
A photograph of a forest path with people walking away, overlaid with a dark text box. The forest has tall, thin trees and a ground covered in fallen leaves. The text box is in the upper right corner.

"Improving ex situ gene conservation: using DNA and simple, affordable proxy metrics."

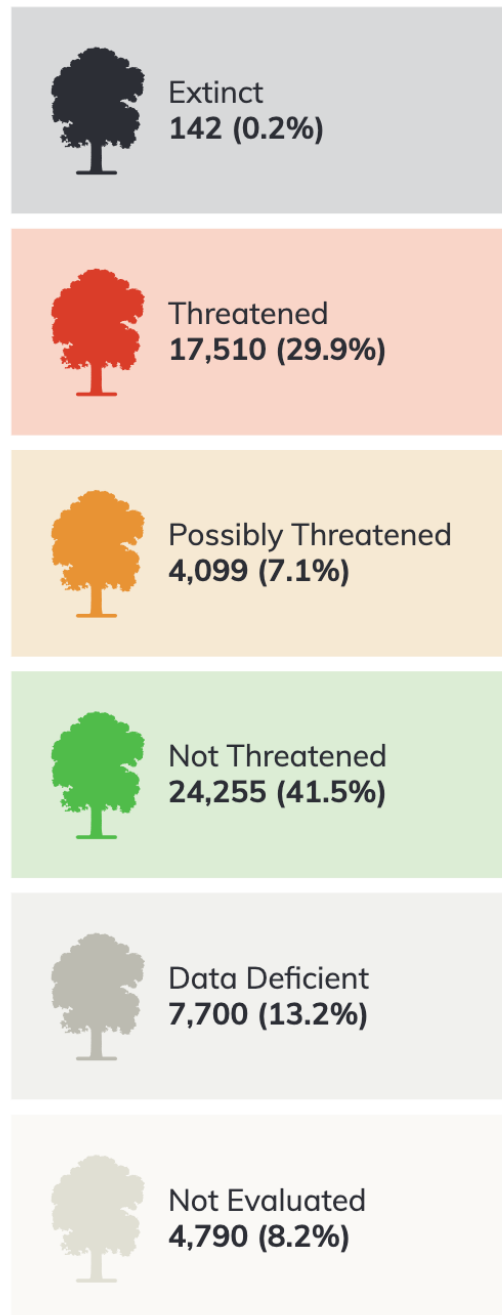
Sean Hoban
The Morton Arboretum
Twitter: [@seanmhoban](#)
Web: www.hobanlab.com

A photograph of a forest path. The path is covered in fallen brown leaves. Several people are walking away from the camera down the path. The trees are tall and thin, with some moss on their trunks. The lighting is soft, suggesting an overcast day or late afternoon. The overall scene is peaceful and natural.

The Morton Arboretum is located on ancestral homelands of the Council of Three Fires—Ojibwe, Odawa, and Potawatomi—and many other tribes that resided on or migrated through this land for generations, including the Illinois, Miami, Sauk, Fox, Kickapoo, and Dakota. I acknowledge and respect the traditional caretakers of this land and their ways of knowing



Number of species





“The global botanic garden and arboretum community is the single strongest force for plant conservation in the world”
-Paul Smith, BGCI

3000 botanic gardens reach >100 million people per year. Mission: contribute to science, education, and conservation, **solving global challenges**



THE
CHAMPION
of TREES



American
Public Gardens
Association



**BOTANIC
GARDENS**
CONSERVATION
INTERNATIONAL



CENTER FOR PLANT
CONSERVATION

The Morton Arboretum

- Educate and inspire... 1 million visitors + 30,000 students / year
- Training, policy work, tree care... in 200+ communities
- Groundbreaking plant science... evolution, community ecology, climate forecasting, soil and root biology, arboriculture
- Tree breeding... selection, improvement, cultivar release
- Science communication & global conservation action



Provide knowledge and tools for conservation

- Gene conservation in situ and ex situ
- Metrics for conservation progress & priorities
- Connect genetic diversity to conservation policy
- Plant health and disease



Emma Spence, Bethany Zumwalde, Bailie Munoz, Alissa Brown, Emily Schumacher, Austin Koontz, Loren Ladd, Kaylee Rosenberger

CONSERVATION THROUGH COLLABORATION: ENSURING GENETIC DIVERSITY IN GARDEN COLLECTIONS

Genetic diversity is central to conservation objectives. Gardens need clear frameworks, tools, and metrics to make progress towards this goal. In this article we show how to measure genetic diversity in collections, why more wild-sourced accessions are needed to meet targets, and why we **MUST** coordinate our efforts.

Working towards the achievement of GSPC Targets 8 and 9.

Target 8:

At least 75 per cent of threatened plant species in *ex situ* collections, preferably in the country of origin, and at least 20 per cent available for recovery and restoration programmes.

Target 9:

70 per cent of the genetic diversity of crops including their wild relatives and other socio-economically valuable plant species conserved, while respecting, preserving and maintaining associated indigenous and local knowledge.

TOWARD THE METACOLLECTION: Coordinating conservation collections to safeguard plant diversity

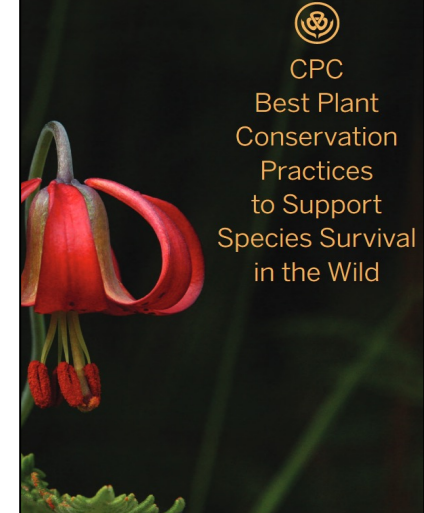


Do we have the space?

The challenge of these Targets is to *strive for high genetic diversity in well-managed collections that are useful for conservation purposes*. This is a real challenge, but the network of thousands of botanical gardens worldwide -- millions of accessions -- can achieve this goal, especially if we work together (Figure 1). Botanical gardens, collections have the capacity, the horticultural and ecological expertise, and the amb

Why genetic diversity?

Genetic diversity is critical for a species to thrive. It helps plants avoid inbreeding, better adapt to environmental change, and better resist pests and diseases. Genetic diversity underlies resilient ecosystems and food security. Keeping high genetic diversity within botanical gardens preserves this critical potential for the future. Genetic diversity also helps show the public the remarkable



Resumen ejecutivo

Febrero 2021

¿Cómo informan los países al Convenio sobre la Diversidad Biológica sobre la diversidad genética y cómo mejorar los informes y el seguimiento de la diversidad genética?

CONTEXTO

- La **biodiversidad** se enfrenta a una amplia gama de presiones, incluidas la degradación del hábitat, el cambio climático, la contaminación y los patógenos de rápida propagación. La diversidad genética intraespecífica es esencial para determinar la capacidad de una población para adaptarse y persistir en respuesta a un entorno cambiante. La diversidad genética es uno de los tres niveles de biodiversidad reconocidos por el Convenio sobre la Diversidad Biológica (CDB) y por otras políticas de conservación nacionales e internacionales.
- **Sin embargo**, las estimaciones del estado y de las tendencias de la diversidad genética siguen sin integrarse de forma rutinaria en los programas de conservación o en los objetivos de la biodiversidad. Esto puede explicarse en parte por la naturaleza técnica de los enfoques genéticos y la desconexión entre la investigación genética y los profesionales de la conservación. Además, se considera la falta de indicadores robustos como una brecha de datos clave que requiere subsanación en el marco global de biodiversidad post-2020.
- **Para comprender cómo** los países signatarios del CDB evalúan y protegen la diversidad genética, hemos realizado una revisión exhaustiva de 114 informes nacionales (quintos y sextos informes). Hemos determinado cómo los países informaron sobre acciones, usos, amenazas, tendencias y especies prioritarias en relación al monitoreo y a la conservación de la diversidad genética.

