

**Genetic diversity
is vital – maintain
all populations at
effective size >500**



This side event was kindly funded by:

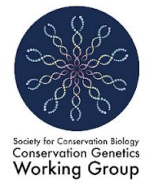


SWEDISH
ENVIRONMENTAL
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AGENCY

Learn more about
conserving genetic diversity



The genetic diversity side-event is proudly co-hosted by over 40 organizations



Genetic Diversity Goal, Target, and Indicators including update on ongoing application of genetic diversity indicators





Stockholm
University



THE COALITION FOR
CONSERVATION GENETICS

What is genetic diversity and why is it important?

Linda Laikre

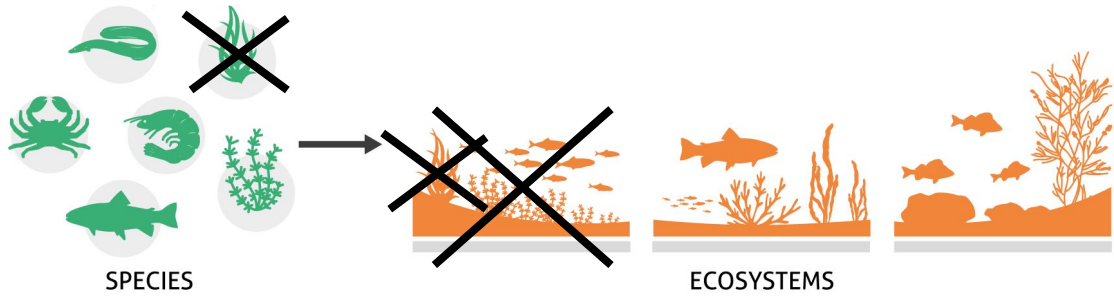
Professor of population genetics at Dept. Zoology, Stockholm University, Sweden
contact: linda.laikre@popgen.su.se



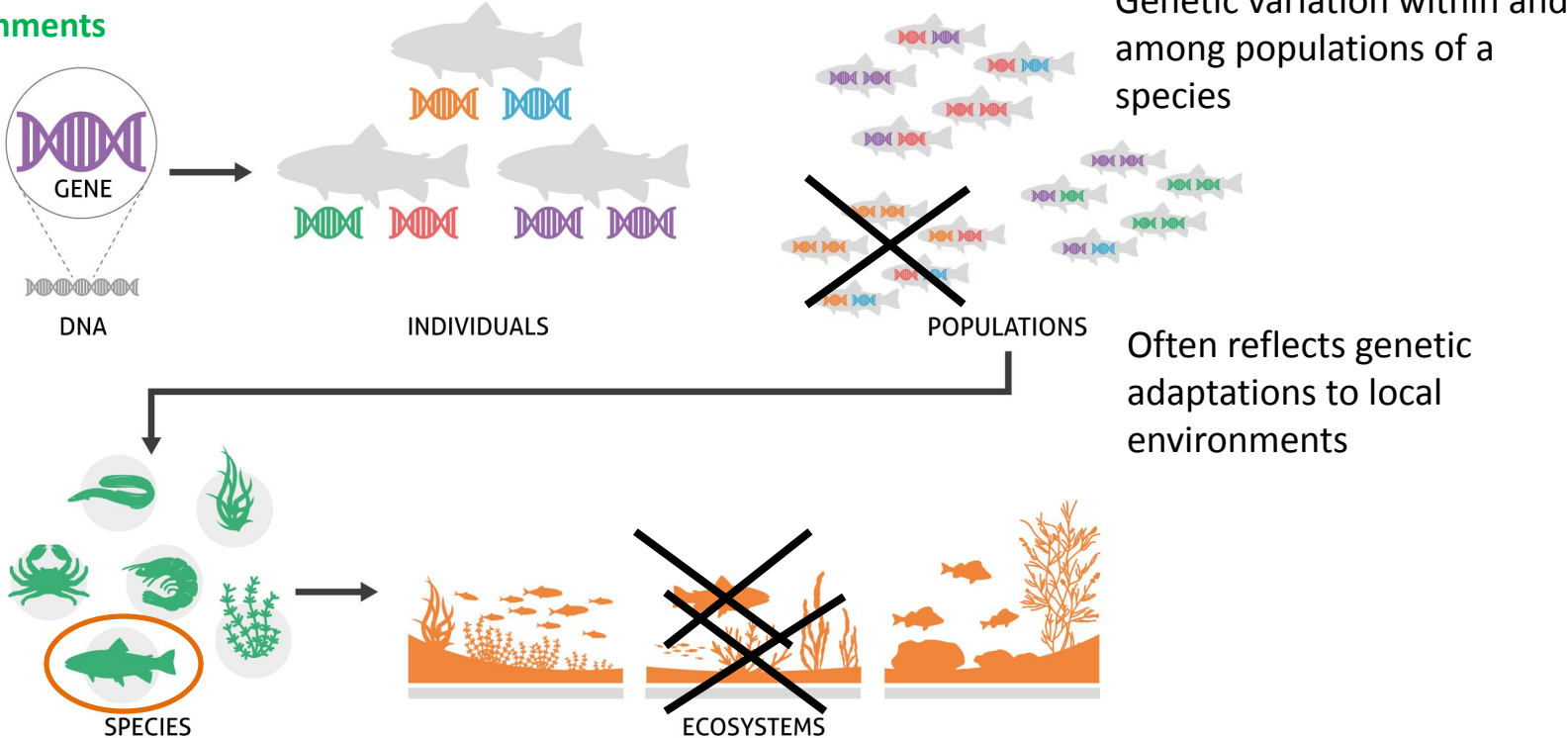
Funded by
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CONSERVATION GENETICS
SPECIALIST GROUP



Genetic diversity – toolbox for evolution, adaptation, survival
the basis for all biodiversity – key in rapidly changing environments



Loss of genetic diversity can have similar effects as loss of species
Genetic diversity within species equally important as species diversity

Our focus: Naturally occurring genetic variation
within and between populations of wild and
domestic species

(Not GMO, LMO, DSI)



High genetic diversity

- High adaptive capacity
- Good potential for long-term survival
- High resilience

Recent example: Corals being able to adapt to warmer ocean temperatures. Genetic diversity within species plays important role.



Morikawa and Palumbi 2019, PNAS



Low genetic diversity

- Low adaptive capacity
- Weak potential for long-term survival
- Low resilience

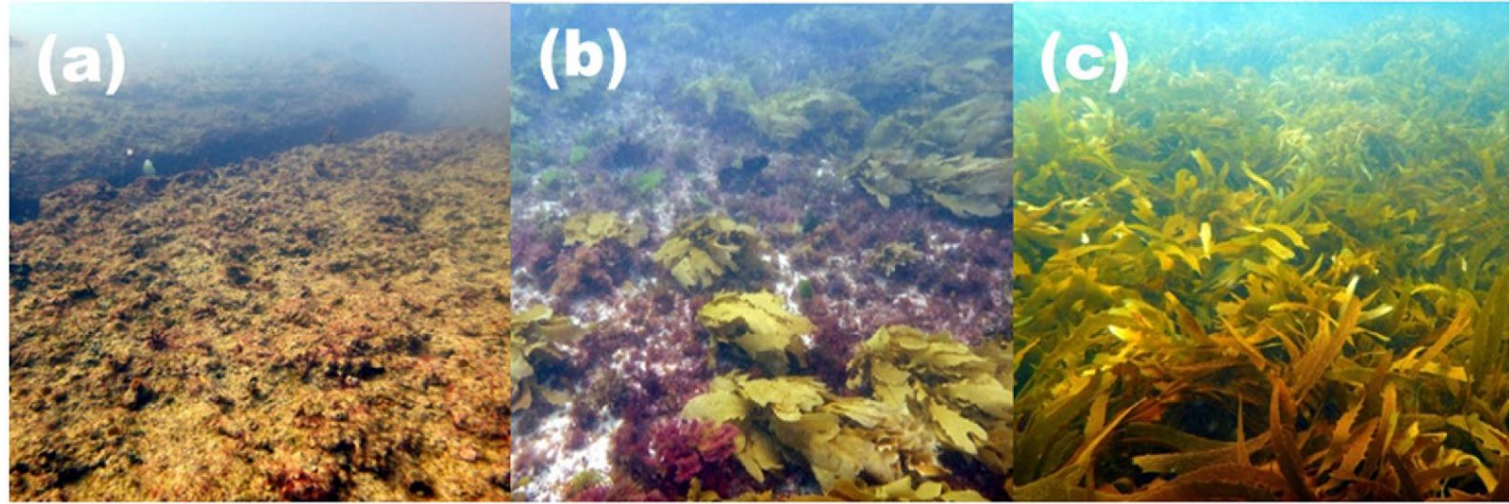
Recent example: Wolf drastic population decline and spinal disorders due to inbreeding (Isle Royale, NA)



