populations in situ and ex situ, maintain all extant (meta-)populations and connectivity among populations, and monitor genetic diversity to guide local and regional conservation management. The indicators monitor that the actions are carried out and are successful. All sections of Fig. 1 (Goal, Action Target, Indicators) are needed and are aligned with the CBD zero draft structure. To summarize, we underline the need to improve the genetic Goal, to add an Action Target to assure that active work will occur, and to use efficient indicators reflecting genetic diversity. These elements could also form future targets for the SDGs and the GSPC.

7. Closing recommendations

For the post-2020 Global Biodiversity Framework Goal 3 of maintaining genetic diversity, we have defined practical genetic diversity indicators based on clear definitions and using available data, which underpin a newly worded Goal and an Action Target. The three indicators are:

- The number of populations [or breeds] within species with an effective population size (Ne) above 500 compared to the number below 500
- The proportion of populations [or geographic range] maintained within species
- The number of species and populations in which genetic diversity is being monitored using DNA based methods

We also propose modifications to current CBD indicators (additions in italics):

- Comprehensiveness of conservation of *all* species
- Number of *resilient, representative, and replicated* plant genetic resources secured in medium or long-term conservation facilities

We note that these two indicators alone are not sufficient. Rather, they can be used as complementary to our three new indicators.

The following CBD indicators may be discontinued.

- "Proportion of local breeds classified as being at risk…" can be subsumed into the new indicator on populations [or breeds] above *Ne* 500
- "The Red List Index..." should not be used because it is not correlated to genetic erosion and because it focuses on global census size, not on size of distinct populations.

We note that genetic data are increasingly available and affordable, and government agencies and others are often able to monitor genetic diversity directly, including using historic samples and models of historic genetic diversity. Genomic technologies and analytical methods are rapidly changing, with genome sequencers now the size and cost of a smartphone, and analytical tools able to estimate gene flow and population sizes many generations in the past. *Within five to ten years, additional indicators of genetic erosion based on large genetic datasets for large numbers of species, with data or inferences reaching back hundreds of years, are likely*. In addition, genetic erosion can in some cases be inferred by monitoring anthropogenic causative factors (e.g., deterioration of habitat, climate change), though the relationship between such factors and genetic erosion is unknown for most species, is sometimes non-linear, multifaceted, and time-lagged (Carvalho et al., 2019). However, if the links between specific causal drivers and genetic erosion are established (Wasserman et al., 2012), monitoring might focus on the *drivers* directly without the need for genetic analysis; this is a critical area of research. Similarly, linking critical thresholds for *Ne* to minimum area requirements of suitable habitat could allow determining if a population confined to a certain *patch size* is large enough to maintain genetic diversity over time. *The indicators we propose should be supplemented as data accumulates and improves.* Indicators could also build on the concept of Essential Biodiversity Variables (EBVs), which are summaries of complex biodiversity data (Navarro et al., 2017)-genetic composition EBVs include allelic diversity, genetic differentiation, and *Ne*.

Progress towards any indicator, including those noted above will require and contribute to capacity-building (Convention on Biological Diversity, 2020; Target 15) for documenting, curating, sharing, and accessing regional and global databases on population demography and genetic diversity information, especially in biodiverse regions. Currently, most collected genetic data (like most biodiversity data) is not easily accessible or lacks sufficient meta-data (Convention on Biological Diversity, 2010b; Pope et al., 2015), and thus cannot be used for monitoring. This situation must change to safeguard genetic diversity. Networks of practitioners (Table 1) must also help interpret and train others to use genetic knowledge, contributing to the zero draft's Target 18: "Promote education and the generation, sharing and use of knowledge relating to biodiversity… ensuring by 2030 that all decision makers have access to reliable and up to date information for the effective management of biodiversity." An additional advance would be to add more genetic diversity definitions (Box 1 and Glossary) to guidance documents for policy, including CBD Biodiversity Glossaries (e.g. https://www.cbd.int/cepa/toolkit/2008/doc/CBD-Toolkit-Glossaries.pdf). Looking forward, we envision a post-2020 framework that recognizes that genetic diversity of all species contributes essentially to supporting human society and the life support systems of the biosphere, and which protects genetic diversity with clear, comprehensive, data-informed policy.

Disclaimer

Any use of trade, firm, or product names is for descriptive purposes only and does not imply endorsement by the U.S. Government. This manuscript does not represent the official finding or policy of any government or institution.