RECOMENDACIONES

Nuestras recomendaciones para la Secretaría del CDB y para los países signatarios tienen como objetivo mejorar el monitoreo y la protección de la diversidad genética para permitir la persistencia de poblaciones y ecosistemas saludables a largo plazo, cumpliendo con el objetivo central del CDB.

1

Aumentar la conciencia y el conocimiento del papel central que juega la diversidad genética en la biodiversidad, proteger y documentar los conocimientos indígenas y locales, y desarrollar la capacidad de los profesionales de la conservación para monitorear y gestionar la diversidad

RESULTADOS PRINCIPALES

- Aunque la mayoría de los países reconocen la importancia de la diversidad genética, el 21% de los Sextos Informes Nacionales no se refirió a ningún objetivo de diversidad genética.
- Solo el 5% de los países reportaron indicadores basados en estudios genéticos o en la protección del conocimiento indígena y local de la diversidad genética.
- Las acciones para conservar la diversidad genética se centraron principalmente en especies agrícolas (cultivos, animales de granja y parientes silvestres de cultivos) en vez de en especies silvestres.

Challenge: conserve options

We need to safeguard genetic, trait, ecological diversity from across species' native distribution

We have limited time, money, resources, space

Tools for the ex situ community to assess and report on our progress

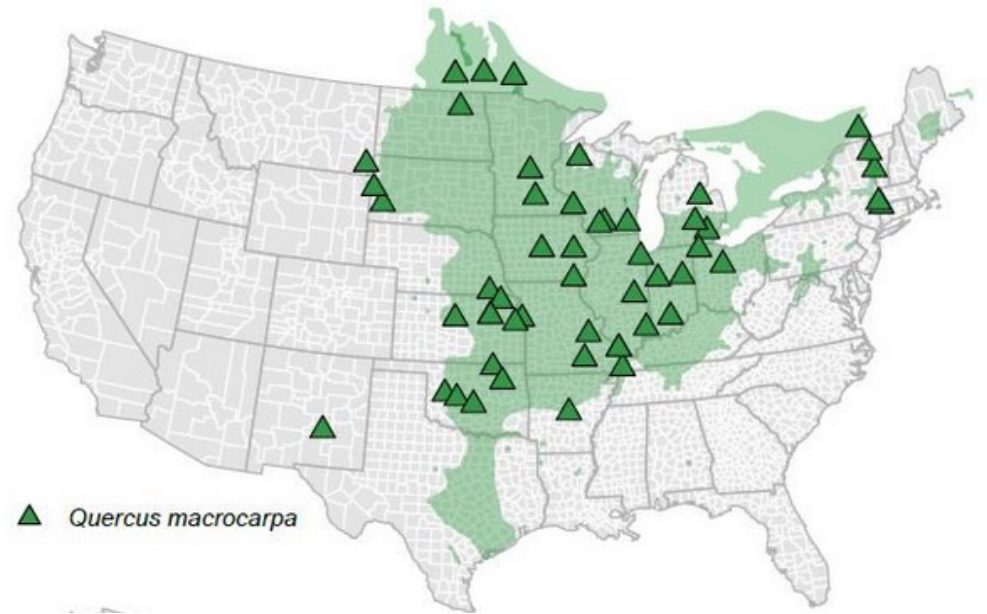


Optimum sampling strategies in genetic conservation

D. R. MARSHALL & A. H. D. BROWN (1975)

There are definite limits to the numbers of samples which can be handled effectively in programmes for the conservation and utilisation of crop genetic resources. These limits are imposed by the financial and personnel resources available to carry out each stage in the process:





Today's talk

1. Context: Genetic diversity and the CBD Kunming Montreal Global Biodiversity Framework
2. Looking back: How have countries reported on their genetic diversity to the CBD, in the past?
3. Looking forward: Tools to assess genetic diversity
 - DNA based studies
 - Simulations
 - Gap analysis
 - Effective size?

The Kunming Montreal Global Biodiversity Framework

The Kunming Montreal Global Biodiversity Framework

- Global treaty among 196 Parties (195 countries plus EU, all UN states except Vatican and USA)
- Created in 1992, in force since 1993
- Commits to
 - Conservation
 - Sustainable use
 - Fair and equitable sharing of benefits
- Requires periodic reporting on state of biodiversity
- *Strategic Plan for Biodiversity 2011-2020*, including the Aichi Biodiversity Targets.



The Kunming Montreal Global Biodiversity Framework

2050 Vision: a world of living in harmony with nature where... biodiversity is valued, conserved, restored and wisely used, maintaining ecosystem services, sustaining a **healthy planet and delivering benefits essential for all people.**

Goal A: ... genetic diversity within populations of wild and domesticated species, is maintained, safeguarding their adaptive potential

Target 4: ... to 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 and sustainable management practices...



Target 4 is our focus today but genetic diversity is relevant to other Targets

- 1 (spatial planning)
- 2 (effective restoration)
- 3 (30% area in effectively governed Pas, OECMs)
- 6 (invasive species)
- 9 (sustainable use of wild species)
- 10 (sustainable fisheries, forestry, agriculture)
- 11 (ecosystem services)

KM GBF Target 4: ... to 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 and sustainable management practices...

- **to maintain and restore the genetic diversity** (do not lose, but *also* perform actions to benefit – connectivity, supplementation)
- **within and between populations** (inbreeding and speed of adaptation, breadth across environments)
- **native, wild and domesticated species** (all native species)
- **maintain adaptive potential** (emphasizes changing environment)

The Kunming Montreal Global Biodiversity Framework

Zero draft Goal A:





















Genetic diversity is maintained or enhanced on average by 2030, and for [90%] of species by 2050



KM GBF Target 4:

... to 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 and sustainable management practices...

Genetic diversity goals and targets have improved, but remain insufficient for clear implementation of the post-2020 global biodiversity framework

Sean Hoban^{1,2}  · Michael W. Bruford³  · Jessica M. da Silva^{4,29}  · W. Chris Funk⁵  · Richard Frankham⁶  · Michael J. Gill⁷  · Catherine E. Grueber⁸  · Myriam Heuertz⁹  · Margaret E. Hunter¹⁰  · Francine Kershaw¹¹  · Robert C. Lacy¹²  · Caroline Lees¹³  · Margarida Lopes-Fernandes¹⁴ · Anna J. MacDonald¹⁵  · Alicia Mastretta-Yanes^{16,17}  · Philip J. K. McGowan¹⁸  · Mariah H. Meek¹⁹  · Joachim Mergeay²⁰  · Katie L. Millette²¹  · Cinnamon S. Mittan-Moreau²²  · Laetitia M. Navarro²³  · David O'Brien²⁴  · Rob Ogden²⁵  · Gernot Segelbacher²⁶  · Ivan Paz-Vinas⁵  · Cristiano Vernesi²⁷  · Linda Laikre²⁸ 