Hedrick et al 2019 in Animal Conservation

High genetic diversity can buffer against environmental extremes

Effects from marine heatwave on kelp forests with different genetic diversity



Low genetic diversity
Strongly affected

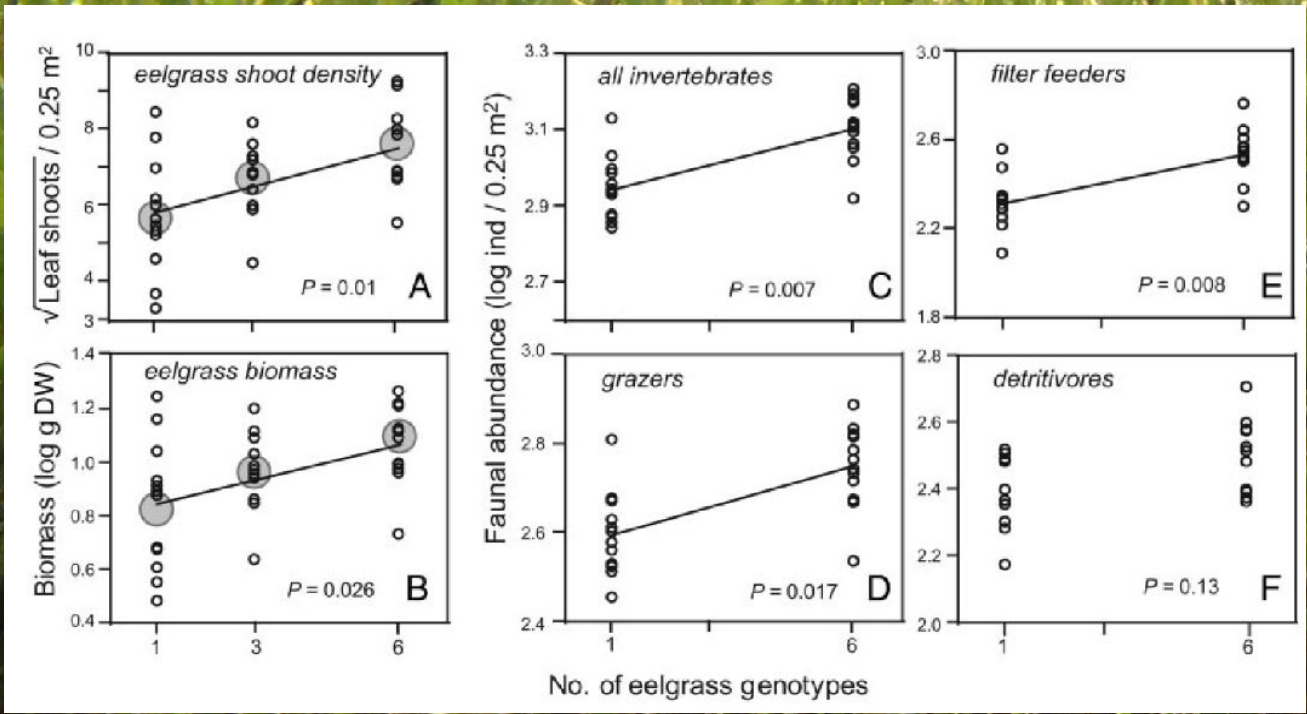
Moderate genetic diversity
Partly affected

High genetic diversity
Not affected

More examples here:
<https://g-bikegenetics.eu/>

Wernberg et al 2018 Scientific Reports (incl. photos)

Genetic variation in eelgrass increase recovery after environmental extremes and increase abundance of associated fauna



Reusch et al. 2005, PNAS
photo: Wiki commons

Genetic diversity allows local adaptation

Rapid adaptation of Atlantic killifish populations to polluted areas in urban estuaries

2017
ECOLOGICAL GENOMICS

The genomic landscape of rapid repeated evolutionary adaptation to toxic pollution in wild fish

Noah M. Reid,¹ Dina A. Proestou,² Bryan W. Clark,³ Wesley C. Warren,⁴
John K. Colbourne,⁵ Joseph R. Shaw,^{5,6} Sibel I. Karchner,^{7,8} Mark E. Hahn,^{7,8}
Diane Nacci,⁹ Marjorie F. Oleksiak,¹⁰ Douglas L. Crawford,¹⁰ Andrew Whitehead^{1*}



More examples at: <https://g-bikegenetics.eu>



G-BIKE



Convention on
Biological Diversity
www.cbd.int

CBD recognizes 3 levels of biodiversity:

- Ecosystems
- Species
- Genetic diversity

But implementation has long lagged behind for genetic diversity.
No CBD target or monitoring so far.

Conserv Genet (2010) 11:349–354
DOI 10.1007/s10592-009-0037-4

COMMENTARY

Genetic diversity is
policy implementat

Linda Laikre

Conservation Biology 2010

**Neglect of Genetic Diversity
Convention on Biological**

LINDA LAIKRE,* FRED W. ALLENDORF,†
DAVID P. GREGOVICH,§ MICHAEL M. HA
KATHERINE C. KENDALL,†† KEVIN McKI
NILS RYMAN,* MICHAEL K. SCHWARTZ,‡
DAVID A. TALLMON,††† BARBARA L. TAY
DONALD M. WALLER,§§§ AND ROBIN S. V.

Conservation Biology 2016

**Aligning science and poli
enlightened conservation**

Carly N. Cook* and Carla M. Sgrò

Post-2020 goals overlook genetic diversity

SCIENCE sciencemag.org

Linda Laikre^{1,2,*}, Sean Hoban^{3,2}, Michael W. Bruford^{4,2},
Gernot Segelbacher^{5,2}, Fred W. Allendorf^{6,2}, Gonzalo
Gajardo⁷, Antonio González Rodríguez^{8,2}, Philip W.
Hedrick⁹, Myriam Heuertz^{10,11}, Paul A. Hohenlohe¹²,
Rodolfo Jaffé^{13,14,2}, Kerstin Johannesson¹⁵, Libby
Liggins¹⁶, Anna J. MacDonald^{17,2}, Pablo Orozco-
terWengel^{1,2}, Thorsten B. H. Reusch¹⁸, Hernando
Rodríguez-Correa¹⁹, Isa-Rita M. Russo^{4,2}, Nils
Ryman¹, Cristiano Vernesi^{20,2,21}



THE COALITION FOR
CONSERVATION GENETICS



Catherine Grueber



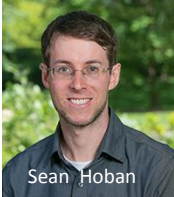
Gernot Segelbacher



Alicia Mastretta-Yanes



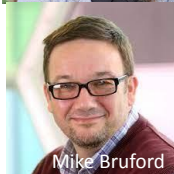
MacDonald



Sean Hoban



Maggie Hunter



Mike Bruford

Improvements for genetic diversity urgent!

International team of conservation genetics researchers provide advice

COP15: Strong quantitative Goal & Target for genetic diversity of all species needed

Also need to measure change – indicators are vital!



Jessica da Silva



Robyn Shaw



David O'Brien



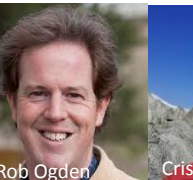
Ivan Parí Vinas



Mariah Meek



Cinnamon Mittan



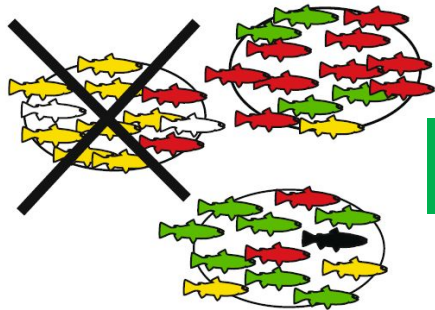
Rob Ogden



Cristiano Vernesi

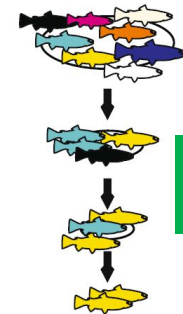


Processes that can result in loss of genetic diversity



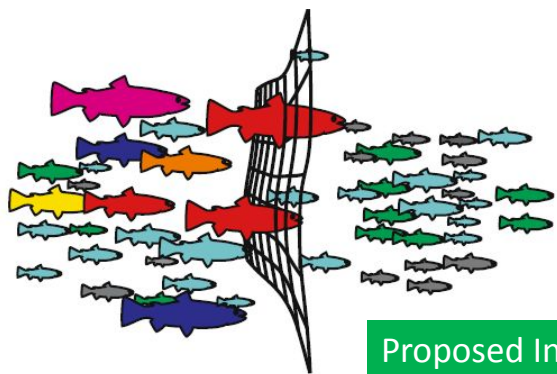
Proposed Indicator 2 (A.8.1)
maintaining populations

1. Loss of genetically distinct populations



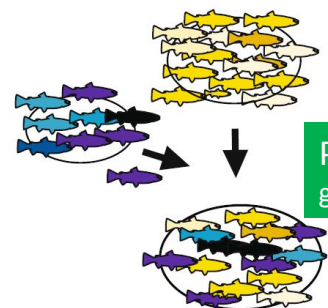
Proposed Indicator 1 (A.5)
effective population size (N_e)

2. Reduced population size



Proposed Indicator 3
genetic monitoring

3. Human induced selection

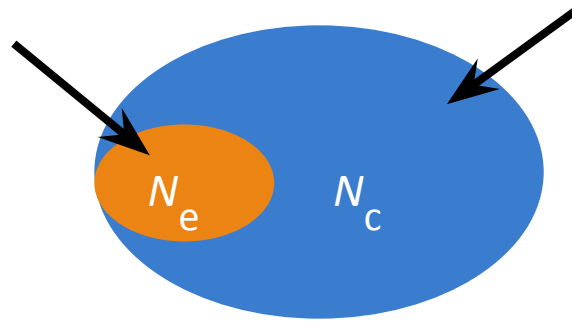


Proposed Indicator 3
genetic monitoring

4. Spread of "alien" populations

Genetic effective population size (N_e)
shows how the population "behaves"
genetically

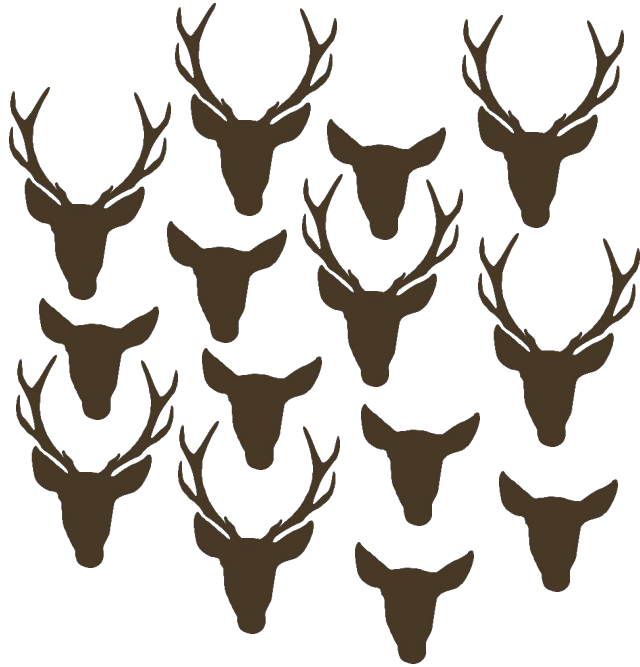
Census size
number of mature individuals (N_c)



