### Why genetic diversity is important and the fundamental concept of N<sub>e</sub>

Linda Laikre contact: linda.laikre@popgen.su.se Dept. Zoology, Stockholm University, Sweden Member of Swedish Council for Biodiversity – advisory body to CBD national focal points, IPBES, etc.













Loss of naturally occurring genetic diversity can have similar effects as loss of species

Genetic diversity within species equally important as species diversity

Slide 3

Importance of genetic diversity and effective population size  $(N_{e})$  Dr. Linda Laikre



#### High genetic diversity

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

Recent example: Corals being able to adapt to warmer ocean temperatures



Morikawa and Palumbi 2019, PNAS

#### Low genetic diversity

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

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



Hedrick et al 2019 in Animal Conservation

### Key questions for conservation

- How fast does my population lose genetic variation?
- Is my population large enough to maintain sufficient levels of genetic diversity?
- N<sub>e</sub> will provide the answer
- (But it can be complex! Our indicator 1 helps!)



The effective population size determines the rate of loss of genetic diversity

#### The effective population size $(N_e)$ is usually much smaller than the census size $(N_c)$

#### Sex ratio is one factor that affects $N_{\rm e}$



 $N_{\rm m}$  = number of mature males;  $N_{\rm f}$  = number of mature females

#### Sex ratio is one factor that affects $N_{\rm e}$



 $N_{\rm m}$  = number of mature males;  $N_{\rm f}$  = number of mature females



If few of adult individuals reproduce and contribute offspring loss of genetic diversity will be faster than if many contribute Other demographic factors also affect N<sub>e</sub> A well-established scientifically accepted rule-of-thumb:

# *N<sub>e</sub>* ≥ 500 Maintains sufficient levels of genetic variation for adaptation

e.g., Franklin 1980; Frankel & Soulé 1981, Ryman & Allendorf 2002; Jamieson & Allendorf 2012

Our proposed indicator 1 for genetic diversity of all species: Indicator 1 \_\_\_\_\_

The number of populations within species with an effective population size (N<sub>e</sub>) above 500 compared to the number below 500

proposed as **Headline** Indicator in the first draft of the CBD Post-2020 Global Biodiversity Framework

This indicator now

CBD/WG2020/3/3/Add.1

Laikre et al 2020; Hoban et al 2020

### How do we assess $N_e$ ?

- From detailed demographic data using equations
- From simulations using demographic data
- From molecular genotypic data

Estimates from thousands of wild and domestic populations are available

### If we do not have $N_e$ estimate – what do we do?

Census size estimates can be used as proxy!

# $N_{\rm e}/N_{\rm c}$ = 0.1 is a good, general proxy!

**Observed mean/median value from several scientific reviews** Frankham 1995, Palstra & Ruzzante 2008, Frasier & Ruzzante 2012, Frankham et al 2019, Hoban et al 2020, 2021



#### Variation around the $N_e/N_c = 0.1$ exists among taxa



## Applying the N<sub>e</sub> indicator



### Explaining genetic diversity indicators in the CBD post-2020 Global Biodiversity Framework

Sean Hoban, Linda Laikre, representing scientists and practitioners from IUCN, SCB, GEO BON, G-BIKE



#### 2010 Target 3.1

Genetic diversity of crops, livestock, and harvested species of trees, fish and wildlife and other valuable species [is] conserved, and associated indigenous and local knowledge [is] maintained

#### 2020 (Aichi) Target 13

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.

#### Draft 1 of CBD post 2020 framework

#### Goal A:

...genetic diversity of wild and domesticated species is safeguarded, with at least 90 per cent of genetic diversity within all species maintained

#### Target 4:

Ensure active management actions to enable the recovery and conservation of species and the genetic diversity of wild and domesticated species, including through ex situ conservation...

#### Why genetic diversity?

 Helps species adapt to environmental and climate change and disease

 Makes ecosystems more resilient to extreme weather and disturbance

 And more! Supports species diversity, communities, and nature's contributions to people

At focus: naturally occurring genetic variation within and between populations of all kinds of species

### **Past indicators**

- 1) Plant and animal genetic resources ... secured in ... conservation facilities
- 2) Proportion of local breeds ... at risk of extinction
- 3) Red List Index for wild relatives...

4) Comprehensiveness of conservation of ... valuable species

### **Past indicators**

- 1) Plant and animal genetic resources ... secured in ... conservation facilities
  - Ignores wild species, does not track genetic diversity
- 2) Proportion of local breeds ... at risk of extinction
  - Ignores wild species
- 3) Red List Index for wild relatives...
  - Does not track well to genetic diversity
- 4) Comprehensiveness of conservation of ... plants
  - Measures actions (but not status)



### **Three indicators**

1) Number of populations [or breeds] within species with an effective population size (Ne) above 500

2) Proportion of populations [or geographic range] maintained

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

Hoban et al 2020, Laikre et al 2020 Further explained in Hoban et al 2021, Lakire et al 2021

### **Three indicators**

1) Number of populations [or breeds] within species with an effective population size (Ne) above 500

2) Proportion of populations [or geographic range] maintained

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

In CBD/SBSTTA/24/INF/2923 May 2021, "Comments from the survey on headline indicators", <u>21 comments supported</u> one or more of these

### **Collaborative development**

Collaboration between four of largest international genetic diversity conservation groups

 GEO BON Genetic Composition Working Group: 180 members, 46 countries
EU Cost Action Genetic Biodiversity Knowledge for Ecosystem Resilience 100+ members, 39 countries
IUCN Conservation Genetics Specialist Group 115 members
Society for Conservation Biology Conservation Genetic Working Group

Improve the acquisition, coordination and delivery of biodiversity observations which are high quality and usable for policy

### **Indicator 1**

The proportion of populations [or breeds] with a genetically effective population size > 500 (A.0.4)

-"Sufficiently large" to prevent genetic erosion/ maintain adaptations

-Related to previous CBD indicator on threatened breeds (similar to populations!)