The Kunming Montreal Global Biodiversity Framework

- Scientific research and consensus (10+ papers)
- Policy briefs and webinars- to NFPs, and with CBD Secretariat

Practical application of indicators for genetic diversity in CBD post-2020 global biodiversity framework implementation

[Henrik Thurfjell](#)^a  , [Linda Laikre](#)^b, [Robert Ekblom](#)^c, [Sean Hoban](#)^d, [Per Sjögren-Gulve](#)^e

Global genetic diversity status and trends: towards a suite of Essential Biodiversity Variables (EBVs) for genetic composition

[Sean Hoban](#), [Frederick I. Archer](#), [Laura D. Bertola](#), [Jason G. Bragg](#), [Martin F. Breed](#), [Michael W. Bruford](#), [Melinda A. Coleman](#), [Robert Ekblom](#), [W. Chris Funk](#), [Catherine E. Grueber](#), [Brian K. Hand](#), [Rodolfo Jaffé](#), [Evelyn Jensen](#), [Jeremy S. Johnson](#), [Francine Kershaw](#), [Libby Liggins](#), [Anna J. MacDonald](#), [Joachim Mergeay](#), [Joshua M. Miller](#), [Frank Muller-Karger](#), [David O'Brien](#), [Ivan Paz-Vinas](#), [Kevin M. Potter](#), [Orly Razgour](#), [Cristiano Vernesi](#), [Margaret E. Hunter](#)  ... [See fewer authors](#) ^



Supporting Implementation of Post-2020 Global Biodiversity Framework



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 114 rapports nationaux (5èmes et 6èmes rapports). Nous avons identifié comment les pays ont rapporté les actions, utilisations, menaces, tendances et espèces prioritaires en lien avec le suivi et 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.

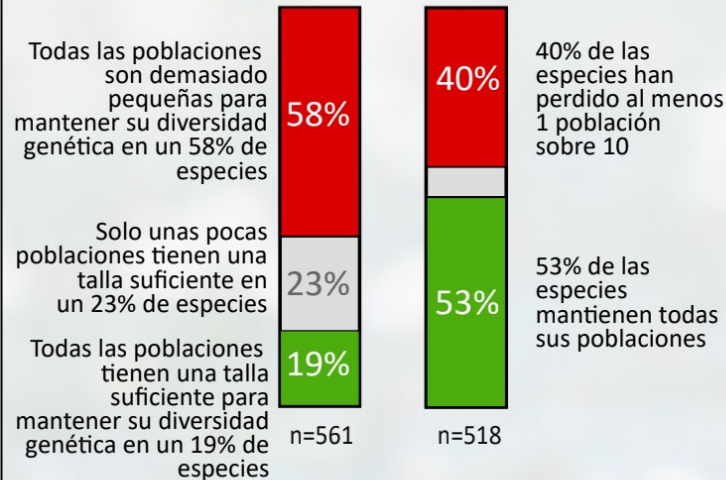
- 1 Promouvoir la sensibilisation et la connaissance du rôle central de la diversité génétique dans la

RÉSULTATS PRINCIPAUX

- Bien que la plupart des pays reconnaissent l'importance de la diversité génétique, 21% des 6èmes rapports nationaux ne faisaient pas référence à un objectif la concernant.
• Seuls 5% des pays ont rapporté des indicateurs basés sur des études génétiques ou sur la protection des connaissances autochtones et locales de la diversité génétique.

Indicador principal 4.A
% de poblaciones dentro de una especie con Ne>500

Indicador complementario
% de poblaciones que se mantienen



¿Cuáles son las necesidades de capacidad?

- El personal (idealmente con conocimiento en bases de datos de biodiversidad, informes nacionales, planes de gestión, etc.) compila y genera la información: alrededor de 400 horas para hacer 100 especies.
• Si se coordina con los esfuerzos de la Lista Roja, este tiempo puede reducirse considerablemente.



JUNE 2022

MONITORING

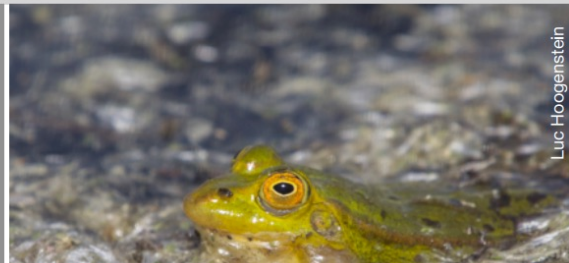
Briefing Note for the Monitoring Framework of the Post-2020 Global Biodiversity Framework

生物多様性条約におけるポスト 2020年生物多様性グローバル枠組のための遺伝的多様性に関するターゲットと指標の提案 政策概要

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

概要

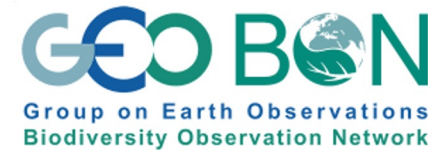
ポスト2020年生物多様性枠組における遺伝的多様性（指標）評価のための遺伝的多様性目標や測定基準は、かけがえのない生物多様性の喪失を防ぎ、生物多様性条約（CBD）のターゲットを達成するために改善されなければなりません。全ての種の遺伝的多様性は適切な測定基準...



Luc Hoogenstein

The Kunming Montreal Global Biodiversity Framework

- Submission of comments on the GBF drafts, SBSTTA
- Attendance in person at COP15, discussed with delegates
- Continuing to work with UNEP WCMC, AHTEG