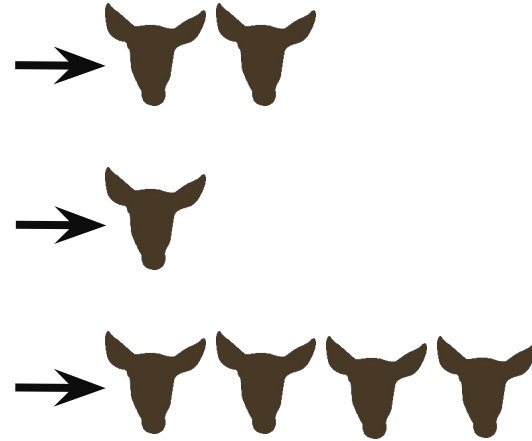
$$1 / 10 = 0.1$$

The effective population size (N_e) determines the rate of loss of genetic diversity
and is much smaller than the census size (~10% on average)

Several demographic factors results in effective population size (N_e) smaller than census size (N_c)

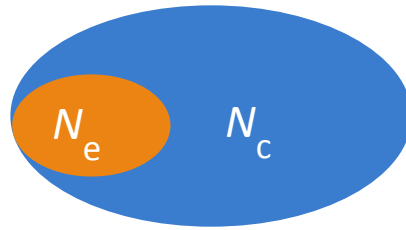


All mature individuals in the population (census size N_c)



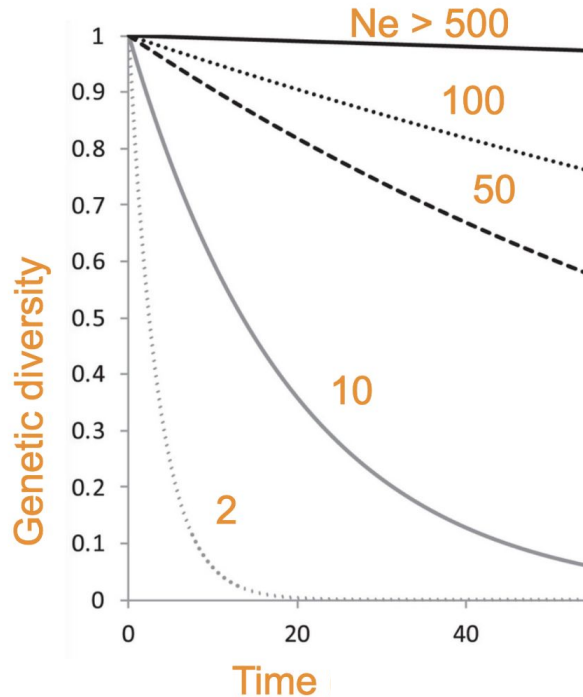
Sex ratio and variation in reproductive success – two important factors that affects N_e

How large must N_e be to avoid rapid loss of genetic diversity?



Well-established, scientifically accepted **rule-of-thumb:**

$N_e > 500$ Maintains sufficient levels of genetic variation for adaptive capacity

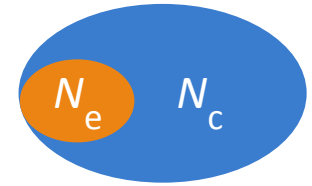


Headline Indicator A.5 of CBD/COP/5/2

The proportion of populations within species with an effective population size (N_e) > 500

N_e can be assessed with:

- demographic data
- genetic data

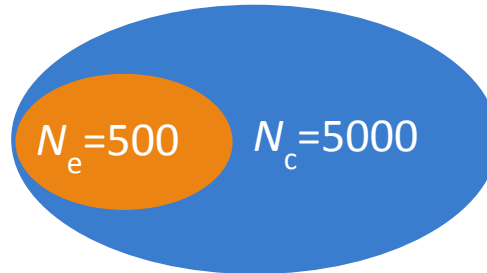


In the absence of such data, census size can be used as proxy

10% of census size is a good proxy

Scientific reviews indicate mean and/or median values close to $N_e/N_c = 0.1$

Frankham 1995, Palstra & Ruzzante 2008, Frasier & Ruzzante 2012, Frankham et al 2019, Hoban et al 2020, 2021



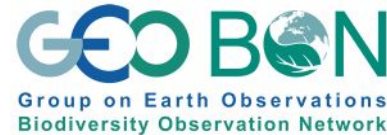
Thank you!

**Support
Headline
Indicator A.5!**

Genetic diversity indicators in the CBD post-2020 Global Biodiversity Framework

Sean Hoban, The Morton Arboretum

IUCN Conservation Genetic Specialist Group
GEO BON Genetic Composition Working Group
representing dozens of scientists & practitioners
from the Coalition for Conservation Genetics



Post 2020 GBF

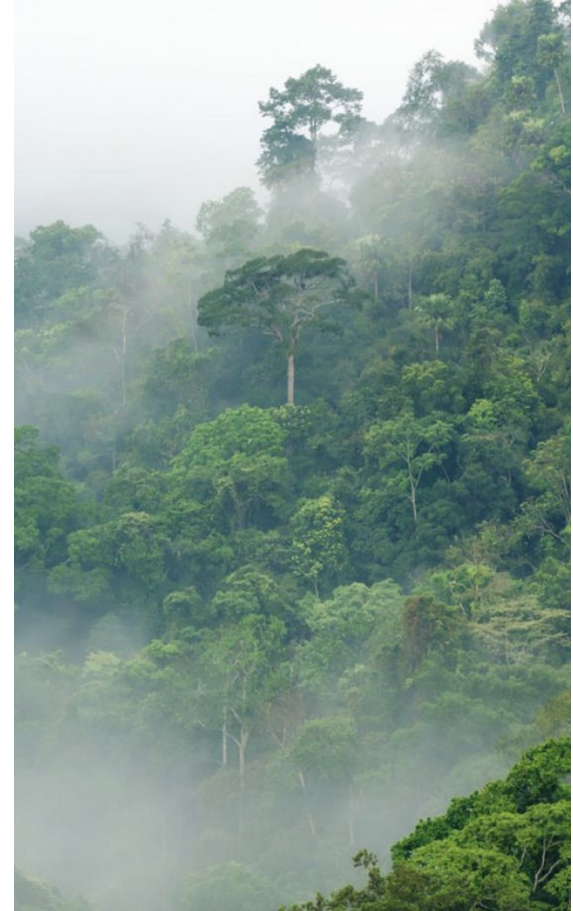
Goal A: ...and all genetically distinct populations, and [at least 95% of] the genetic diversity within populations of native wild and domesticated species, are maintained, safeguarding their adaptive potential

Target 4: ... and maintain and restore the genetic diversity within and between populations of native wild and domesticated species [to maintain their adaptive potential] including through in situ and ex situ conservation...

relevant to Target 12: connectivity, Target 3: protected areas, Target 5 and 9: harvest

Genetic diversity within and between populations of species

- ◆ **Helps species adapt** to environmental and climate change and disease
- ◆ **Makes ecosystems more resilient** to extreme weather and disturbance
- ◆ **And more!** Supports ecosystem services, nature's contributions to people, & restoration success



How to maintain genetic diversity and restore conditions to ensure that species can adapt?

- (1) Maintain sufficiently large populations (N_e 500)
- (2) Prevent loss of distinct populations
- (3) If possible, monitor with DNA and use for management



Three indicators of genetic diversity status

- (1) Proportion of populations [or breeds] within species with an effective population size (N_e) above 500
- (2) Proportion of distinct populations maintained
- (3) Number of species & populations in which genetic diversity is being monitored using DNA based methods

Other complementary indicators (genetic scorecard, a.48, comprehensiveness, a.51, breeds and seed banks, a.52, a.53)

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



SBSTTA/24/INF/29 May 2021

“Survey on headline indicators”, 21 comments supported one or more of these



Geneva and Bonn, 2022

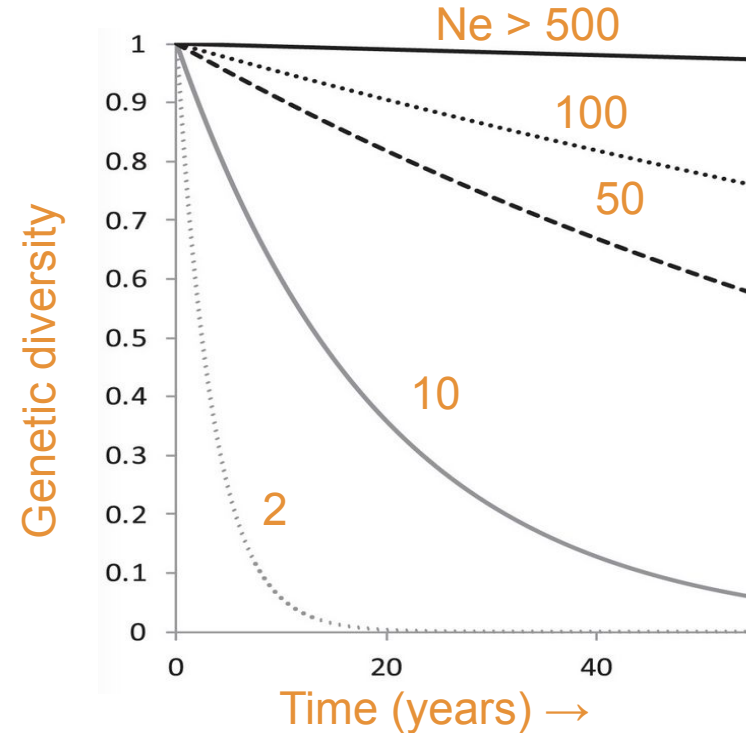
Supportive, but Parties wished to know more about relevance, feasibility, and data availability



The proportion of populations [or breeds] with an effective population size (N_e) above 500 (A.5)

Relevant: “Sufficiently large” to prevent genetic erosion/ inbreeding, and maintain adaptive capacity