CRediT authorship contribution statement

Sean Hoban: Conceptualization, Writing - original draft, Writing - review & editing. **Michael Bruford**: Conceptualization, Writing - review & editing. **Josephine D'Urban Jackson**: Conceptualization, Writing - review & editing. **Margarida Lopes-Fernandes**: Conceptualization, Writing - review & editing. **Myriam Heuertz**: Conceptualization, Writing - review & editing. **Paul A. Hohenlohe**: Conceptualization, Writing - review & editing. **Per Sjögren-Gulve**: Conceptualization, Writing - review & editing. **Gernot Segelbacher**: Conceptualization, Writing - review & editing. **Cristiano Vernesi**: Conceptualization, Writing - review & editing. **Sally Aitken**: Writing - review & editing. **Laura D. Bertola**: Writing - review & editing. **Paulette Bloomer**: Writing - review & editing. **Martin Breed**: Writing - review & editing. **Hernando Rodríguez-Correa**: Writing - review & editing. **W. Chris Funk**: Writing - review & editing. **Catherine E. Grueber**: Writing - review & editing. **Margaret E. Hunter**: Writing - review & editing. **Rodolfo Jaffe**: Writing - review & editing. **Libby Liggins**: Conceptualization, Writing - original draft, Writing - review & editing. **Joachim Mergeay**: Writing - review & editing. **Farideh Moharrek**: Writing - review & editing. **David O'Brien**: Writing - review & editing. **Rob Ogden**: Writing - review & editing. **Clarisse Palma-Silva**: Writing - review & editing. **Ivan Paz-Vinas**: Data curation, Formal analysis, Writing - review & editing. **Jennifer Pierson**: Writing - review & editing. **Uma Ramakrishnan**: Writing - review & editing. **Murielle Simo-Droissart**: Writing - review & editing. **Naoki Tani**: Writing - review & editing. **Lisette Waits**: Writing - review & editing. **Linda Laikre**: Conceptualization, Writing - review & editing.

Declaration of competing interest

The authors declare that they have no known competing financial interests or personal relationships that could have appeared to influence the work reported in this paper.

Acknowledgements

We would like to acknowledge funding from the EU Framework Horizon 2020 through the COST Action 18134 'Genomic Biodiversity Knowledge for Resilient Ecosystems'-GBIKE. This work has benefited from an "Investissement d'Avenir" grant managed by Agence Nationale de la Recherche (CEBA, ref. ANR-10-LABX-25-01), funding via The Morton Arboretum Center for Tree Science, Swedish Research Council Formas, Grant Number: FR-2016/0005, Swedish Research Council, Grant Number: 2019-05503. We also thank Jerker Lokrantz/Azote for preparing Fig. 1. The open access was financed through the SwEPA and BIBSAM.

Appendix A. Supplementary data

Tables S1 and S2 and Fig. S1 compile estimates of *Ne/Nc* from several reviews and new data. Supplementary data to this article can be found online at https://doi.org/10.1016/j.biocon.2020.108654.

References

Aguilar, R., Quesada, M., Ashworth, L., Herrerias-Diego, Y., Lobo, J., 2008. Genetic consequences of habitat fragmentation in plant populations: susceptible signals in plant traits and methodological approaches. Mol. Ecol. 17, 5177–5188.

Allendorf, F.W., Hohenlohe, P.A., Luikart, G., 2010. Genomics and the future of conservation genetics. Nat. Rev. Genet. 11, 697–709.

Alsos, I.G., Ehrich, D., Thuiller, W., Eidesen, P.B., Tribsch, A., Schönswetter, P., Lagaye, C., Taberlet, P., Brochmann, C., 2012. Genetic consequences of climate change for northern plants. Proc. Biol. Sci. 279, 2042–2051.

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. The Morton Arboretum., Lisle, IL.

Biodiversity Indicators Partnership, 2011. Guidance for national biodiversity indicator development and use. UNEP World Conservation Monitoring Centre, Cambridge, UK, pp. 40.

Blanchet, S., Prunier, J.G., Paz-Vinas, I., Saint-Pé, K., Rey, O., et al., 2020. A river runs through it: the causes, consequences and management of intraspecific diversity in river networks. Evol. Appl. https://doi.org/10.1111/eva.12941.

Bowman, J., Greenhorn, J.E., Marrotte, R.R., McKay, M.M., Morris, K.Y., Prentice, M.B., Wehtje, M., 2016. On applications of landscape genetics. Conserv. Genet. 17, 753–760.