Analysis of 114 National Reports to the CBD

Aichi Target 13

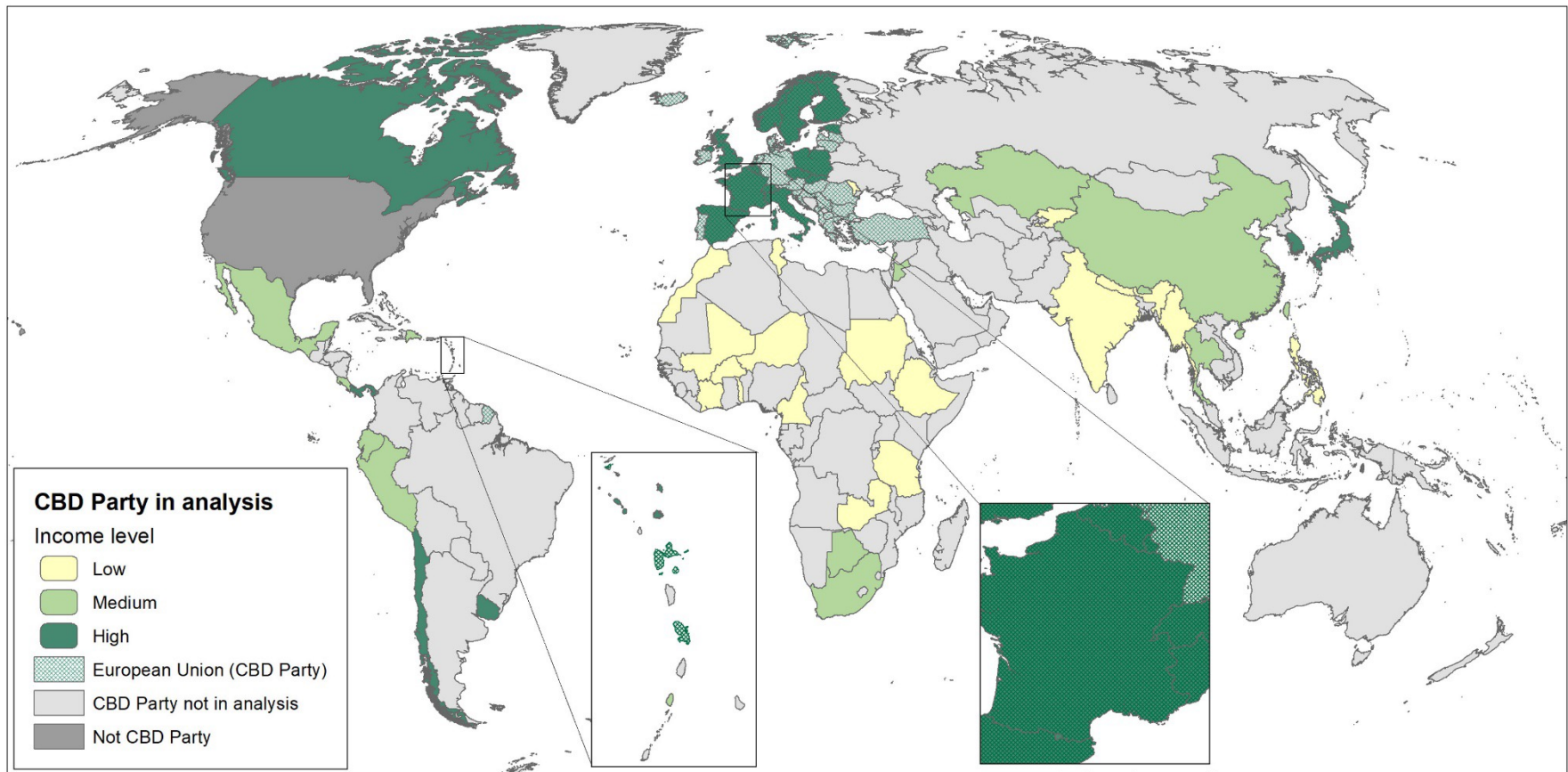
By 2020, the genetic diversity of cultivated plants and farmed and domesticated animals and of wild relatives, including other socio-economically as well as culturally valuable species, is maintained,

and strategies have been developed and implemented

for minimizing genetic erosion and safeguarding their genetic diversity.

Analysis of 114 National Reports to the CBD

- National reports are the means of reporting to the CBD; obligated every 4 years
- We assessed the content of National Reports submitted by 57 countries in 2014 and 2018 – the two most recent cycles of reporting
- Selected countries represent varying income levels, geography, biodiversity, and primary language



Analysis of 114 National Reports to the CBD

- We assessed genetic diversity with respect to biodiversity *status, threats, actions, obstacles, and progress towards targets*
- Caveat: NRs are summaries; some conservation actions or knowledge in a country may not be included due to limited time, space, knowledge, capacity or access to data by the report writers

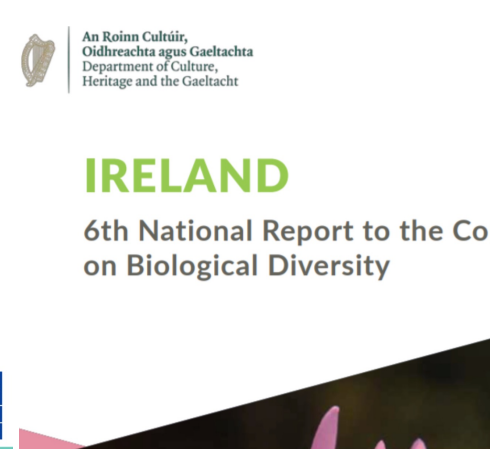
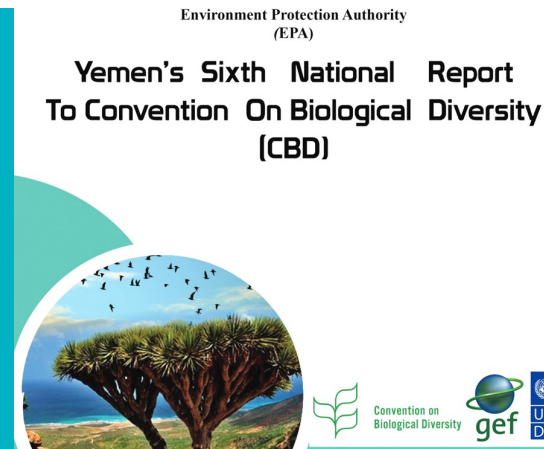


Genetic diversity is considered important but interpreted narrowly in country reports to the Convention on Biological Diversity: Current actions and indicators are insufficient

[Sean Hoban](#)^{a y1}  , [Catriona D. Campbell](#)^{b1} , [Jessica M. da Silva](#)^{c d1} ,
[Robert Ekblom](#)^{e y1} , [W. Chris Funk](#)^{f y1} , [Brittany A. Garner](#)^{g1} , [José A. Godoy](#)^{h1} ,
[Francine Kershaw](#)ⁱ¹ , [Anna J. MacDonald](#)^{b j y1} , [Joachim Mergeay](#)^{k l y1} ,
[Melissa Minter](#)^{m1} , [David O'Brien](#)ⁿ¹ , [Ivan Paz Vinas](#)^{o p1} , [Sarah K. Pearson](#)^{q1} ,
[Sílvia Pérez-Espona](#)^{r s y1} , [Kevin M. Potter](#)^{t1} , [Isa-Rita M. Russo](#)^{u y1} ,
[Gernot Segelbacher](#)^{v y1} , [Cristiano Vernesi](#)^{w y1} , [Margaret E. Hunter](#)^{x y1} 

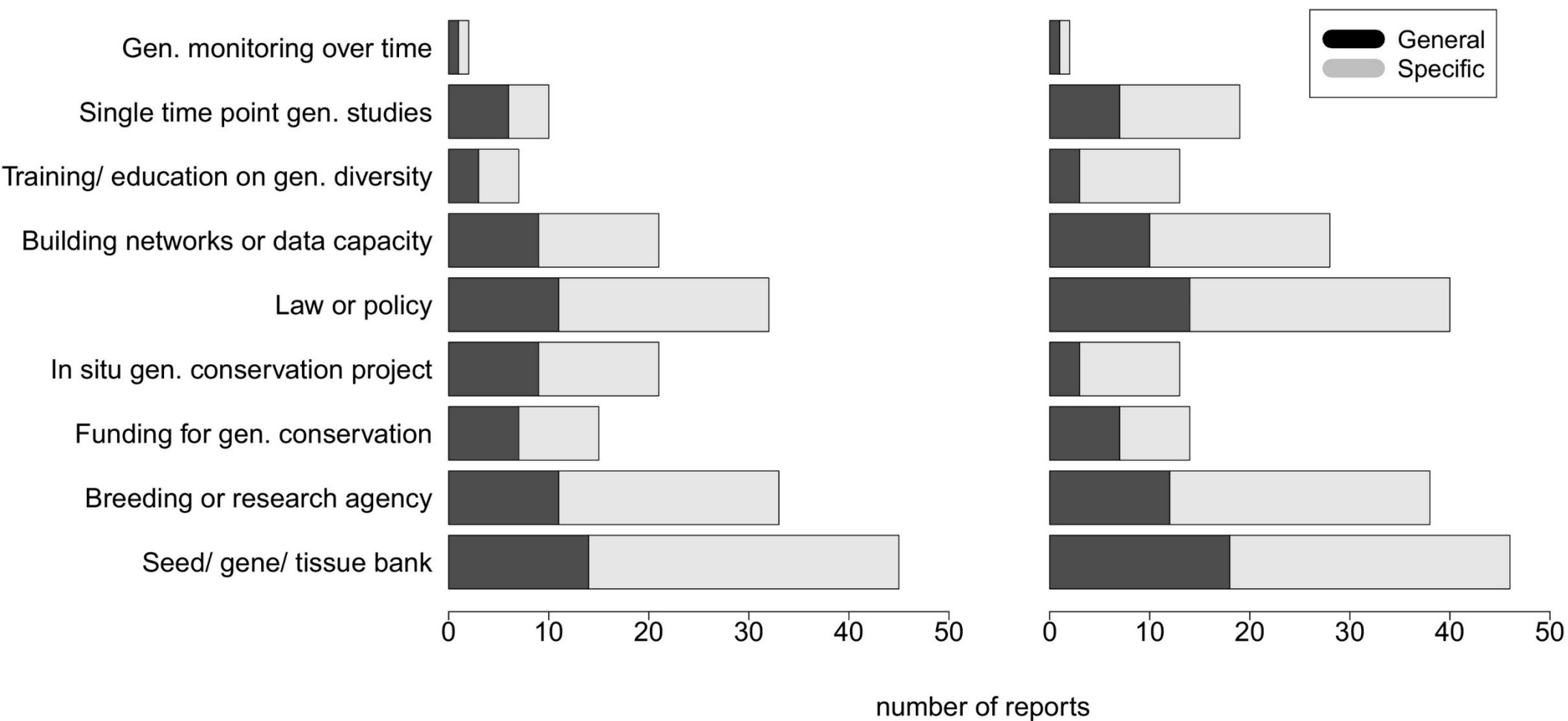
Analysis of 114 National Reports to the CBD