Understandable: Related to previous CBD indicator on threatened breeds

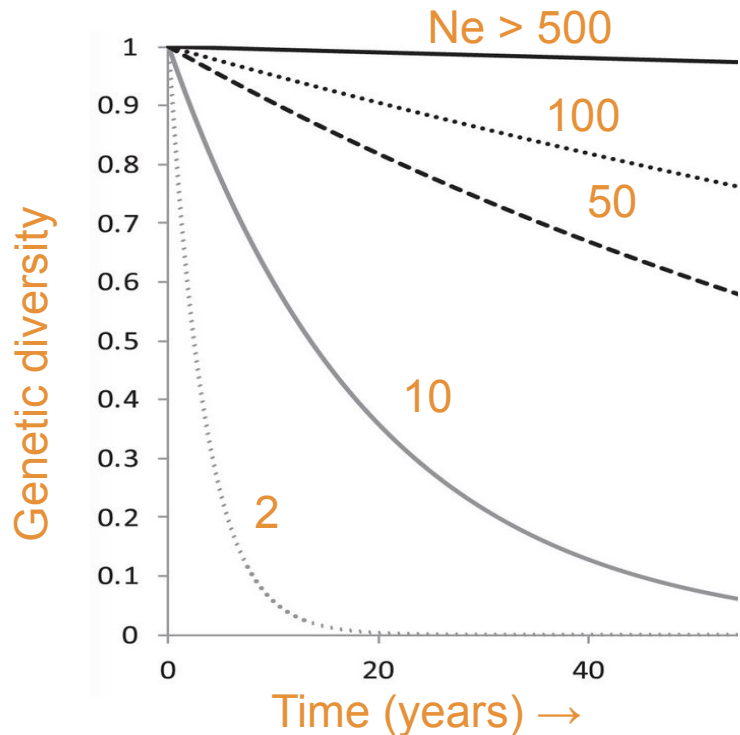


The proportion of populations [or breeds] with an effective population size (N_e) above 500 (A.5)

Feasible, measurable, data available.

Use $1/10^{\text{th}}$ of census size (no DNA)

- Species management reports
- Red List assessments data
- Citizen scientists counts
- From area of suitable habitat



Proportion of distinct populations maintained (A.8.1)

Relevant: Maintain genetic adaptations

Understandable: People can see adaptations to different habitats



Proportion of distinct populations maintained (A.8.1)

Feasible, measurable, data available:

- Species management reports (no DNA data)
- IUCN Red List Population assessments data
- National databases, habitat maps, GBIF
- Citizen science



Number of species & populations in which genetic diversity is being monitored using DNA based methods

Relevant: Knowledge helps management

Accessible: Easy to count, report on



(Non DNA) Data are available!

- Assessed data availability in Red List for >22,000 species
- Ne: some census data available for 30% of species
- Populations: some range data available for 20% of species

NATUR
VÅRDS
VERKET 

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Data are usable!

- Calculations for 62 mammals and 17 reptiles
- 51% of mammal populations $< N_e$ 500
- 16% of mammals have populations lost
- 3% of species with genetic studies

Genetic indicators capture a conservation concern- genetic loss- not otherwise known at this scale

Gaining momentum

- 9 countries, ~100 species per country: Australia, Belgium, Colombia, France, Japan, Mexico, South Africa, Sweden, USA
- Includes biodiversity agencies of the countries



INRAE



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Opportunities

- Useful even beyond CBD reporting, e.g. for decisions about species management

Iterative, participatory improvement

Garner et al 2020, Schmidt et al 2022 (ecoevoarxiv), Rivers et al 2014, Vitorino et al 2019, Willoughby et al 2015, van Oosterhout 2021, Hoban et al 2022a and b

**Linking Indicators
to Goal A and Target 4
text being discussed**

Goal A

Intermediate option:

... and all genetically distinct populations, and [at least 95% of] the genetic diversity within populations of native wild and domesticated species, are maintained, safeguarding their adaptive potential.

Indicator

1: The proportion of populations within species with an effective population size > 500 (Headline indicator A.5)

helps maintain genetic diversity **within populations**, which helps them adapt quickly

Goal A

Intermediate option:

... and all genetically distinct populations, and [at least 95% of] the genetic diversity within populations of native wild and domesticated species, are maintained, safeguarding their adaptive potential.

Indicator

2: Proportion of populations maintained within species

(Component Indicator A.8.1/
Complementary Indicator)

helps conserve **among population** genetic diversity to preserve options for the species

Target 4

...maintain and restore the genetic diversity **within and between** populations of native wild and domesticated species [to maintain their adaptive potential] including through in situ and ex situ conservation,

Indicators

Populations $N_e > 500$ (A.5)

**Proportion of populations maintained
(A.8.1)**

**Number of species and populations
monitored using DNA-based methods for
management**

**genetic scorecard (a.48),
comprehensiveness indicator (a.51),
others (a.52, a.53)**

Also

Target 12: connectivity

Target 3: “representative protected areas”

Target 5 and 9: overharvest, sustainable harvest

Indicators

Populations $N_e > 500$ (A.5)

Proportion of populations maintained (A.8.1)

Number of species and populations monitored using DNA-based methods for management

**genetic scorecard (a.48),
comprehensiveness indicator (a.51)**

**Reference to the maintenance of genetic diversity
both within and between populations
for ALL species
is CRITICAL for both Goal A and Target 4
and is connected to indicators,
which also support other targets**

Conclusion: SMART and useful

- Indicators are sensitive to genetic change, feasible, scalable, data available and are garnering Party interest

Specific (clear and quantitative)

Measurable (data is available)

Achievable (the work can be done)

Relevant (connected to genetic conservation)

Time bound (repeat every five years)

National Application of Genetic Indicators in 9 Countries



Jessica da Silva¹ & Alicia Mastretta-Yanes²



¹South African National Biodiversity Institute (SANBI); j.dasilva@sanbi.org.za

²Comisión Nacional para el Conocimiento y Uso de la Biodiversidad (CONABIO); amastretta@conabio.gob.mx

SANBI
Biodiversity for Life



CONABIO
COMISIÓN NACIONAL PARA
EL CONOCIMIENTO Y USO
DE LA BIODIVERSIDAD

Purpose:

- Show that the indicators are feasible
- Demonstrate how countries calculate the indicators for species
- Demonstrate how countries calculate national metrics
- Showcase resources available for countries to start their genetic indicator journey

~100 species per country

Selection based on a variety of criteria:

1. Representatives across a range of plants, animals and fungi
 - a. Wild and domesticated
2. Diverse ecosystems / habitats
3. Mix of life-histories traits
4. Range of conservation statuses/values
5. Data is likely to be available



How to get data?

Published
data

Experts or
local knowledge
holders

National
monitoring
databases

Flexibility in the overall approach, but with standardized methods

*Assessment with or **without** genetic data*

Focus on the two proposed indicators



Published data



Rose's Mountain Toadlet
(*Capensibufo rosei*)



2 locations, under threat

JUSTIFICATION

Listed as Critically Endangered in view of the very restricted area of occupancy (AOO) of 1.5 km², its small extent of occurrence (EOO) of 25 km², with all individuals known from only two threat-defined locations that are considered severely fragmented, and a continuing decline in the extent and quality of its habitat.



Published data



Rose's Mountain Toadlet
(*Capensibufo rosei*)

Conserv Genet (2018) 19:349–363
DOI 10.1007/s10592-017-1008-9



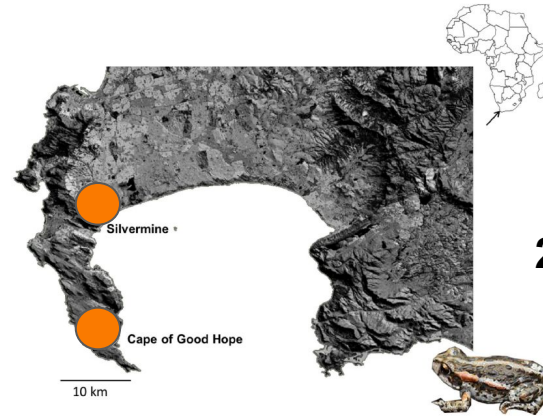
RESEARCH ARTICLE

Conservation genetics of an endemic and threatened amphibian (*Capensibufo rosei*): a leap towards establishing a genetic monitoring framework

Jessica M. da Silva^{1,2} · Krystal A. Tolley^{1,3}

Fading out of view: the enigmatic decline of Rose's mountain toad *Capensibufo rosei*

E. R. CRESSEY, G. J. MEASEY and K. A. TOLLEY



6 historical populations

2 populations remaining

no natural connectivity

Populations maintained

(Indicator 2):

$$2/6 = 0.33$$



Published data



Rose's Mountain Toadlet
(*Capensibufo rosei*)

MSc thesis



Estimating the Population Size of a Rare and Elusive Species: the Case of Rose's Mountain Toadlet

FRANCOIS S. BECKER^{1,2}

Capture-Mark-Recapture

Effort: 30-60 min

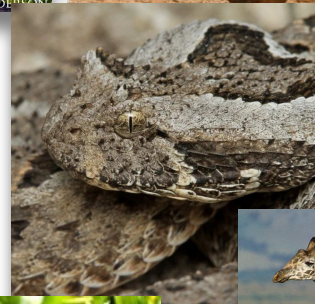
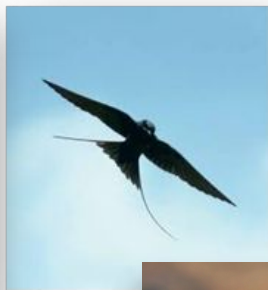
Pop 1 (Silvermine): $N_c = 2,168$ → $N_e = 216.8$

Pop 2 (Cape of Good Hope): $N_c = 1,849$ → $N_e = 184.9$

Populations $N_e > 500$

(Indicator 1):

$$0/2 = 0.00$$





Existing resources

SANBI Biodiversity for Life South African National Biodiversity Institute

Red List of South African Plants

Red List statistics | Summary of recent changes | National Red List categories | Assessment methods


Browse

- Genera: A
- Genera: B
- Genera: C
- Genera: D
- Genera: E
- Genera: F
- Genera: G


Home

Threatened Species Programme

In one of the continent's largest collaborative conservation programmes, South African Plants Online provides up to date information on the status of threatened plants.