Brown, G.R., Gill, G.P., Kuntz, R.J., Langley, C.H., Neale, D.B., 2004. Nucleotide diversity and linkage disequilibrium in loblolly pine. Proc. Natl. Acad. Sci. 101 (42), 15255–15260.

Bruford, M.W., Davies, N., Dulloo, M.E., Faith, D.P., Walters, M., 2017. Monitoring changes in genetic diversity. In: The GEO Handbook on Biodiversity Observation Networks. Springer, Cham, pp. 107–128.
Carvalho, C.S., Lanes, É.C.M., Silva, A.R., Caldeira, C.F., Carvalho-Filho, N., Gastauer, M., Imperatriz-Fonseca, V.L., Nascimento Júnior, W., Oliveira, G., Siqueira, J.O., Viana, P.L., Jaffé, R., 2019. Habitat loss does not always entail negative genetic consequences. Front. Genet. 10, 1011.
Ceballos, G., Ehrlich, P.R., Dirzo, R., 2017. Biological annihilation via the ongoing sixth mass extinction signaled by vertebrate population losses and declines. Proc. Natl. Acad. Sci. U. S. A. 114, E6089–E6096.
Clark, J.S., 2010. Individuals and the variation needed for high species diversity in forest trees. Science 327, 1129–1132.
Convention on Biological Diversity, 2001. Global Biodiversity Outlook 1 [WWW Document]. URL. https://www.cbd.int/gbo1/ (accessed 3.9.20).
Convention on Biological Diversity, 2006. Global Biodiversity Outlook 2. (Secretariat of the Convention on Biological Diversity).
Convention on Biological Diversity, 2010a. Strategic Plan for Biodiversity 2011–2020, including Aichi Biodiversity Targets.
Convention on Biological Diversity, 2010b. Global Biodiversity Outlook (GBO-3), in: Convention on Biological Diversity.
Convention on Biological Diversity, 2020. Zero Draft of the Post-2020 Global Biodiversity Framework. (Convention on Biological Diversity).
Do, C., Waples, R.S., Peel, D., Macbeth, G.M., Tillett, B.J., Ovenden, J.R., 2014. NeEstimator v2: re-implementation of software for the estimation of contemporary effective population size (Ne) from genetic data. Mol. Ecol. Resour. 14, 209–214.
Doyle, R.W., 2016. Inbreeding and disease in tropical shrimp aquaculture: a reappraisal and caution. Aquac. Res. 47, 21–35.
Environment, D.G., 2017. Reporting under Article 17 of the Habitats Directive: Explanatory notes and guidelines for the period 2013-2018. Brussels.
Erdelen, W.R., 2020. Shaping the Fate of Life on Earth: The Post-2020 Global Biodiversity Framework. Global Policy 11 (3), 347–359.
Food and Agriculture Organization of the United Nations, 2014. The state of the world's forest genetic resources.
Frankham, R., 1995. Effective population size/adult population size ratios in wildlife: a review. Genet. Res. 66, 95–107.
Frankham, R., Bradshaw, C.J.A., Brook, B.W., 2014. Genetics in conservation management: revised recommendations for the 50/500 rules, Red List criteria and population viability analyses. Biol. Conserv. 170, 56–63.
Funk, W.C., Chris Funk, W., McKay, J.K., Hohenlohe, P.A., Allendorf, F.W., 2012. Harnessing genomics for delineating conservation units. Trends Ecol. Evol. https://doi.org/10.1016/j.tree.2012.05.012.
Gaut, B.S., Seymour, D.K., Liu, Q., Zhou, Y., 2018. Demography and its effects on genomic variation in crop domestication. Nat Plants 4, 512–520.
Gomez-Uchida, D., Palstra, F.P., Knight, T.W., Ruzzante, D.E., 2013. Contemporary effective population and metapopulation size (Ne and meta-Ne): Comparison among three salmonids inhabiting a fragmented system and differing in gene flow and its asymmetries. Ecology and evolution 3 (3), 569–580.
Griffiths, K.E., Balding, S.T., Dickie, J.B., Lewis, G.P., Pearce, T.R., Grenyer, R., 2015. Maximizing the phylogenetic diversity of seed banks. Conserv. Biol. 29, 370–381.
Guerrant, E.O., Havens, K., Vitt, P., 2014. Sampling for effective ex situ plant conservation. Int. J. Plant Sci. 175, 11–20.
Hammer, K., Laghetti, G., 2005. Genetic Erosion – examples from Italy1,2. Genet. Resour. Crop. Evol. 52, 629–634.
Harlan, J.R., 1975. Our vanishing genetic resources. Science 188, 617–621.
HELCOM, B., 2007. HELCOM Baltic Sea action plan. Krakow, Poland. 15. pp. 2007.