- **Countries noted the value of genetic diversity** for resilience to environmental or climate change, productivity in agriculture/ forestry/ fisheries, developing new varieties
- 70% and 79% of countries had a national-level genetic diversity target in the 5th and 6th NRs (**thus 21-30% lacked such a target**)
- 13% of countries reported on **strategies for minimizing genetic erosion**, even though Aichi Target 13 called for such strategies



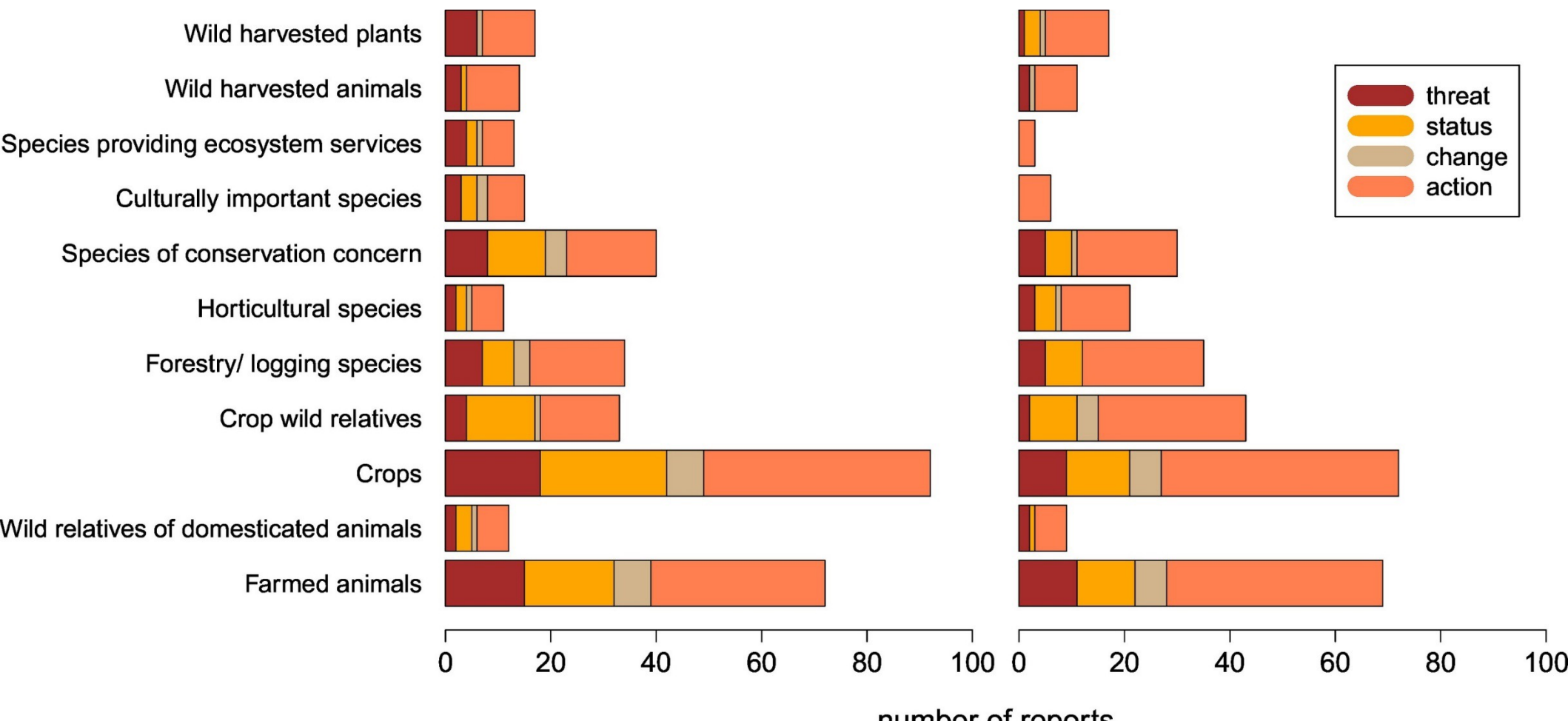
Analysis of 114 National Reports to the CBD

- Common genetic diversity actions related to seed banks, research agencies or breeding programs, and laws or policies (all ex situ)
- Genetic studies, genetic monitoring, training were rarely mentioned



Analysis of 114 National Reports to the CBD

- When genetic diversity was mentioned regarding specific species we categorized the text as relating to action, threat, status or change
- Neglected species included wild harvested species, species providing cultural value or ecosystem services, and horticultural species



Analysis of 114 National Reports to the CBD

We conclude that in reporting to the CBD- the largest and most comprehensive instrument for directing biodiversity conservation globally- Parties focused on a small set of genetic diversity conservation actions, a biased subset of species, and insufficient indicators or genetic monitoring programs.