THE IUCN RED LIST OF THREATENED SPECIES™



RED LIST OF SOUTH AFRICAN SPECIES

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FIELD GUIDE TO SNAKES AND OTHER REPTILES OF SOUTHERN AFRICA




KZN Biodiversity Status Assessment Report – 2021

Biodiversity Asset: Blue Swallow (*Hirundo atrocaerulea*)



Group	Birds
Common Name	Blue Swallow
Scientific Name	<i>Hirundo atrocaerulea</i>
Assessment period	2020/2021 breeding season

Accessibility: Investigate

STAATSKOERANT, 6 DESEMBER 2019

No. 42887 19

GOVERNMENT NOTICES • GOEWERMENTSKENNISGEWINGS

DEPARTMENT OF ENVIRONMENTAL AFFAIRS

NO. 1567

06 DECEMBER 2019

NATIONAL ENVIRONMENTAL MANAGEMENT: BIODIVERSITY ACT, 2004 (ACT NO. 10 OF 2004)

BIODIVERSITY MANAGEMENT PLAN FOR THE BONTEBOK (*DAMALISCUS PYGARGUS*)



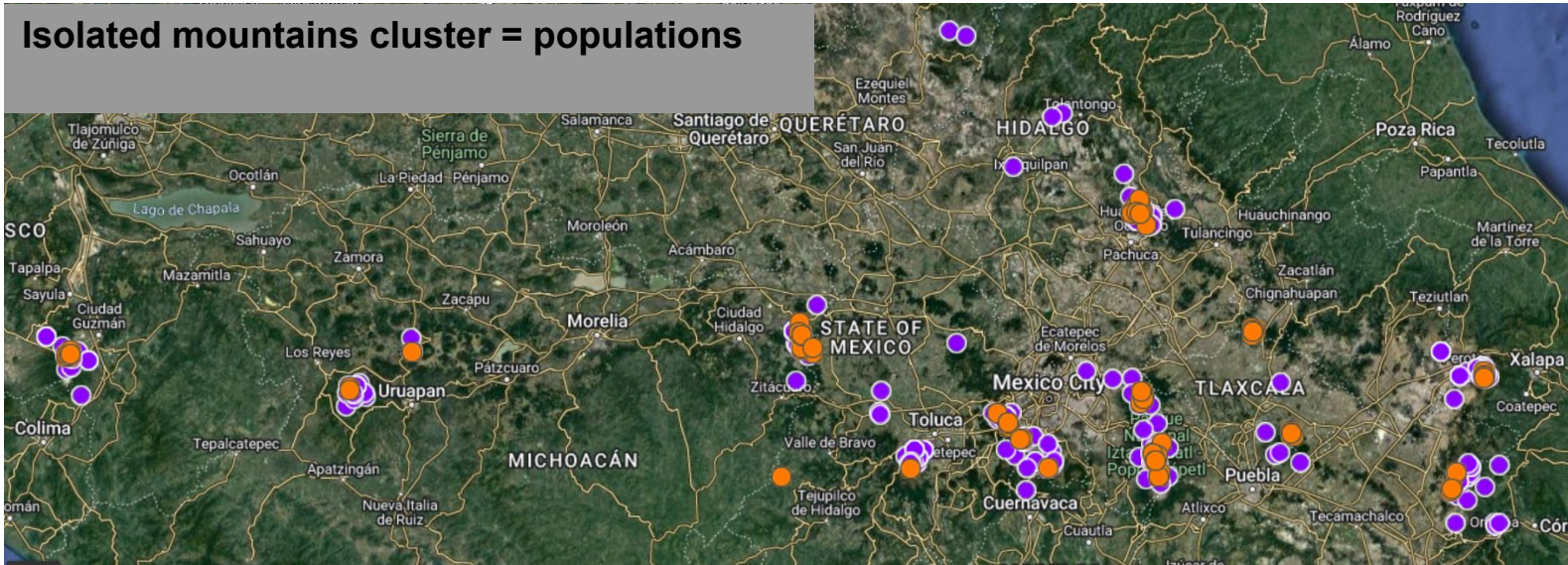
Citizen science and experts/local consultations



Occurrence data from
Collections and iNaturalist (citizen sci)



Mexican mountain juniper
(*Juniperus monticola*)





Citizen science and experts/local consultations

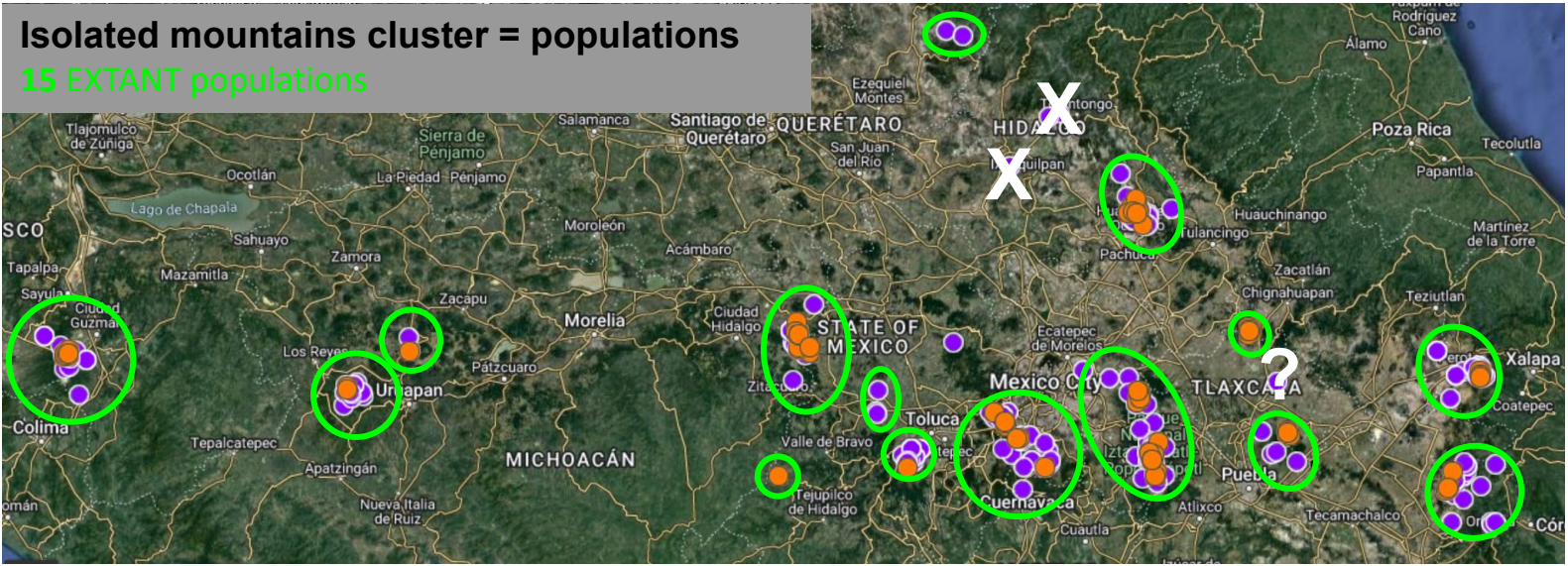


Occurrence data from
Collections and iNaturalist (citizen sci)



Mexican mountain juniper
(*Juniperus monticola*)

Isolated mountains cluster = populations
15 EXTANT populations



populations maintained indicator = 15/17 = 0.88



Citizen science and experts/local consultations



Mexican mountain juniper
(*Juniperus monticola*)



Approximate census size

Based on local botanists and park rangers

WHAT'S THE RANGE OF THE NC FOR POPULATION 1?

- < 5,000 by much
- < 5,000 but not by much (tens or a few hundred less)
- > 5,000 but not by much (tens or a few hundred more)
- > 5,000 by much
- estimate is a range including both less and greater than 5,000 (e.g. "3,000 to 10,000")

- 4 populations **more** than 5,000 individuals → **Ne > 500**
- 7 populations **less** than 5,000 individuals → **Ne < 500**

populations = $4/11 = 0.36$
Ne > 500 indicator



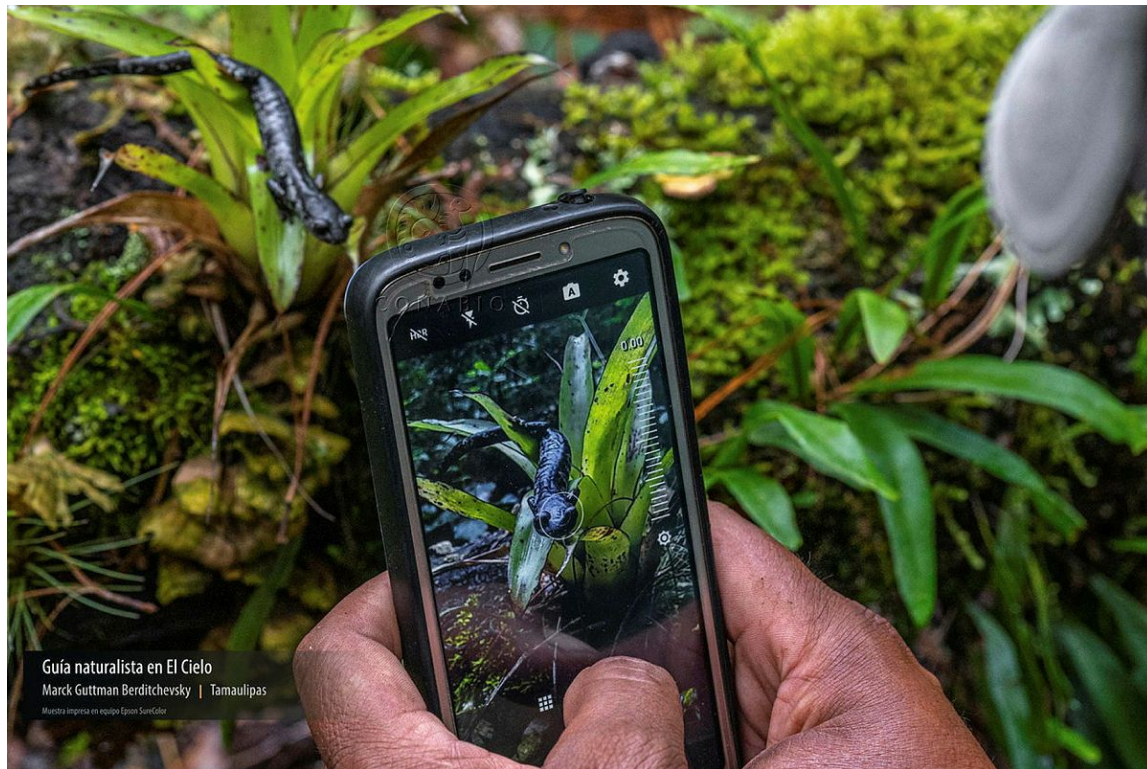
Existing data sources









aVerAves



PROYECTO
agro
biodiversidad
mexicana.