Hill, J., Enbody, E.D., Pettersson, M.E., Sprehn, C.G., Bekkevold, D., Folkvord, A., Laikre, L., Kleinau, G., Scheerer, P., Andersson, L., 2019. Recurrent convergent evolution at amino acid residue 261 in fish rhodopsin. Proc. Natl. Acad. Sci. 116 (37), 18473–18478.
Hoban, S., 2019. New guidance for ex situ gene conservation: sampling realistic population systems and accounting for collection attrition. Biol. Conserv. 235, 199–208.
Hoban, S., Arntzen, J.A., Bruford, M.W., Godoy, J.A., Rus Hoelzel, A., Segelbacher, G., Vilà, C., Bertorelle, G., 2014. Comparative evaluation of potential indicators and temporal sampling protocols for monitoring genetic erosion. Evol. Appl. 7, 984–998.
Hodges, J., 1992. The Management of Global Animal Genetic Resources. Proceedings of an FAO Expert Consultation, Roma.
Holliday, J.A., Aitken, S.N., Cooke, J.E.K., Fady, B., González-Martínez, S.C., Heuertz, M., Jaramillo-Correa, J.-P., Lexer, C., Staton, M., Whetten, R.W., Plomion, C., 2017. Advances in ecological genomics in forest trees and applications to genetic resources conservation and breeding. Mol. Ecol. 26, 706–717.
Hollingsworth, P.M., O'Brien, D., Ennos, R.A., Yahr, R., Neaves, L., et al., 2020. Scotland's Biodiversity Progress to 2020 Aichi Targets: Conserving Genetic Diversity – Development of a National Approach for Addressing Aichi Biodiversity Target 13 that Includes Wild Species. Scottish Natural Heritage, Inverness.
Hössjer, O., Laikre, L., Ryman, N., 2016. Effective sizes and time to migration–drift equilibrium in geographically subdivided populations. Theor. Popul. Biol. 112, 139–156.
Hughes, A.R., Stachowicz, J.J., 2009. Ecological impacts of genotypic diversity in the clonal seagrass Zostera marina. Ecology 90, 1412–1419.
IPBES, 2019. Summary for policymakers of the global assessment report on biodiversity and ecosystem services of the Intergovernmental Science-Policy Platform on Biodiversity and Ecosystem Services. S. Díaz, et al. (eds.). IPBES, Bonn, Germany. 56 pages.
IUCN, 2016. A global standard for the identification of key biodiversity areas. Iucn (international Union For Conservation of Nature).
IUCN, 2019. The IUCN Red List of Threatened Species. Version 2019-3 [WWW Document]. IUCN 2020. URL. https://www.iucnredlist.org.
IUCN, 2020. IUCN position: zero draft of the post-2020 Global Biodiversity Framework. In: February 2020. Italy, Rome.
Jamieson, I.G., Allendorf, F.W., 2012. How does the 50/500 rule apply to MVPs? Trends Ecol. Evol. 27, 578–584.
Khoury, C.K., Amariles, D., Soto, J.S., Diaz, M.V., Sotelo, S., Sosa, C.C., Ramírez-Villegas, J., Achicanoy, H.A., Velásquez-Tibatá, J., Guarino, L., León, B., Navarro-Racines, C., Castañeda-Álvarez, N.P., Dempewolf, H., Wiersema, J.H., Jarvis, A., 2019. Comprehensiveness of conservation of useful wild plants: an operational indicator for biodiversity and sustainable development targets. Ecol. Indic. 98, 420–429.
Koskela, J., Lefèvre, F., Schueler, S., Kraigher, H., Olrik, D.C., et al., 2013. Translating conservation genetics into management: Pan-European minimum requirements for dynamic conservation units of forest tree genetic diversity. Biol. Conserv. 157, 39–49.
Lacy, R.C., Pollak, J.P., 2017. Vortex: A Stochastic Simulation of the Extinction Process. Chicago Zoological Society, Brookfield, Illinois, USA.
Lacy, R.C., Ballou, J.D., Pollak, J.P., 2012. PMx: software package for demographic and genetic analysis and management of pedigreed populations: PMx software for pedigree analysis. Methods Ecol. Evol. 3, 433–437.
Laikre, L., 2010. Genetic diversity is overlooked in international conservation policy implementation. Conserv. Genet. 11, 349–354.
Laikre, L., Hoban, S., Bruford, M.W., Segelbacher, G., Allendorf, F.W., et al., 2020. Post-2020 goals overlook genetic diversity. Science 367, 1083–1085.
Leigh, D.M., Hendry, A.P., Vázquez-Domínguez, E., Friesen, V.L., 2019. Estimated six per cent loss of genetic variation in wild populations since the industrial revolution. Evol. Appl. 12, 1505–1512.