-Also a GEO BON EBV

### **Indicator 1**

The proportion of populations [or breeds] with a genetically effective population size > 500 (A.0.4)

Data sources:

- Genetic assessments of Ne, or software (Neogen)
- National agencies & NGOs track census of endangered or important species
- Citizen scientists counts
- IUCN Red List Population assessments , LPI data
- From area of suitable habitat

use Nc\*0.1 or Nc\*(Ne/Nc ratio from taxa)



#### **Endangered Species Act reports**





#### TABLE 1-ERIGERON MAGUIREI POPULATION INFORMATION

Meta-population	Population	Minimum population estimate (number of known sites) per land owner*						
		BLM SITLA		USFS	NPS	Total		
Northern San Rafael Swell	Calf Canyon**	500(10) 60(1)	87(2)			587(12)		
Central San Rafael Swell	Coal Wash	100(6)	***unkown			100(6)		
	Link Flats	9,000(9) 200(4)	50(1)			250(5)		
Southern San Rafael Swell	John's Hole Segers Hole	300(3) 100(2)	***unkown ***unkown			300(3) 100(2)		
Capitol Reef	Deep Creek Capitol Reef			1,500(2)	100,000(29) 30,000(15)	101,500(31) 30,000(15)		
	Waterpocket Fold				20,000(42)	20,000(42)		
	Totals	10,260(35)	1,137(5)	1,500(2)	150,000(86)	162, <del>897(</del> 128)		
	Percent	6.30	0.70	0.92	92.08	100.00		



Buffalo Creek and Goosepond Creek, Oglethorpe County, Georgia: Wood found about 50 individuals in the first site which is the original area of discovery. Twenty-five individuals were observed in the second subpopulation, some of which spread onto

private land.

 Oconee National Forest, Jasper and Baldwin County, Georgia: With the leadership of John Jensen and Tom Patrick from Georgia Department of Natural Resources, Lobdell and Thompson located the "large population of *Q. oglethorpensis* and *Q. shumardii*" present within the park. Upon visiting the same area, Jordan Wood observed 100 individuals (mature and immature) with another 400 found to the north,

#### Scientific literature, Living Planet Index data, etc.



Mean N Ν  $LDNe N_{b}$ Mean  $N_{\rm b}$ UC 5 65 (49–79) 20 (13-48) 6 HM 5 (3–5) 66 (52-80) 4 4 DY 5 116 (84–179) 10 (3–34) 6 LC 338 (250-798) 31 (11-117) 6 6 LO 5 5 470 (372–625) 44 (23–188) WC 783 (530–1148) 31 (21-52) 6 6 **STBC** 5 917 (587–1405) 28 (14–54) 6 LB 5 1184 (877–1383) 52 (34-83) 4 CC 5 1862 (1471–5246) 74 (65–99) 4 UO 6 6 2569 (1949–3835) 62 (41-87) BC 4693 (4044-6132) 355 (267–567) 6 4 7 WN 4 7801 (6713–10 032) 178 (110-267)





Table 1 Population summary statistics from twelve CR brook trout pop

### **Indicator 2**

Proportion of distinct populations [or geographic range] maintained (Component)

-Maintain genetic adaptations

-Related to Species Habitat Index, but focuses on loss of distinct populations

-Relates to GEO BON EBV

### **Indicator 2**

Proportion of distinct populations [or geographic range] maintained (Component)

Data sources:

- GBIF (Global Biodiversity Information Facility)
- National agencies, NGOs (e.g. forest inventories)
- Citizen scientists (iDigBio)
- IUCN Red List Population assessments
- Map of Life
- Scientific assessments

#### Map of Life- species' range maps



#### Red List Assessment maps (sometimes include original extent)



# Calflora- a regional species' occurrence database (with dates)



	Calflora Ot	oservation Search				▼ MAP	► TOOLS			
Clic	ck on 🖍 to sele	ct a record. Click on columr	i title to sort.		82 records	► LEGEND				
	ID	Plant	Date	Source	County	TTP	Ananeim	Josnua Tree	COLORADO	5
	DAV214662	Quercus cedrosensis Cedros island oak	2015-03-19	Consortium of California Herbaria	?	Мар	Satellite		RESERVA	K
	mu8840	Quercus cedrosensis Cedros island oak	2015-03-05		?					
	oe6382	Quercus cedrosensis Cedros island oak	2014-03-22	San Diego Native Plant Society	San Diego	de la	San Diego	0 Mexicali		a
	wb1194-2868	Quercus cedrosensis Cedros island oak	2013-05-02		San Diego		Tijuan	San Luis Rio Colorado	San Luis Río Colorado	12)
Ø	UCR-239439	Quercus cedrosensis Cedros island oak	2012-03-20	Consortium of California Herbaria	?		Ensepada		Reserva de la Biosfera Alto Golfo	
Ø	SD223000	Quercus cedrosensis Cedros island oak	2012-03-20	Consortium of California Herbaria	?	-X-		) [] 	de	
	SD246069	Quercus cedrosensis Cedros island oak	2009-05-10	Consortium of California Herbaria	?			- 8 BAJ CALOFO		
	SD161398	Quercus cedrosensis Cedros island oak	2005-04-26	Consortium of California Herbaria	?					
	DAV329044	Quercus cedrosensis Cedros island oak	2005-03-10	Consortium of California Herbaria	San Diego	Google		Map data ©202	1 Google, INEGI	
						🗏 🕂 31.3196, -	118.4910			

### **Indicator 3**

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

-Knowledge helps management

-Supports GEO BON EBVs

-Fund monitoring, applied research, communication

### **Indicator 3**

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

Data sources:

- Search of journal articles (google scholar)
- Search of government publications
- Search of datasets (GenBank, Dryad, etc)
### The coming of age of conservation genetics in Latin America: what has been achieved and what needs to be done

Juan Pablo Torres-Florez<sup>1</sup> · Warren E. Johnson<sup>2</sup> · Mariana F. Nery<sup>3</sup> · Eduardo Eizirik<sup>4</sup> · María A. Oliveira-Miranda<sup>5</sup> · Pedro Manoel Galetti Jr<sup>1</sup>

### A survey of studies in the Americas (2013)

<b>Table 2</b> Number ofconservation genetics papers,number of species studied ineach country, IUCN red list	Country	Research papers	Studied species	IUCN stud- ied species
species studied for each country and the total IUCN red listed species for each country. The megadiverse countries are indicated in bold	Argentina	20	25	13
	Bolivia	2	2	1
	Brazil	225	257	92
	Chile	34	83	35
	Colombia	12	25	24
	Costa Rica	10	12	5
	Cuba	2	2	1
	Dominican Republic <sup>a</sup>	3	1	1
	Ecuador	18	39	35
	El Salvador	1	1	0
	Guatemala	2	3	2
	Haiti <sup>a</sup>	0	0	0
	Honduras	0	0	0
	Mexico	83	88	57



Biological Conservation Volume 209, May 2017, Pages 130-136



### And in Europe (2014)

### Conservation genetics in the European Union – Biases, gaps and future directions



# **IUCN CGSG developing method for countries**

Published literature over a defined time period (eg 2015-2019)



- 122 studies
- 108 species
- 89 animals
- 30 plants
- 3 fungi
- 110 wild
- 12 domestic





- 79 studies
- 80 species
- 46 animals
- 32 plants
- 1 fungi
- 68 wild
- 11 domestic



# Are they ready for use?

Our case studies show that Parties can already leverage national data sources for reporting on numerous species

Indicator 1: Global data source for Ne is envisioned

Indicator 2: Potential for integration with Map of Life

Indicator 3: Approach in development but IUCN CGSG

# A strong Goal

# Goal and Milestone should be connected to indicators

# A strong Goal

# 2050 Goal

Indicator 2Prevent the loss of distinct populations and<br/>maintain at least 95% of genetic diversity within<br/>populations of all wild and domesticated species,<br/>and restore conditions ensuring evolutionary<br/>adaptive potential.

# A strong Goal

# 2050 Goal

Indicator 2
 Indicator 1
 Indicator 1
 Indicator 1
 Indicator 3
 Indicator 3

# **2030 Milestone**

- Indicator 1 The proportion of populations sufficiently large enough to maintain genetic diversity has increased [by at least 10%],
- Indicator 2 the proportion of genetically distinct populations maintained is [100%], and
- Indicator 3 strategies and monitoring programs are being developed and initiated.

# A clear, measurable Target

By 2030, the genetic diversity of wild and domestic populations is **maintained, protected, managed, and monitored,** in situ and ex situ, at levels ensuring [95%] of population diversity [in perpetuity].

Progress is measured by indicators- large populations, no loss of populations, and monitoring

(Hoban et al 2020, O'Brien et al 2020)

### Two page policy brief translated in 8 languages

### Genetic diversity targets POLICY BRIEF and indicators proposed for the CBD post-2020 Global Biodiversity Framework

To accompany: 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

#### **Executive Summary**

Genetic diversity goals and metrics to assess genetic diversity (indicators) in the post-2020 biodiversity framework must be improved to prevent the irreplaceable loss of biodiversity and to meet the Convention on Biological Diversity (CBD) targets. Genetic diversity within **all species** must be conserved, measured, and monitored using appropriate metrics. Suitable for the post-2020 framework, we propose a genetic Goal with a recommended Action Target, and suggest three new genetic indicators, plus changes to current CBD indicators.

#### Background

Genetic diversity contributes to supporting human society and the life support systems of the biosphere. It is decreasing globally due to human actions. This diversity enables species to adapt, maintains ecosystem services (e.g. water filtration, food), and is essential to ensure the resilience of species and ecosystems to climate change. The "zero draft" of the CBD's post-2020 framework follows the 2011-2020 CBD strategy to conserve biodiversity, for which few targets have been met. **Maintaining genetic diversity is recognised in the** 

# Like many species, pool frogs (Pelophylax lessonae) live in multiple

ike many species, pool frogs (Pelophylax lessonae) live in multiple onnected populations, which should be considered when measuring enetic diversity

#### Proposed indicators

To meet global conservation goals, we propose that genetic diversity within all species needs to be conserved, measured, and monitored using appropriate metrics.

We propose three new indicators for the post-2020 CBD framework, to be used in addition to modifications to the current CBD's zero draft indicators. One indicator alone is insufficient for monitoring progress towards the CBD genetic

### **Proposed Indicators**

The number of populations [or breeds] within species with an effective population size > 500 compared to the number < 500

Ne lower than 500 means that a population has a reduced ability to adapt to environmental change. If no genetic, demographic, or pedigree data is available on a species, Ne can be roughly approximated as 1/10 (i.e. 10%) of the population census size (number of adults).

The proportion of (sub)populations [or geographic range] maintained within species

The loss of genetically distinct wild populations, or the agricultural equivalent - breeds, landraces, or varieties - will result in large losses of genetic diversity within species. This indicator **compares the number of genetically distinct populations, relative to a historic baseline.** Alternatively, a percentage of the species historic range which is maintained would suffice.

The number of species and populations in which genetic diversity is being monitored using DNA-based methods

To safeguard genetic diversity we need to know the level of genetic diversity within and among populations, environmental drivers of that diversity, and how connected the populations are. However, **this indicator cannot be relied on alone** as it may simply reflect a greater ability to gain this information OR more species being targeted for conservation genetic research efforts.