Group	Species	populations Ne > 500	populations maintained
	<i>Pelophylax lessonae</i>	0	1
	<i>Rana dalmatina</i>	0.125	1
	<i>Alces alces</i>	1	1
	<i>Canis lupus</i>	0	1
	<i>Lutra lutra</i>	0	0.8
	<i>Siluris glanis</i>	0	0.38
	<i>Coregonus albula morphotype trybomi</i>	0	0.25
	<i>Dendrocopos leucotos</i>	0	0.17
	<i>Mertensia maritima</i>	0	1
	<i>Gymnadenia nigra</i>	0	0.75
	<i>Lopinga achine</i>	1	1
	<i>Phengaris arion</i>	0.375	0.46
Total (mean)		0.30	0.68

Calculating the genetic diversity indicators is feasible for all taxonomic groups and generates a country level indicator



... and more joining!

Icons by Andrew Doane, Georgiana Ionescu, Wolf Böse, Christian Brunner, Yanti & Bakunetsu Kaito from the Noun Project

Standardized tool for data collection

▶ **Section 1: Assessor and Country information**

▶ **Section 2: Species Taxonomy**

▼ **Section 3: Indicator 2**

QUESTIONS IN THIS SECTION DIRECTLY HELP IN QUANTIFYING INDICATOR 2, AND WILL INFORM THE SECTION ON INDICATOR 1 BY STIPULATING THE NUMBER OF POPULATIONS YOU WILL BE ASKED TO COMPLETE WITH RESPECT TO POPULATION NAME AND SIZE.

NUMBER OF EXTINCT (KNOWN) POPULATIONS WITHIN THE COUNTRY OF ASSESSMENT *
Type -999 if unknown
1 ▾

TYPE THE NAME OR REGION OF THE EXTINCT POPULATIONS, SEPARATED BY A SEMICOLON (;)"
Alfajayucan, Hidalgo; Cardonal, Hidalgo

NUMBER OF EXTANT (KNOWN) POPULATIONS WITHIN THE COUNTRY OF ASSESSMENT *
Type -999 if unknown
10 ▾

COULD OTHER POPULATIONS EXIST IN THE COUNTRY OF ASSESSMENT?
i.e., Does the number of known populations cover the entire range of the species within the country of assessment?

It is highly likely that no other populations exists in the country (e.g., extensive surveys have been conducted and/or habitat expected to be unsuitable)

It is possible that other populations exist but these have not been clearly defined

Unknown

WHAT YEAR OR TIME PERIOD IS THIS POPULATION STRUCTURE BASED ON? *
2010-2020

BROADLY, WHICH OF THE FOLLOWING CATEGORIES BETTER DEFINES HOW POPULATIONS ARE DEFINED FOR THIS SPECIES? *
Refer to Guidance Document and Kobo User Manual for examples of each option.

Genetic clusters/clades

Geographic boundaries

Ecological or Biogeographic proxies

Traits (e.g., behavioural, morphological, physiological)

Management Units (demography/ migration)

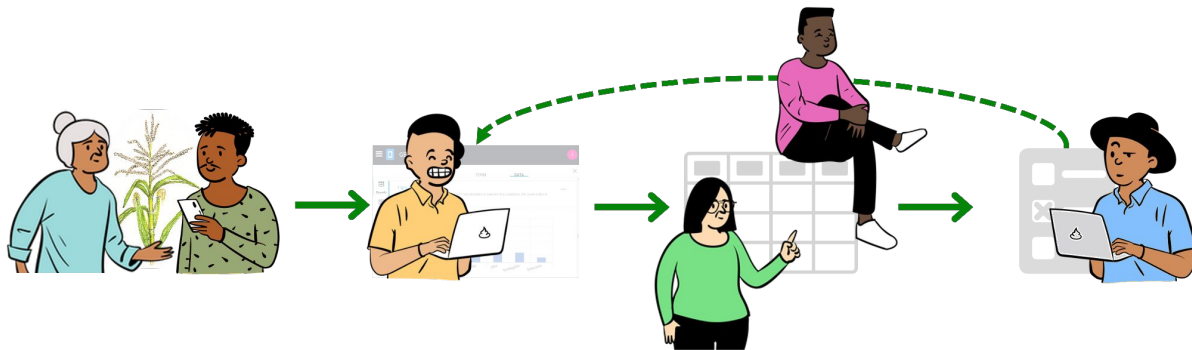
Other



Genetic Diversity Web Form example

Guidance documents and capacity building

Detailed advice and workshops on how to undertake the genetic monitoring at the country level for a set of species, as well as how to answer each question of the web-form.



People illustrations by Open Peeps, icos by The Noun Project.
 Illustrations from [Adriana Iwasaki and Héctor Tobón](#)

Overview

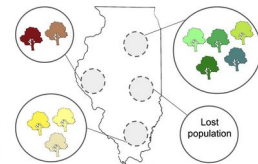
In 2020, Laikre, Hoban and colleagues outlined an approach to assess genetic diversity status and trends *without requiring any genetic data (e.g. DNA sequence)*, using 'genetic indicators'. The indicators were developed in response to a recognized gap in reporting to the U.N. Convention on Biological Diversity (CBD). There was a need for tools to report on 'genetic erosion' and 'safeguarding' or 'maintaining' genetic diversity, within and among populations of species. Two indicators allow a fairly standardized and rapid way to assess *whether a species is likely to be losing or has lost genetic diversity* by quantifying critical aspects of demography that generally correlate to genetic diversity: (1) the size of each population (number of adult individuals), and (2) the geographic range or number of populations relative to historic conditions. A third indicator on genetic knowledge/ genetic studies has also been proposed.

The logic behind these indicators is simple. (1) Small populations lose genetic diversity, and very small populations lose genetic diversity very quickly (Frankham 2021). (2) Loss of populations can result in loss of unique genetic adaptations (Exposito Alonso et al 2022). So, measuring population size and loss of populations is a fairly good proxy or summary of genetic diversity status, without ever measuring the DNA diversity itself.

The indicators should be applied to a *curated, representative set of species* (represent a range of habitats, taxonomic groups, traits, etc.)- 100 to several thousand species per country, depending on a country's biodiversity, data capacity, and resources for CBD reporting. Approximately 100 species is likely a minimum to represent diverse habitats, taxonomic groups, commonness/ rarity, and threat status. However, if 100 cannot be collected, any amount of data is important.

The first two genetic diversity indicators are:

1. The first indicator is based on comparing the **effective population size of each population N_e to a critical threshold** (e.g. $N_e = 500$). For many species, it is sufficient and appropriate to use the **census size N_c (the number of living adults) as a proxy for N_e , and a threshold of $N_c = 5000$ mature individuals**. Below this threshold, a population rapidly loses genetic diversity, can become inbred, and starts to lose ability to adapt to environmental change.



	Indicator 1: Populations large enough to maintain genetic diversity	Indicator 2: Populations still exist (not lost)
2020	1 of 3	3 of 4

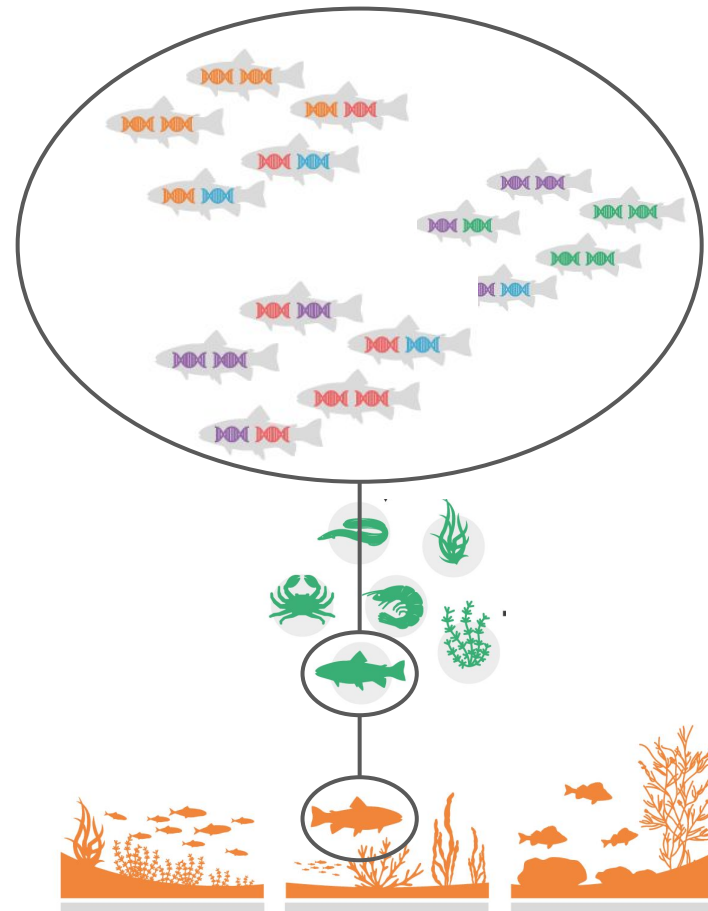
Fig 1: Illustration of genetic diversity indicators, for four populations in Illinois, USA, measured in the year 2020. One tree = 1000 plants. Colors show genetic diversity. In 2020, one population is extinct, and 2 of 3 are too small.