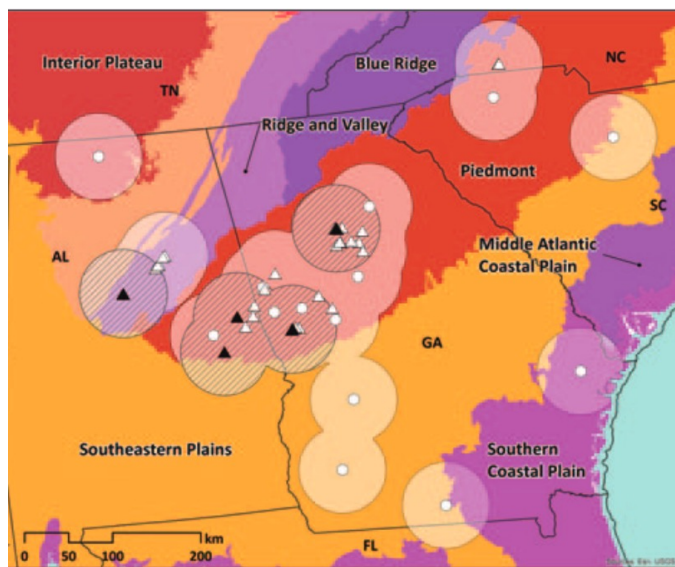
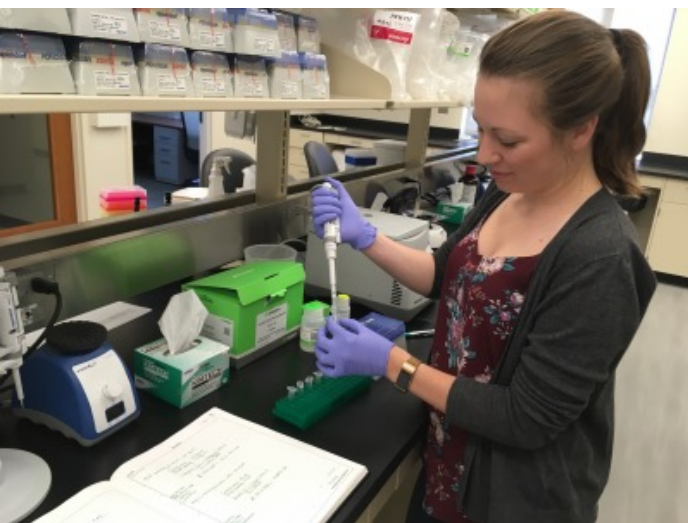
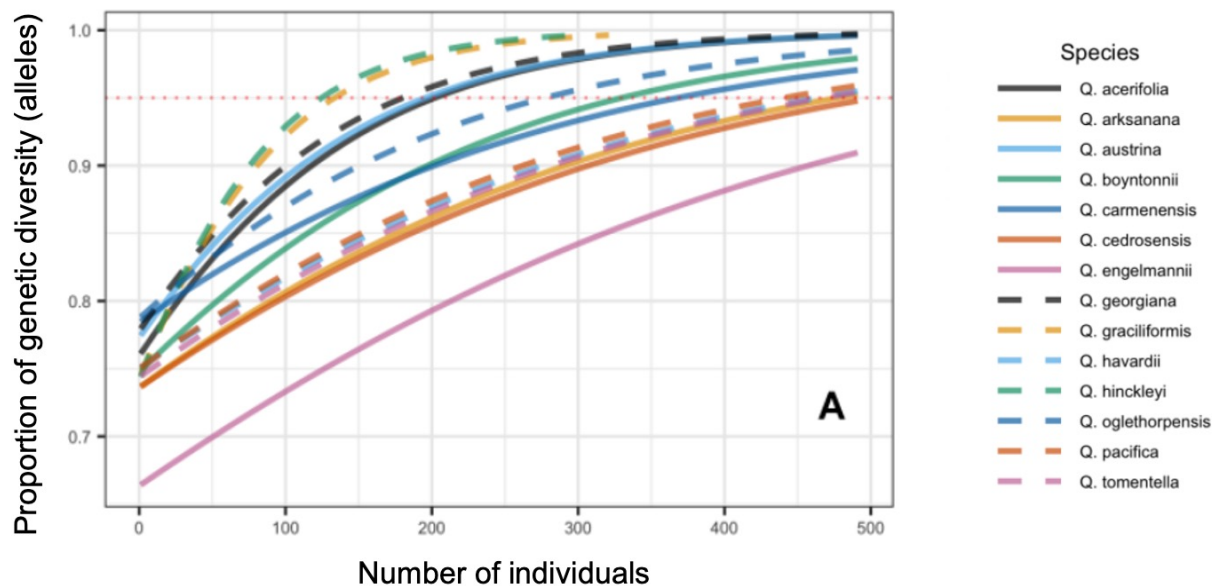
- Report on genetic diversity in all species (can focus on subsets)
- Report on genetic studies, genetic knowledge, in situ/ ex situ links, local knowledge/ use of genetic diversity
- Improved Glossary for terms relating to genetic diversity; foster communication and collaboration across science-policy
- Develop national strategies on genetic diversity



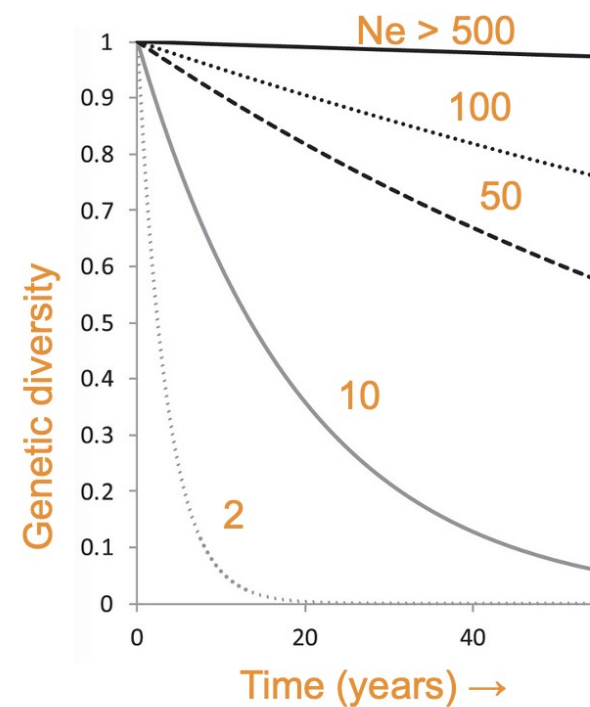
Assessing genetic diversity ex situ

Assessing genetic diversity ex situ

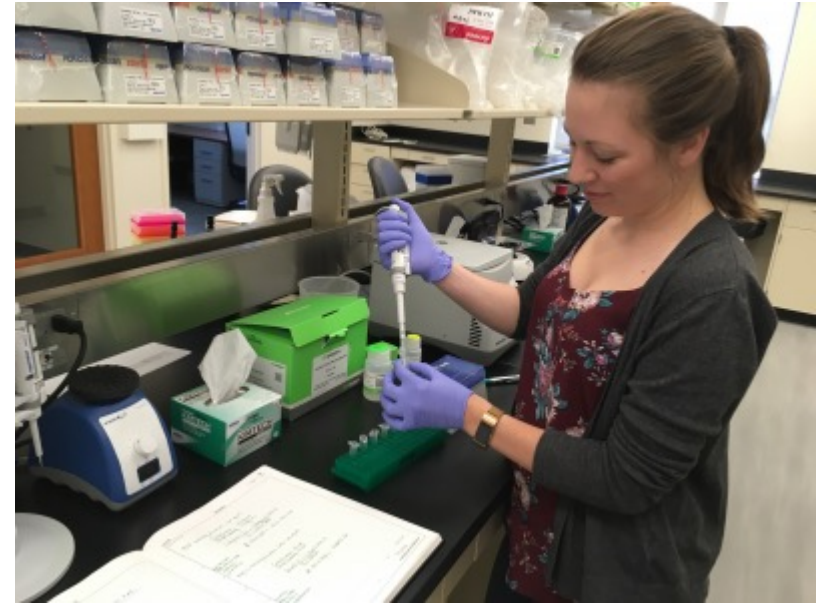
1. DNA based studies
2. Simulations
3. Gap analysis
4. Effective population size



- ▲ Wild provenance source of ex situ living specimen
- △ Geolocated native occurrence record
- County centroid native occurrence record