#### Edits to current CBD Zero Draft Goal 3 indicators

Do not use IUCN Red List Index as a genetic indicator
 Ensure minimum requirements for *ex situ* collections are representative, replicated, and resilient

**Effective population size (Ne)** is an estimate of the genetic population size. *Ne* is smaller than census size because not all individuals in a population reproduce, and those that do can have different numbers of offspring. Factors like population inbreeding may reduce *Ne* further.

### 2030 Goal

Maintain existing genetic diversity and halt the loss of genetic diversity **within all species**. Develop and initiate strategies to avoid future genetic diversity loss.

### 2050 Goal

Secure and **restore adaptive potential** and **longterm maintenance** of genetic diversity within populations of species.

### **Action Target**

Halt loss, retain, safeguard and restore the genetic diversity and adaptive potential of species and populations, in the wild and in captivity/collections, assuring that by 2030: populations have an effective population size >500, genetic diversity and genetic connectivity is monitored using DNA-based methods in populations of key species, and loss of distinct populations within species has been halted.



Microcycas calocoma (critically endangered). Most ex situ

# **Genetic indicators are SMART**

- **Specific** (clear and quantitative)
- **Measurable** (data is available)
- Achievable (the necessary actions are feasible)
- **Relevant** (connected to genetic conservation)
- **Time bound** (DNA and proxy data available, time goals)

# Global Commitments to Conserving and Monitoring Genetic Diversity Are Now Necessary and Feasible

SEAN HOBAN<sup>®</sup>, MICHAEL W. BRUFORD<sup>®</sup>, W. CHRIS FUNK<sup>®</sup>, PETER GALBUSERA, M. PATRICK GRIFFITH, CATHERINE E. GRUEBER<sup>®</sup>, MYRIAM HEUERTZ, MARGARET E. HUNTER, CHRISTINA HVILSOM, BELMA KALAMUJIC STROIL, FRANCINE KERSHAW, COLIN K. KHOURY, LINDA LAIKRE, MARGARIDA LOPES-FERNANDES, ANNA J. MACDONALD, JOACHIM MERGEAY<sup>®</sup>, MARIAH MEEK, CINNAMON MITTAN<sup>®</sup>, TAREK (Hoban et al 2021)



### Statement on genetic diversity in CBD, dated December 22, 2020

In the context of the Convention on Biological Diversity post-2020 Framework, and towards a mutual aim of conserving all biodiversity, we the "Conservation Genetic Coalition"<sup>1</sup> make the following statements regarding genetic diversity in this Framework. We invite Parties to use the following wordings in their interventions and comments to the CBD. If Parties would like assistance in drafting genetic diversity language in their comments, please write to

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

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

### I. INTRODUCTION

This information document<sup>1</sup> focuses on the evidence-based consideration, protection, and monitoring of genetic diversity in the post-2020 Global Biodiversity Framework (GBF), to prevent genetic diversity loss and improve its contributions to species, ecosystems, and society. "Genetic diversity" is the diversity in DNA sequences and traits within species which allows populations to adapt, evolve and survive over time. This document presents the current state of knowledge that genetic diversity within all species- not just agricultural species- contributes to (a) species' survival, ecosystem resilience and productivity, and (b) nature's contribution to people. Genetic diversity is the foundation of species and ecosystem diversity,

### Policy brief on National Reports, genetic diversity- 15 languages

#### November 2020

How do Parties report to the Convention on Biological Diversity on genetic diversity and how can reporting and monitoring be improved?

### BACKGROUND

- Biodiversity is facing a wide range of pressures, including habitat degradation, climate change, pollution, and fast-spreading pathogens. Genetic diversity - the variation within a species - plays a central role in a population's ability to adapt and persist in response to a changing environment. Genetic diversity is one of three levels of biodiversity recognized by the Convention on Biological Diversity (CBD), and other national and international conservation policies.
- However, estimates of the status and trends of genetic diversity are not yet routinely integrated into conservation programmes or biodiversity targets. This can be partly explained by the technical nature of genetic approaches, and the disconnect between genetics research and conservation practitioners. Furthermore, the lack of reliable indicators is recognised as a key data gap for the post-2020 biodiversity framework.
- To better understand how CBD signatory Parties assess and protect genetic diversity, we conducted a thorough review of 114 5<sup>th</sup> and 6<sup>th</sup> National Reports to determine how countries reported actions, uses, threats, trends, and priority species for genetic diversity monitoring and

#### **KEY FINDINGS**

- Although most countries recognize the importance of genetic diversity, 21% of 6<sup>th</sup> National Reports did not refer to a genetic diversity target.
- Only 5% of countries reported indicators based on genetic studies or protection of Indigenous and local knowledge of genetic diversity.
- Actions to conserve genetic diversity primarily focused on agricultural species (cultivated crops, farm animals, and crop wild relatives) rather than wild species.
- The top three genetic diversity indicators reported by countries included the number of genetic resources in conservation facilities, the number of plant genetic resources known/surveyed, and Red List status. However, these indicators do not reliably measure genetic erosion.

#### RECOMMENDATIONS

Our recommendations to the CBD Secretariat and Parties aim to enhance monitoring and protection of genetic diversity for long-term persistence of populations and healthy ecosystems, fulfilling the core goal of the CBD.

> Increase awareness and knowledge of the central role of genetic diversity in biodiversity, protect and document Indigenous and local knowledge, and build capacity among conservation practitioners to monitor and manage genetic diversity.

Develop and implement standardized guidance for routine genetic management, long-term monitoring, and reporting of the genetic diversity status, threats, actions, and trends for wild and socioeconomically important species.

2

3

Implement improved genetic diversity-focused targets and indicators (Hoban et al. 2020) for the post-2020 CBD framework to enable monitoring of genetic diversity trends and progress towards these targets.



Amend the CBD National Reports templates and provide guidance and resources to encourage and enable consistent and clear reporting on insitu and ex-situ genetic diversity monitoring in wild and socioeconomically important species.