2. The second indicator is based on comparing the **current number of populations that exist to a prior/ historic assessment of the number of populations**. This reflects **loss of populations** to human-induced changes, with 50-200 years ago as a baseline (depending on the country). If counts of populations existing and lost are not available, a proportion (or

Yes, *you* can!

- **DNA data needed?** Not necessarily, census and population data can be used exclusively
- **Enough data?** Yes, for 100+ species/ country
- **Time consuming?** No, 1 month, 3 people on average
- **Flexible? Save time/ money?** Yes, use diverse data (reports, local knowledge, existing in-country databases)
- **Can my country start reporting?** Yes!
- **Can my country report it every 5 years?** Yes!

Leverage existing biodiversity
knowledge and monitoring data to
include genetic diversity -
one of the main components of
biodiversity and of Goal A.



Gracias, Merci, 谢谢你, Thank you, Obrigada, Tack, благодарю вас, Grazie, شكرا, Danke

**Genetic diversity
is vital – maintain
all populations at
effective size >500**



Questions?

**Genetic diversity
is vital – maintain
all populations at
effective size >500**



Words from:

Lucia Ruíz - WWF

Johan Abenius - Swedish delegation

COP15 in
Montreal

Welcome to our exhibition booth!

Area A0, booth number 409 (see floorplan [here](#))



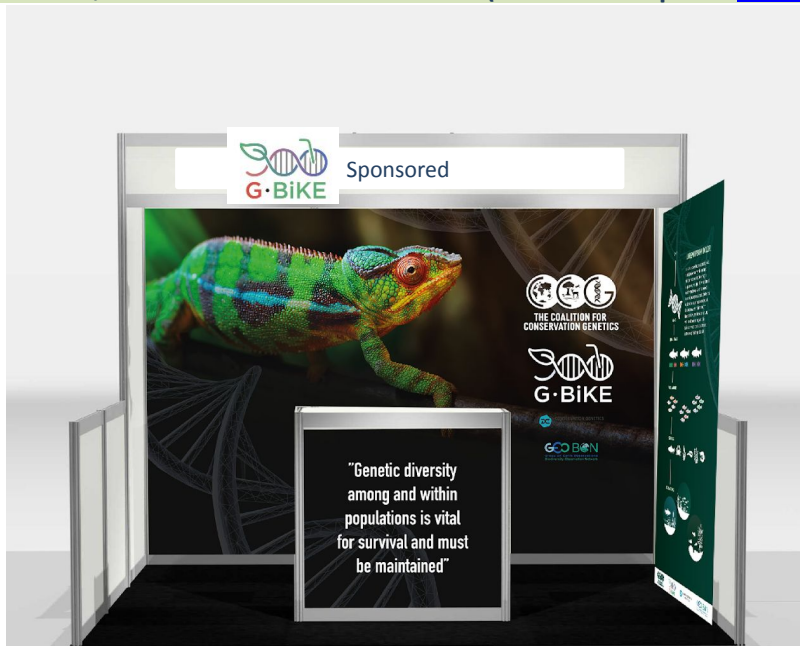
Society for Conservation Biology
Conservation Genetics
Working Group



Society for Conservation Biology



EUROPEAN COOPERATION
IN SCIENCE & TECHNOLOGY



We are available through COP5 for
questions and discussions

Cristiano Vernesi



Maggie Hunter



Alicia Mastretta
Yanes



Jessica da Silva



Ivan Paz-Vinas



Sean Hoban

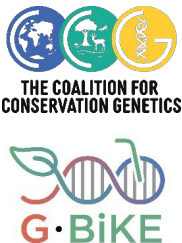


Linda Laikre



Resources online

- <https://coalitionforconservationgenetics.org/>
- <https://g-bikegenetics.eu/en>



- Policy briefs in many languages
- Publications
- Statements to the CBD
- Fact sheets
- Videos
- Contact information

Objectifs et indicateurs de diversité génétique proposés pour le Cadre Mondial de la Biodiversité de la CBD pour l'après-2020

NOTE DE POLITIQUE

Hoban et al., 2020. Genetic diversity targets and indicators in the CBD post-2020 Global Biodiversity Framework must be improved. *Biological Conservation*. <https://doi.org/10.1016/j.biocon.2020.108654>

Résumé

Les objectifs de diversité génétique et les paramètres pour l'évaluer (indicateurs) dans le cadre de la biodiversité de l'après-2020 doivent être mis au point pour prévenir la perte irremplaçable de biodiversité et pour atteindre les objectifs de la Convention sur la Diversité Biologique (CDB). La diversité génétique au sein de toutes les espèces doit être conservée, mesurée et surveillée à l'aide de paramètres appropriés. Pour le cadre post-2020, nous proposons un objectif génétique avec un Cadre d'Action recommandé, et ajoutons trois nouveaux indicateurs génétiques, ainsi que des modifications au niveau des indicateurs actuels de la CDB.



Coverage de nouvelles espèces, des populations de Lézards (Phyllotis leucurus) vivant en populations connectées entre elles, ce qui doit être pris en compte pour mesurer la diversité génétique

Contexte

La diversité génétique contribue au soutien de la société humaine et des systèmes de maintien de la vie dans la biosphère. Elle diminue à l'échelle mondiale en raison des actions humaines. Cette diversité permet aux espèces de s'adapter, maintient les services écosystémiques (p. ex. la filtration de l'eau, la pollinisation) et est essentielle pour assurer la résilience des espèces et des écosystèmes face au changement climatique. Le "point zéro" du cadre de l'après-2020 de la CDB suit la stratégie (2011-2020) de la CDB pour la conservation de la biodiversité, pour laquelle peu d'objectifs ont été atteints. Le maintien de la diversité génétique est reconnu dans la stratégie post-2020 comme l'un des cinq principaux objectifs pour 2050. Cependant,

- 1. L'objectif pour la diversité génétique du projet zéro de la CDB est basé et inspiré (Lowe et al., 2020; Isenring, 2020).
- 2. Il n'y a pas de Cadre d'Action pour 2030 en matière de diversité génétique.
- 3. Les indicateurs actuels de diversité génétique de la CDB négligent la plupart des espèces sauvages car ils se limitent aux espèces domestiquées et aux espèces sauvages qui leur sont apparentées. Les espèces sauvages sont indistinguables à l'échelle et au services des écosystèmes, en particulier dans le contexte du changement climatique.
- 4. Les indicateurs actuels sont également inappropriés pour un suivi adéquat de l'évolution de la diversité génétique.

Indicateurs proposés

Pour atteindre les objectifs mondiaux de conservation, nous proposons que la diversité génétique au sein de toutes les espèces soit conservée, mesurée et surveillée à l'aide de paramètres appropriés.

Nous proposons trois nouveaux indicateurs pour le cadre post-2020 de la CDB, à utiliser en sus des modifications apportées aux indicateurs actuels du projet zéro de la CDB. Un seul indicateur est insuffisant pour suivre les progrès vers l'objectif de la CDB en matière de diversité génétique. Ces indicateurs :

- sont applicables à toutes les espèces,
- sont disponibles immédiatement,
- sont adaptables, c'est-à-dire qu'ils peuvent être calculés au niveau local, régional ou mondial,
- peuvent être agrégés entre les espèces et entre les différents groupes taxonomiques,
- ne nécessitent pas de données génomiques (indicateur 1 et 2)

Pour plus de détails, veuillez lire notre article ou contacter Sean Hoban shoban@biodiversity.org et Linda Latire linda.latire@gbikgenetics.eu

Genomic Biodiversity Knowledge for resilient Ecosystems



Variabilidad Genética – clave en la adaptación al cambio ambiental

Conclusiones principales

Los seres humanos dependemos de los ecosistemas. Es en nuestro propio interés el actuar y estar vigilantes frente a la pérdida de biodiversidad causada por el hombre y por el cambio climático.

- La diversidad genética es la variación a nivel del ADN. Es la base de las diferencias biológicas, tanto entre especies como entre individuos de la

Recomendaciones principales

Evitar la extinción de las especies y salvaguardar los ecosistemas requiere de actuaciones urgentes e integrales.

- Conservar y restaurar la diversidad genética para mantener la viabilidad de especies y ecosistemas y

Note Politique

Février 2021

Comment les pays rendent-ils compte de la diversité génétique à la Convention sur la Diversité Biologique et comment améliorer les rapports et le suivi de cette diversité?

CONTEXTE

- La biodiversité est confrontée à un large éventail de pressions, notamment la dégradation de l'habitat, le changement climatique, la pollution et les agents pathogènes à propagation rapide. La diversité génétique intraspécifique joue un rôle essentiel pour déterminer la capacité d'une population à s'adapter et à se maintenir en réponse à un environnement changeant. La diversité génétique est l'un des trois niveaux de biodiversité reconnus par la Convention sur la Diversité Biologique (CDB) et d'autres politiques de conservation nationales et internationales.
- Or, les estimations de l'état et des tendances de la diversité génétique ne sont pas encore considérées de façon systématique dans les programmes de conservation ou dans les objectifs de biodiversité. Cela peut s'expliquer en partie par la nature technique des approches génétiques et par le manque de connexions entre la recherche en génétique et les acteurs de la conservation. En outre, le manque d'indicateurs fiables est reconnu comme étant une lacune clé à combler dans le cadre global pour la biodiversité post-2020.
- Pour mieux comprendre comment les pays signataires de la CDB évaluent et protègent la diversité génétique, nous avons procédé à un examen approfondi de 134 rapports nationaux (bièmes et bièmes rapports). Nous avons identifié comment les pays ont rapporté les actions, réalisations, menaces, tendances et espèces prioritaires en lien avec la conservation de la diversité génétique.

RECOMMANDATIONS

Nos recommandations au Secrétariat de la CDB et aux pays signataires ont pour objectif d'améliorer le suivi et la protection de la diversité génétique pour contribuer au maintien des populations et des écosystèmes sains dans le long terme, objectif principal de la CDB.