Assessing genetic diversity ex situ



Assessing genetic diversity ex situ




Species	Number Plants
<i>P. ekmanii</i>	93
<i>P. sargentii</i>	99
<i>Z. decumbens</i>	205
<i>Z. lucayana</i>	244
<i>Q. georgiana</i>	36
<i>Q. oglethorpensis</i>	145
<i>Q. boyntonii</i>	77
<i>H. waimeae</i>	16
<i>H. hanneriae</i>	43
<i>M. pyramidata</i>	40
<i>M. asheii</i>	14

11 taxa in 5 genera
Palms, cycads, oaks,
magnolias, hibiscus

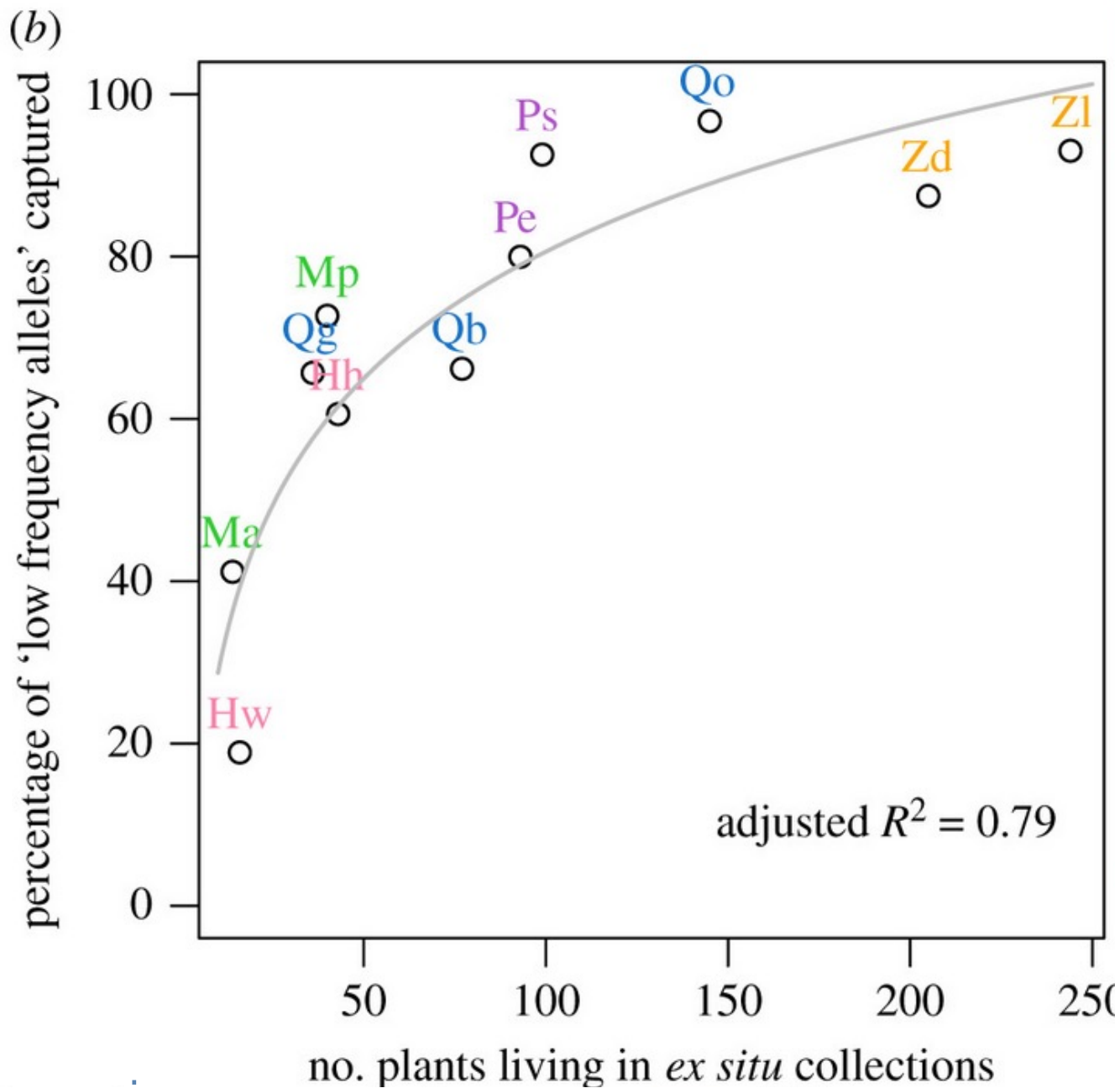
Assessing genetic diversity ex situ

Species	Number Plants	Genetic Diversity
P. ekmanii	93	0.88
P. sargentii	99	0.95
Z. decumbens	205	0.85
Z. lucayana	244	0.95
Q. georgiana	36	0.73
Q. oglethorpensis	145	0.94
Q. boyntonii	77	0.70
H. waimeae	16	0.40
H. hannerae	43	0.69
M. pyramidata	40	0.80
M. asheii	14	0.79

Assessing genetic diversity ex situ

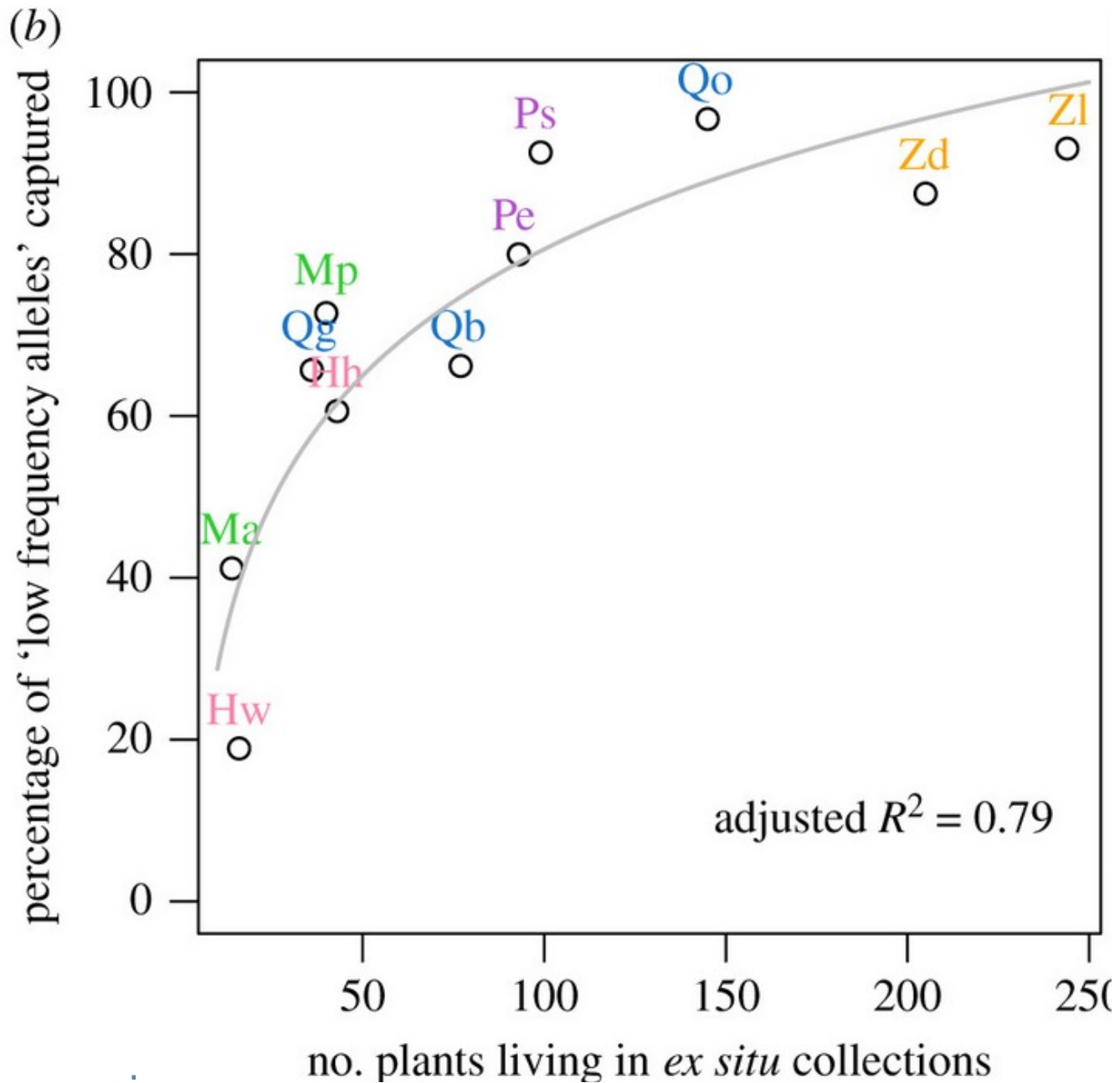
Species	Number Plants	Genetic Diversity	Gold standard
P. ekmanii	93	0.88	
P. sargentii	99	0.95	
Z. decumbens	205	0.85	
Z. lucayana	244	0.95	
Q. georgiana	36	0.73	
Q. oglethorpensis	145	0.94	
Q. boyntonii	77	0.70	
H. waimeae	16	0.40	
H. hanneriae	43	0.69	
M. pyramidata	40	0.80	
M. asheii	14	0.79	