Maruyama, T., Kimura, M., 1980. Genetic variability and effective population size when local extinction and recolonization of subpopulations are frequent. Proc. Natl. Acad. Sci. U. S. A. 77, 6710–6714.
Marzo, B.C., Sánchez-Montes, G., Martínez-Solano, I., 2020. Contrasting demographic trends and asymmetric migration rates in a spatially structured amphibian population. Integrative Zoology.
Maunder, M., Lyte, B., Dransfield, J., Baker, W., 2001. The conservation value of botanic garden palm collections. Biol. Conserv. 98, 259–271.
Miraldo, A., Li, S., Borregaard, M.K., Flórez-Rodríguez, A., Gopalakrishnan, S., Rizvanovic, M., Wang, Z., Rahbek, C., Marske, K.A., Nogués-Bravo, D., 2016. An Anthropocene map of genetic diversity. Science 353, 1532–1535.
Morikawa, M.K., Palumbi, S.R., 2019. Using naturally occurring climate resilient corals to construct bleaching-resistant nurseries. Proc. Natl. Acad. Sci. https://doi.org/10.1073/pnas.1721415116.
Navarro, L.M., Fernández, N., Guerra, C., Guralnick, R., Kissling, W.D., et al., 2017. Monitoring biodiversity change through effective global coordination. Curr. Opin. Environ. Sustain. 29, 158–169.
Ogden, R., Chuven, J., Gilbert, T., Hosking, C., Gharbi, K., et al., 2020. Benefits and pitfalls of captive conservation genetic management: evaluating diversity in scimitar-horned oryx to support reintroduction planning. Biol. Conserv. 241, 108244.
Ouborg, N.J., van Treuren, R., van Damme, J.M.M., 1991. The significance of genetic erosion in the process of extinction. Oecologia. https://doi.org/10.1007/bf00317601.
Outhwaite, C.L., Gregory, R.D., Chandler, R.E., Collen, B., Isaac, N.J.B., 2020. Complex long-term biodiversity change among invertebrates, bryophytes and lichens. Nat Ecol Evol 4, 384–392.
Palstra, F.P., Fraser, D.J., 2012. Effective/census population size ratio estimation: a compendium and appraisal. Ecol. Evol. 2, 2357–2365.
Palstra, F.P., Ruzzante, D.E., 2008. Genetic estimates of contemporary effective population size: what can they tell us about the importance of genetic stochasticity for wild population persistence? Mol. Ecol. 17, 3428–3447.
Palstra, F.P., Ruzzante, D.E., 2011. Demographic and genetic factors shaping contemporary metapopulation effective size and its empirical estimation in salmonid fish. Heredity 107 (5), 444–455.
Paz-Vinas, I., Quéméré, E., Chikhi, L., Loot, G., Blanchet, S., 2013. The demographic history of populations experiencing asymmetric gene flow: combining simulated and empirical data. Mol. Ecol. 22 (12), 3279–3291.
Pérez-Espona, S., Consortium, C, et al., 2017. Conservation genetics in the European Union–biases, gaps and future directions. Biol. Conserv. 209, 130–136.
Pinsky, M.L., Palumbi, S.R., 2014. Meta-analysis reveals lower genetic diversity in overfished populations. Mol. Ecol. 23, 29–39.
Ploetz, R.C., 2015. Management of Fusarium wilt of banana: a review with special reference to tropical race 4. Crop Prot. 73, 7–15.
Pope, L.C., Liggins, L., Keyse, J., Carvalho, S.B., Riginos, C., 2015. Not the time or the place: the missing spatio-temporal link in publicly available genetic data. Mol. Ecol. 24, 3802–3809.
Prieto, I., Violle, C., Barre, P., Durand, J.-L., Ghesquiere, M., Litrico, I., 2015. Complementary effects of species and genetic diversity on productivity and stability of sown grasslands. Nat Plants 1, 15033.
Raffard, A., Santoul, F., Cucherousset, J., Blanchet, S., 2019. The community and ecosystem consequences of intraspecific diversity: A meta-analysis. Biol. Rev. 94 (2), 648–661.
Reusch, T.B.H., Ehlers, A., Hämmerli, A., Worm, B., 2005. Ecosystem recovery after climatic extremes enhanced by genotypic diversity. Proc. Natl. Acad. Sci. U. S. A. 102, 2826–2831.
Royal Botanic Gardens, K., 2016. State of the World's Plants. (Royal Botanic Gardens).
Rubidge, E.M., Patton, J.L., Lim, M., Burton, A.C., Brashares, J.S., Moritz, C., 2012. Climate-induced range contraction drives genetic erosion in an alpine mammal. Nat. Clim. Chang. 2, 285–288.
Ryman, N., Laikre, L., Hössjer, O., 2019. Do estimates of contemporary effective size tell us what we want to know? Mol. Eco. 28, 1904–1918.