1. Promouvoir la sensibilisation et la connaissance du rôle central de la diversité génétique dans la biodiversité, rapporter et protéger les connaissances autochtones et locales, et renforcer les moyens des acteurs de la conservation pour mieux surveiller et gérer la diversité génétique.
2. Favoriser et mettre en œuvre des directives standardisées pour la gestion génétique, le suivi à long terme, et pour faire rapport de l'état, des menaces, des actions et des tendances en lien avec la diversité génétique chez les espèces sauvages et celles ayant une importance socio-économique.
3. Mettre en œuvre des objectifs et des indicateurs améliorés localisés sur la diversité génétique (Hoban et al., 2020) dans le cadre de la CDB post-2020, afin de permettre le suivi de la diversité génétique au cours du temps et les progrès effectués pour atteindre ces objectifs.
4. Modifier les modèles de réunion des rapports nationaux de la CDB et fournir des conseils et des ressources pour encourager et permettre la rédaction de rapports cohérents et clairs concernant le suivi de la diversité génétique (in situ et ex situ) chez les espèces sauvages et celles ayant une importance socio-économique.

RÉSULTATS PRINCIPAUX

- Bien que la plupart des pays reconnaissent l'importance de la diversité génétique, 21% des bièmes rapports nationaux ne faisaient pas référence à un objectif la concernant.
- Seuls 5% des pays ont rapporté des indicateurs basés sur des données génétiques ou sur la protection des connaissances autochtones et locales de la diversité génétique.
- Les actions de conservation de la diversité génétique se sont principalement focalisées sur les espèces agricoles (espèces cultivées, animaux de ferme et espèces sauvages apparentées) plutôt que sur les espèces sauvages.
- Les trois principaux indicateurs de diversité génétique rapportés par les pays signataires sont le nombre de ressources génétiques préservées dans des installations de conservation, le nombre de ressources phylogénétiques connues / répertoriées et le statut de la Liste rouge. Or, ces indicateurs ne mesurent pas de manière fiable l'érosion génétique.
- Dans l'ensemble, l'attention limitée accordée au suivi de la diversité génétique, en particulier chez les espèces sans valeur économique, empêche toute tentative d'évaluation globale des changements de diversité génétique au cours du temps.

DIRECTIONS FUTURES

La CDB et les pays signataires ont la possibilité de s'assurer que des objectifs de diversité génétique soient effectivement mis en œuvre pour améliorer la conservation de la biodiversité. Le groupe de travail GEO BON sur la composition génétique et ses partenaires ont en mesure de fournir une expertise continue à la CDB et aux pays signataires au fur et à mesure qu'ils élaborent et mettent en œuvre des objectifs pour surveiller et protéger la diversité génétique.

Préparé par le «Group on Earth Observations Biodiversity Observation Network» (GEO BON) pour les personnes intéressées par la diversité génétique pour la biodiversité post-2020.

Contact: Dr Sean Hoban, shoban@biodiversity.org or Dr Margaret Hunter, mhunter@gbike.acz

Voir le rapport complet pour des recommandations détaillées: Hoban et al. (2020). An analysis of genetic diversity actions, indicators and targets in 134 National Reports to the Convention on Biological Diversity (<https://doi.org/10.1016/j.biocon.2020.108654>)



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Online

- New paper on indicators, for policy maker audience
- <https://doi.org/10.22541/au.166627692.27077414/v1>

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

Sean Hoban, Jess da Silva, Alicia Mastretta-Yanes, Catherine Grueber, Myriam Heuertz, Maggie Hunter, Joachim Mergeay, Ivan Paz-Vinas, Keiichi Fukaya, Fumiko Ishihama, Rebecca Jordan, María Camilla Latorre, Anna J. MacDonald, Victor Rincon-Parra Per Sjögren-Gulve, Naoki Tani, Henrik Thurfjell, Linda Laikre

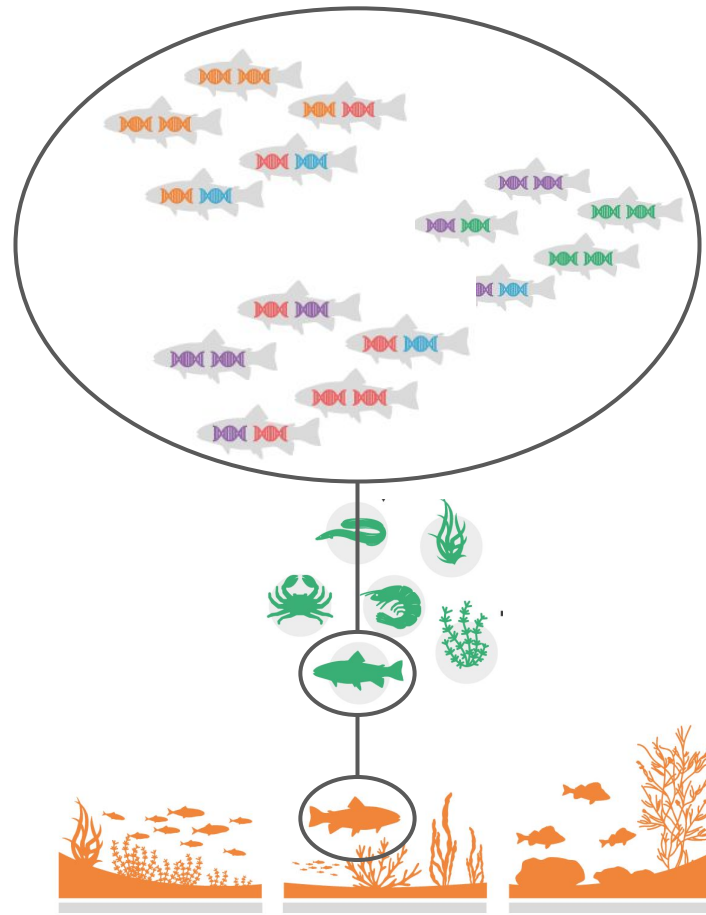
Online

- New paper on ‘decoding’ genetic diversity wording
- <https://doi.org/10.22541/au.166785459.91522683/v1>

Genetic diversity Goals and Targets have improved, but remain insufficient

Sean Hoban*; Michael W. Bruford; Jessica M. da Silva; Richard Frankham; W. Chris Funk; Michael J. Gill; Catherine E. Grueber; Myriam Heuertz; Margaret E. Hunter; Francine Kershaw; Robert C. Lacy; Caroline Lees; Margarida Lopes-Fernandes; Anna J. MacDonald; Alicia Mastretta-Yanes; Philip JK McGowan; Mariah H. Meek; Joachim Mergeay; Katie L. Millette; Cinnamon S. Mittan-Moreau; Laetitia M Navarro ; David O'Brien; Rob Ogden; Ivan Paz-Vinas; Gernot Segelbacher; Cristiano Vernesi; Linda Laikre*

We can leverage existing biodiversity knowledge and monitoring data to **monitor and report genetic diversity**, one of the main components of biodiversity and of Goal A and Target 4.



Sponsors



Mike Bruford

Co-hosts



Te Kāwanatanga o Aotearoa
New Zealand Government



SWEDISH SPECIES INFORMATION CENTRE



Frequently asked questions

How many species? ALL species?

Each country reports the indicator value based on a representative sample of at least 100 species (counting only populations within the country).

Representing different habitat types, lifespan, taxonomic group, and threat status/ rarity

Do genetic diversity Goals, Target 4, or indicators involve submitting or sharing Digital Sequence Information (DSI)?

No. The first two genetic diversity indicators are simply counts of populations meeting a criteria (effective size threshold or being extant). Only counts and proportions would be reported. DSI is not reported; Parties do not submit DSI.

The indicator on counts of genetic diversity studies for conservation purposes is also simply a count of studies and no DSI is shared when reporting, at all.

How much time does it take?

On average 2 hours per species to gather the data (from maps, reports, experts, or database analysis) + 0.5 hours to enter data

Plus 10 hours to learn the protocols/ training

8-9 weeks for 1 person

1 week for team of 8 persons

Can it be done now?

Yes, training materials are ready, data collection tools are ready

Could begin as soon as early 2023

Why multiple indicators- effective size (N_e) of 500 within populations, and maintaining all distinct populations?

Genetic diversity ***within*** populations allows sufficient variation within each population to adapt to local conditions over time and to avoid inbreeding consequences.

Genetic diversity ***between*** populations ensures the whole species can maintain enough adaptation for changing environments.

Both are essential for species survival and for supporting resilient ecosystems.

Why not other indicators?

LPI - overall population change- very good for 'population abundance' part of Goal A; but does not consider N_e 500- not genetic diversity

RLI - nearness to extinction; not closely correlated with genetic processes

Ecosystem/ habitat extent or quality - does not consider genetic processes, N_e 500, distinct populations

What skills/ technical knowledge is needed

To gather the data for indicator calculations, only a general biology or environmental science training is needed.

Do the two suggested headline indicators require using DNA-based techniques?

No. Genetic data/ molecular techniques are not required.

The Ne and populations maintained indicators can be reported using only census counts of individuals and field observations, which can be compiled

When genetic data is available for some species, it can be used to directly measure effective population size (N_e), and/or to help define populations.

How often to report?

Every 4 to 5 years, optional for more frequent if it is useful to the country (e.g. 2 years)

This matches the time scale of much environmental change and population change, and genetic processes (especially new offspring/ generations)

What is a population?

Use available knowledge and pragmatic approach

- population designations from the report or experts consulted, which reflect knowledge of the species biology, history and dispersal
- discrete patches such as forest or lakes
- ecoregions or biogeographic regions as proxies
- geographic (and migration) barriers such as mountains/ valleys, or hydrological zones, which may promote local adaptation
- grid cells based on species' dispersal.

Are the indicators SMART?

Specific (clear and quantitative)

Measurable (data is available)

Achievable (the work can be done)

Relevant (connected to genetic conservation)

Time bound (repeat every five years)

Is guidance in place to start applying the suggested indicators, for reporting on Goal A and Target 4 on genetic diversity?

Nine countries are already compiling data for these indicators. Supporting materials are being produced to support all countries in reporting on these indicators in a reliable, robust manner, and are available