# Feedback from Parties, others

- Support for advancing genetic diversity indicators, Target
- Questions
  - Do indicators apply to all species
  - What is a population
  - Data sources, quality of dataset
  - How many species to report on
- Request for case study examples
- Requests for future webinars and Q&A

# Making this feasible

- Ongoing: Webinars for focal points & support staff- indicator explanation, establish in-country connections.
- 2021: IUCN WCC session; motion on genetic diversity
- 2021-2022: Testing the indicators with Parties; Developing data infrastructure, online resources
- 2022: Complete guidance manual for the three genetic diversity indicators, in consultation with practitioners and focal points from as many countries as possible

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# **Our recommendations- summary**

- Indicators are sensitive to change, scalable, data available and are garnering Party interest
- Clear, measurable Target and Goal, connected to the indicators
- Plan to work with Parties to trial indicators

Questions?



South African National Biodiversity Institute

# Genetic diversity indicators: a South African perspective

Jessica da Silva j.dasilva@sanbi.org.za

Celebrating biodiversity for the benefit and enjoyment of all South Africans

### **Ecosystem Data**





## **Ecosystem data**

- Threat status
- Protection level

Spatial distribution of ecosystem protection level for each realm: (A) terrestrial, (B) marine, (C) sub-Antarctic territory including the PEIs and surrounding seas, (D) river, (E) inland wetland, (F) estuarine (represented as circles for graphic purposes).

# Species data

- Occurrence records
- IUCN Red List status
  & trends

Hermanun

pe Town

Stellenboact





### **Reporting on Genetic Diversity**



# **Genetic Diversity Indicators and Monitoring**

To date, ad hoc application of genetic diversity indicators & monitoring research

Majority on threatened species across a range of taxonomic groups







African Penguin









Seagrass \* Temporal genetic monitoring

# **Genetic Diversity Indicators and Monitoring**

**Commercial interest** 



Kingklip



#### South African Abalone



Indigenous chickens



Indigenous sheep





Cheetah

Cape Buffalo

### Cultural & social significance

# **Prioritizing Species**

- Threatened
- Endemic
- Social & cultural importance
- Commercial harvesting
- Wild relatives of crops and breeds
- Wildlife ranching

# **Prioritizing Species**

#### Table 3. Status of all indigenous taxa assessed. NT is Near Threatened, DD is Data Deficient, FW is freshwater

Taxon	Birds	Mammals	Reptiles	Amphibians	Butterflies	Plants	FW fishes	Dragonflies	Seabreams	Linefish (bony)	Linefish (cartilaginous)	Corals	
Extinct	0	5	2	0	3	36	0	2	0	0	0	0	
Threatened	84	57	24	16	78	2 804	42	20	9	12	2	9	3 157
NT, DD, <mark>R</mark> are	49	56	25	17	62	3 366	21	13	9	36	13	34	
Least Concern	599	218	346	92	656	14 195	55	127	24	31	11	52	
Total	732	336	397	125	799	20 401	118	162	42	79	26	95	
Endemics	38	57	209	62	418	13 763	58	28	15	2	2	0	
% Extinct	0%	1%	1%	0%	0.4%	0.2%	0%	1%	0%	0%	0%	0%	
% Threatened all taxa	11%	17%	6%	13%	10%	14%	36%	13%	21%	13%	7%	9%	
% Endemics	5%	17%	53%	50%	52%	67%	49%	17%	35%	3%	7%	0%	_
% Endemics threatened	24%	39%	7%	26%	18%	20%	66%	36%	33%	0%	0%	na	315

# **Prioritizing Species**

# Criteria:

- Threatened
- Endemic
- Not well protected

- 3 157 (353 animals, 2 804 plants)
  - **315** (181 animals, 134 plants)
  - 255 (105 plants, 150 animals)

# Amphibians

			Indicator 1		Indicator 2	Indicator 3	
	Taxon	Number of Populations	Pops with Ne > 500	Pops with Ne < 500	Remaining populations	Temporal genetic monitoring	
CR	Capensibufo rosei	5 (2 extant)	1	1	40%	Yes (2 pops)	$\checkmark$
EN	Sclerophrys pantherina	6 (5 extant)	Unknown	≥1	83%	Yes (1 pop)	$\checkmark$

#### Capensibufo rosei



Indicator 1 = 0.50Indicator 2 = 0.40 Ideal values 1.0 (100%  $N_e > 500 \&$  maintained)

#### Sclerophrys pantherina



Indicator 1 = Unknown (but likely 0.00) Indicator 2 = 0.83

# **Reptiles**

**RA = available upon reanalysis** 

	·		Indicator 1		Indicator 2	Indicator 3
	Taxon	Number of Populations	Pops with Ne > 500	Pops with Ne < 500	Remaining populations	Temporal genetic monitoring
CR	Psammobates geometricus	2-3	RA	RA	100%	No
EN	Bradypodion thamnobates	1	RA	RA	100%	RA
VU	Smaug giganteus	5	RA	RA	100%	No

### Smaug giganteus



Mature individuals = 67 700 (48% decline)

### Psammobates geometricus



Mature individuals = 800 (> 90% habitat transformed)



Bradypodion thamnobates

Mature individuals = ?