Santamaría, L., Mendez, P.F., 2012. Evolution in biodiversity policy–current gaps and future needs. Evol. Appl. 5 (2), 202–218.
Sjögren, P., 1988. Metapopulation biology of Rana lessonae Camerano on the Northern periphery of its range. Comprehensive Summaries of Uppsala Dissertations 157.
Sjögren, P., 1991. Genetic variation in relation to demography of peripheral pool frog populations (Rana lessonae). Evol. Ecol. 5, 248–271.
Society for Conservation Biology, 2020. Position Paper on the Convention on Biological Diversity's Zero Draft (of January 6, 2020) of the Post-2020 Global Biodiversity Framework. (Society for Conservation Biology).
Spielman, D., Brook, B.W., Frankham, R., 2004. Most species are not driven to extinction before genetic factors impact them. Proc. Natl. Acad. Sci. 101 (42), 15261–15264.
Taylor, H.R., Dussex, N., van Heezik, Y., 2017. Bridging the conservation genetics gap by identifying barriers to implementation for conservation practitioners. Global Ecology and Conservation 10, 231–242.
Tittensor, D.P., Walpole, M., Hill, S.L., Boyce, D.G., Britten, G.L., Burgess, N.D., Butchart, S.H., Leadley, P.W., Regan, E.C., Alkemade, R., Baumung, R., 2014. A mid-term analysis of progress toward international biodiversity targets. Science 346 (6206), 241–244.
Van der Walt, K.-A., Swartz, E.R., Woodford, D., Weyl, O., 2017. Using genetics to prioritise headwater stream fish populations of the Marico barb, Enteromius motebensis Steindachner 1894, for conservation action. Koedoe 59, 381.
Walters, C., Berjak, P., Pammenter, N., Kennedy, K., Raven, P., 2013. Plant science. Preservation of recalcitrant seeds. Science 339, 915–916.
Wang, J., Santiago, E., Caballero, A., 2016. Prediction and estimation of effective population size. Heredity 117, 193–206.
Waples, R.S., 2002. Definition and estimation of effective population size in the conservation of endangered species. In: Beissinger, S.R., McCullough, D.R. (Eds.), Population Viability Analysis. The University of Chicago Press, Chicago & London, pp. 147–168.
Waples, R.S., Gaggiotti, O., 2006. INVITED REVIEW: What is a population? An empirical evaluation of some genetic methods for identifying the number of gene pools and their degree of connectivity. Mol. Ecol. 15 (6), 1419–1439.
Waples, R.S., Do, C., Chopelet, J., 2011. Calculating Ne and Ne/N in age-structured populations: a hybrid Felsenstein-Hill approach. Ecology 92, 1513–1522.
Wasserman, T.N., Cushman, S.A., Shirk, A.S., Landguth, E.L., Littell, J.S., 2012. Simulating the effects of climate change on population connectivity of American marten (Martes americana) in the northern Rocky Mountains, USA. Landsc. Ecol. 27, 211–225.
Willoughby, J.R., Sundaram, M., Wijayawardena, B.K., Kimble, S.J.A., Ji, Y., Fernandez, N.B., Antonides, J.D., Lamb, M.C., Marra, N.J., DeWoody, J.A., 2015. The reduction of genetic diversity in threatened vertebrates and new recommendations regarding IUCN conservation rankings. Biol. Conserv. 191, 495–503.
Wu, H.X., 2019. Benefits and risks of using clones in forestry – a review. Scand. J. For. Res. 34, 352–359.