# Developing country perspective



# **Resources & Capacity**



South African National Biodiversity Institute

# THANK YOU!

Jessica da Silva j.dasilva@sanbi.org.za



Celebrating biodiversity for the benefit and enjoyment of all South Africans



# CONABIO's example approach to evaluate genetic diversity indicators

Alicia Mastretta-Yanes

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26<sup>th</sup> July 2021



### INDICATORS

The number of populations within species with an effective population size (N<sub>e</sub>) above 500 compared to the number below 500

The proportion of populations maintained within species The number of species and populations in which genetic diversity is being monitored using DNA-based methods

### **Select species**

**Data needs** 

Defining **populations** within species

Genetic **or** abundance data to estimate Ne Determining if populations still exist

Performing/systematizing DNA-based studies



### **Choosing species: selection criteria**

For each of Mexico's major ecosystems:











### **Choosing species: selection processes**





Preliminary list



Confirm data availability

Images credits: The Noun Project & Open Peeps



Workshop with experts



Final species list


CONSIGN NACIONAL PARA EL CONOCIMIENTO Y USO DE LA BIODIVERSIDAD INDICATORS

per of populations species with an opulation size (N<sub>e</sub>) PO 0 compared to the per below 500

The proportion of populations maintained within species The number of species and populations in which genetic diversity is being monitored using DNA-based methods

#### **Defining populations within species**

#### Easy for isolated habitats!



## Not so easy for widespread ecosystems





The proportion of populations maintaine within species The number of species and populations in which genetic diversity is being monitored using DNA-based methods

#### **Defining populations within species**

**Proxies of genetic diversity** to define areas holding potentially genetically differentiated populations



INDICATORS

The proportion of populations maintained within species The number of species and populations in which genetic diversity is being monitored using DNA-based methods

#### **Defining populations within species**

**Proxies of genetic diversity** to define areas holding potentially genetically differentiated populations



Environmental drivers Holdridge life zones Literature review

- Spatially represented by:
  - Biogeo provinces
  - Edaphology
  - Watersheds

**Historical drivers** Phylogeographic patterns





INDICATORS

itions an The proport te (N<sub>e</sub>) populations m to the within spo The number of species and populations in which genetic diversity is being monitored using DNA-based methods

#### **Defining populations within species**

**Proxies of genetic diversity** to define areas holding potentially genetically differentiated populations



Environmental drivers Holdridge life zones **Historical drivers** Phylogeographic patterns **Proxies of Genetic Diversity** 



INDICATORS

itions an The propor ze (N<sub>e</sub>) populations m to the within sp The number of species and populations in which genetic diversity is being monitored using DNA-based methods

#### **Defining populations within species**

**Proxies of genetic diversity** to define areas holding potentially genetically differentiated populations





CONSIÓN NACIONAL PARA EL CONOCIMIENTO Y USO DE LA BIODIVERSIDAD

The num	ber of pop	pulations
within	species w	vith an
	0 compar	ed to the

The proportion of pulations maintained within species

INDICATORS

ne number of species and populations in which genetic diversity is being monitored using DNA-based methods



#### Genetic or abundance data to estimate Ne









#### Genetic or abundance data to estimate Ne





CONABIO COMISIÓN NACIONAL PARA EL CONOCIMIENTO Y USO DE LA BIODIVERSIDAD



The proportion of

INDICATORS

n of p itained get ies

populations in which genetic diversity is being monitored using DNA-based methods

#### **Indicator 1**

#### **Data examples**



#### Teosintes: wild relatives of maize



#### Zea mays ssp. parviglumis Most known populations ~ 1,800 samples ~ 34,000 SNPs

Similar sampling for all Zea taxa

Diana Rivera-Rodríguez, Jesús Sánchez et al *in prep* 





CONSIÓN NACIONAL PARA EL CONOCIMIENTO Y USO DE LA BIODIVERSIDAD The number of populations within species with an effective population size (N above 500 compared to the number below 500

The proportion of populations maintained within species

INDICATORS

ne number of species and populations in which <u>penetic diversity is being</u> monitored using DNA-based methods

#### **Indicator 2**

#### **Determining if populations still exist**





The number of popul within species wit effective population s above 500 compared number below 5

The proportion of populations maintained within species

**INDICATORS** 

he number of species and populations in which senetic diversity is being monitored using DNA-based methods



#### **Determining if populations still exist**

Potentially genetically differentiated **populations** 

#### Data to assess if populations exist:

Occurrence data:





CONABIO COMISIÓN NACIONAL PARA EL CONOCIMIENTO Y USO DE LA BIODIVERSIDAD INDICATORS

The proportion of populations maintained within species he number of species and populations in which genetic diversity is being monitored using DNA-based methods

#### **Indicator 2**

#### **Data examples**

#### + Data to assess if populations exist:

#### Occurrence data:

#### Juniperus monticola

- Representative of alpine grasslands
- Large range, narrow
   habitat

Already studied



Collections iNaturalist 10/13



https://enciclovida.mx/especies/155226-juniperus-monticola



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The proportion of populations maintained within species The number of species and populations in which genetic diversity is being monitored using DNA-based methods

#### **Indicator 2**



#### (PGD x SDM or occurrences)

#### Hylocharis leucotis

- Representative of pineoak forests
- Large range, broad habitat



#### Data examples

+ Data to assess if populations exist:



Zamudio Beltrán et al (2020) Biol. Journal Linneal Soc



Collections

iNaturalist

eBird



The number of populati within species with a effective population size above 500 compared to number below 500

The proportion of populations maintained within species

INDICATORS

populations in which senetic diversity is being monitored using DNA-based methods



#### **Determining if populations still exist**

Potentially genetically differentiated **populations** 

Data to assess if populations exist:

Occurrence data: aVerAves



Ecosystem integrity:



(PGD x SDM or occurrences)

or



Naturally isolated populations



The number of populations within species with an effective population size (Ne) above 500 compared to the number below 500

The proportion of populations maintained within species

INDICATORS

The number of species and populations in which genetic diversity is being monitored using DNA-based methods



#### Performing or systematizing DNA-based studies





The number of populations within species with an effective population size (N<sub>e</sub>) above 500 compared to the number below 500

The proportion of populations maintained within species

INDICATORS

The number of species and populations in which genetic diversity is being monitored using DNA-based methods

#### **Indicator 3**

#### Performing or systematizing DNA-based studies

We already identified genetic studies of 491 / 2,678 Mexican species at risk



Published data of many species more is available





The number of populations within species with an effective population size (N<sub>e</sub>) above 500 compared to the number below 500

The proportion of populations maintained within species

INDICATORS

The number of species and populations in which genetic diversity is being monitored using DNA-based methods

#### **Indicator 3**

#### Performing or systematizing DNA-based studies

We already identified genetic studies of 491 / 2,678 Mexican species at risk https://enciclovida.mx





Zamudio Beltrán et al (2020) Biol. Journal Linneal Soc

#### **Summary workflow**







Iready tudied Umbrel

Workshop with experts

Subset of species including representatives of:

- Each of Mexico's major ecosystems
- Major taxonomic groups
- Contrasting dispersal abilities
- Different forms of rarity



potentially genetically differentiated populations



indicator 2 Occurrences and/or ecosystem integrity to evaluate if populations still exist







indicators 1 & 3 Abundance and/or genetic data from already studied species



COMISIÓN NACIONAL PARA EL CONOCIMIENTO Y USO DE LA BIODIVERSIDAD

## Thank you

Alicia Mastretta-Yanes amastretta@conabio.gob.mx







Royal Botanic Garden Edinburgh

### A scorecard approach to assessing genetic diversity

#### David O'Brien,

Pete Hollingsworth, Tarek Mukassabi and Rob Ogden









## Convention on Biological Diversity

#### Target 13 - Genetic Diversity Maintained

- By 2020, the genetic diversity of cultivated plants and farmed and domesticated animals and of wild relatives, including other socioeconomically as well as culturally valuable species, is maintained, and strategies have been developed and implemented for minimizing genetic erosion and safeguarding their genetic diversity
- Target 13 reviewed across 50 nations (38 Englishspeaking, 9 Spanish, 10 French) across all continents (inc. Antarctica)
- Somewhat variable, but main focus on cultivated and domesticated species. <u>Hoban et al. 2021</u>
- What will post-2020 look like?

# What were Scotland and the UK reporting?

- Number of flowering plant accessions at UK holding institutes
- Number of accessions for priority crop wild relatives in gene banks
- Number of crop wild relatives in nature conservation sites
- Number of collections of Scottish landraces *ex situ*
- Population size of 'at risk' native domesticated mammals
- Status of two native species of deer
- BUT What about all the other species, inc. those of conservation concern?

## Key questions for CBD reporting

"...other socio-economically valuable species, as well as for selected wild species of plants and animals."

- What taxa to include in the "other" category?
  - "Other socio-economically as well as culturally valuable species"
  - "Selected wild species of plants and animals"
- What can we do that is feasible for in situ?
  - Starting assumption is that the system needs to cope with no direct genetic data being available
  - But requires some knowledge of where the species lives and its biology
- How best to summarise *ex situ* representation of genetic diversity?
  - Again assuming that direct genetic data may not be available

# Genetics scorecard – choosing species?

#### • Five criteria

- National conservation priority wild species (e.g. freshwater pearl mussel);
- Species of national cultural importance (e.g. golden eagle);
- Species providing key ecosystem services (e.g. Sphagnum papillosum);
- Species of importance for wild harvesting (food and medicine) (e.g. blaeberry);
- Economically important game species (e.g. red deer)

## What's in each species' scorecard?

- Summary of relevant genetic conservation issues for the species, key issues, species traits  $\rightarrow$  susceptibility to genetic problems.
- A statement of international importance of national genetic diversity for the species, to contextualise the assessment.
- Evaluation of key genetic risks facing *in situ* populations: Diversity, functional diversity, unique evolutionary lineages, hybridisation, low turnover
- Overall *in situ* threat assessment based on expert opinion leading to a 'low-medium-high' genetic risk categorisation based on species attributes and the risks faced by the species.
- A statement of confidence on the overall *in situ* threat assessment. This step aims to transparently capture the level of certainty among experts as to the risk categorisation.
- The level of representation in *ex situ* collections. This step was undertaken for plant species which are particularly well suited to holding *ex situ* collections in seed banks.

Scie	ntific name	Pinus sylvestris	Common Name	Scots pine	
GB I	UCN Category	LC	T13 Status	Moderate risk Mitigation effective	
Creates Ordensie Burvey data Ordensie Ordensie Burvey data Ordensie Ordensie Burvey data Ordensie Ordensie Burvey data					
	Background	Hermaphrodite, wind pollinated, widely distributed tree. Present in 84 natural stands, often small and fragmented (dark circles on map, light circles are plantations). Natural stands represent only 10% of trees in Scotland. Genetic marker studies show large amounts of neutral genetic diversity. Some evidence of adaptive differentiation in Scotland from west to east (Salmela, 2011; Donnelly <i>et al.</i> , 2018).			
	Current threats	Plant pathogens represent the major emerging threat ( <i>Dothistroma septosporum</i> races introduced on Corsican and lodgepole pine) (Piotrowska <i>et al.</i> , 2018).			
Context	Contribution of Scottish population to total species diversity	Molecular evidence for putative separate lineage in north western Scotland, although nuclear markers indicate very low differentiation, even from continental Europe (Ennos <i>et al.</i> , 1997). Scotland does, however, contain a uniquely oceanic adapted population (Ennos <i>et al.</i> , 1997; Donnelly <i>et al.</i> , 2018).			



risk summary

## Which species were included?

- Mix of taxonomic groups Basidiomycota, Ascomycota, bryophytes, vascular plants, Mollusca, Arthropoda, Chordata (fish, amphibian, bird, mammal)
- Some bias to vascular plants and chordates inevitable next do marine spp.



Hollingsworth et al. (2020a) https://www.natur e.scot/scotlandsbiodiversityprogress-2020aichi-targetsconserving-geneticdiversitydevelopmentnational



Hollingsworth et al. (2020b) https://www.natu re.scot/scotlandsbiodiversityprogress-2020aichi-targets-aichitarget-13-geneticdiversitymaintained

## What next?

- Incorporate Essential Biodiversity Variables (EBV)
- Marine species
- Harmonise genetic conservation monitoring and strategies between sectors – forestry, agriculture, horticulture and wild species
- Greater incorporation of genomic data into monitoring
- Expanding the scorecard's use beyond Scotland collaboration with University of Benghazi, Libya.





## Thank you









APPLYING PROPOSED GENETIC INDICATORS TO CBD: A HANDFUL CASES FROM SWEDEN

> Dr. Per Sjögren-Gulve The Wildlife Analysis Unit of the Swedish EPA

1

Naturvårdsverket | Swedish Environmental Protection Agency



#### (1) effective size ( $N_e$ ), (2) proportion of populations maintained



- Scientific & indigenous knowledge, co-operation scientists & experts
  - "citizen science"  $\rightarrow$  national and/or international data base(s).
- Ecological census and estimation methods, geographic distinctness.
- Genetic methods: N<sub>e</sub> from (repeated) genetic screening,
  - + evaluation/validation of connectivity(+ evaluation of population distinctness).



### PSG Slide 3 G-BIKE Applying two Hoban et al. indicators



- In Sweden and Fennoscandia (SE+NO+FI)
  - Sweden & Finland are MSs of the EU (e.g., Natura 2000),
  - all three have ratified the Bern Convention and the CBD,
  - IUCN-redlist and EU species status assessments help.
- National Species Information Centres exist

   → data bases for storing species records/observations, e.g.
   https://www.gbif.org/dataset/38b4c89f-584c-41bb-bd8f-cd1def33e92f
- Genetic monitoring unusual, but likely to be used much more.





#### Some comparative species cases from Sweden



Photo: © Karl-Olof Bergman



- The butterfly Lopinga achine NT
  - (1) the conservative  $N_e/N_c$  "0.1 rule"  $\Rightarrow$  census size  $N_c = 5000$

metapopulation sizes: > 6100 (Östergötland) + c. 7000 (Gotland)

(2) 100% distinct metapop.s remain, recovery program exists



Naturvårdsverket | Swedish Environmental Protection Agency

PSG Slide 5 G-BIKE Applying two Hoban et al. indicators

#### cases from Sweden (contin.)



Photo: © David Simcox



- The large blue Maculinea arion NT
  - (1) the conservative N<sub>e</sub>/N<sub>c</sub> "0.1 rule" ⇒ census size 5000 (meta)populations sizes 2020: ⇒ total (7500 12500) 2 x 5000
    (2) % of metapopulations: 77%; decreasing, recovery program exists





#### cases from Sweden (contin.)



Photo: © Per Sjögren-Gulve

• The pool frog (*Pelophylax lessonae*) VU

(1) the conservative  $N_e/N_c$  "0.1 rule"

 $\Rightarrow$  census size 5000

census estimate from year 2020:

⇒ (3000-9000) 100+4900

(2) Metapopulation  $\Rightarrow$  local extinctions and recolonizations, 100% distinct metapop.s remain, recovery program exists.



PSG Slide 7

## GOBINE Applying two Hoban et al. indicators

#### cases from Sweden (contin.)



Photo: © Kimmo Pöri

• The wolverine Gulo gulo VU

(1) the conservative  $N_e/N_c$  "0.1 rule"



⇒ census size 5000

- − genomic & simulation studies:  $N_e/N_c = 0.248 \Rightarrow$  census size = 2018
- − (meta)population size year 2019 (SE+NO+FI):  $\Rightarrow$  total N<sub>c</sub> = 1398

(2) 100% of populations remain, increasing, management plans exist

Increased genetic monitoring + co-management btw countries.


## PSO GOBINE Applying two Hoban et al. indicators



- (1) the conservative  $N_e/N_c$  "0.1 rule"  $N_e$  500  $\Rightarrow$  census size 5000
- − from genetic linkage disequilibrium  $\Rightarrow$  N<sub>e</sub> = 16, 32, 38, 68 and 81
- (2) 100% of breeds/populations remain, management plans exist.



## PSG Slide 9 G-BIKE Applying two Hoban et al. indicators

## The handful cases of wild species from Sweden

Taxon	# N <sub>e</sub> > 500 (i.e, N <sub>c</sub> > 5000)	# N <sub>e</sub> < 500	Remain. pop.
Lopinga butterfly	2 pop. (100%)	0 pop.	100%
Maculinea butterfly	2 pop. (40%)	3 pop. (60%)	77%
Pelophylax frog	0 pop. (0%)	2 pop.	100%
Gulo wolverine	0 pop. (0%)	1 transboundary population	100%

(1)  $N_e$  indicator =  $\frac{N_e > 500}{N_e < 500}$  = (100%+40%+0%+0%)/4 = **35%** (mean) at the species level

(2) Remaining distinct populations within species: average = **94%** 

Noting: Sweden has 202 RE and 219 CR species with  $N_e$ < 500



## PSG Slide 10 G-BIKE Applying two Hoban et al. indicators

- Test during 2021 by the Swedish Species Information Centre:
  - 21 740 species were assessed for the Swedish 2020 redlist
  - 654 of them were Data Deficient (DD)
  - 21 086 species (EX+RE+CR+EN+VU+NT+LC) from 25 taxonomic categories
  - To how many of these species from which organism groups can the Hoban et al. (2020) indicators (1) and (2) be applied to assess whether  $N_c > 5000 (N_e > 500)$  OR  $N_c < 5000 (N_e < 500)$  and the proportion of remaining genetically distinct populations ?
  - Prel.: more detailed test for certain organism groups
  - Reporting before the end of 2021.



PSG Slide 11



Thank you!

Contact: per.sgulve@gmail.com