Assessing genetic diversity ex situ



Hoban et al 2020
Proceedings B, "Taxonomic
similarity does not.."

100 to 200 plants?



Hoban et al 2020
Proceedings B, "Taxonomic
similarity does not.."

A multi use tool

- Relatedness- how related (inbred) are individuals
 - 74% of samples are full siblings
- Redundancy- is each allele or population “backed up” (still conserved if one is lost)
 - 95% of alleles in 2+ copies; 73% of alleles in 10+ copies
- Representation: each location
 - Three of four populations have 50+ samples ex situ, one population only has 6 samples all at one garden



Assessing genetic diversity ex situ with DNA

Main message:

- DNA studies can identify how much genetic diversity is conserved
- DNA studies can identify other aspects relevant to managing and enhancing a collection in the future



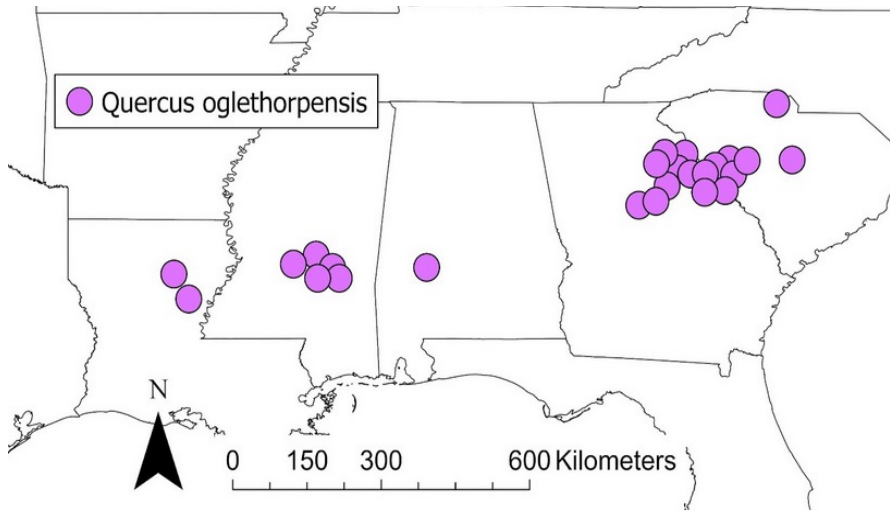
Improving collections with simulations

Improving collections with simulations

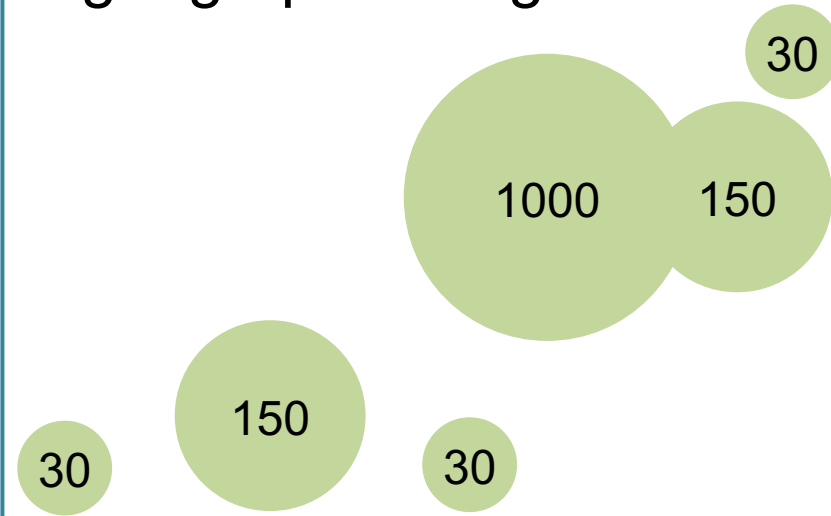
Novel approach: Use simulations to estimate minimum sample size needed

Improving collections with simulations

1. Species geographic ranges



2. Modeled geographic ranges



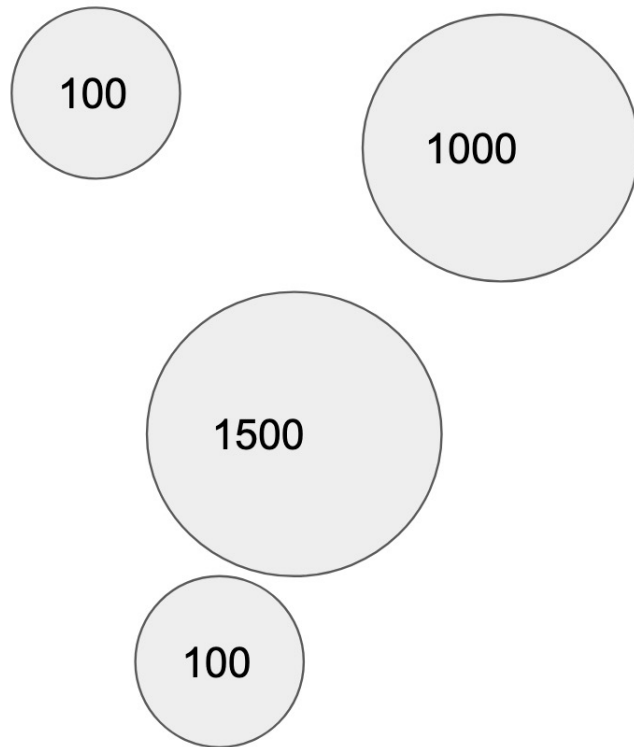
3. Simulated seed sampling



4. Evaluate how each sampling did

Improving collections with simulations

Model of species geographic range and demography

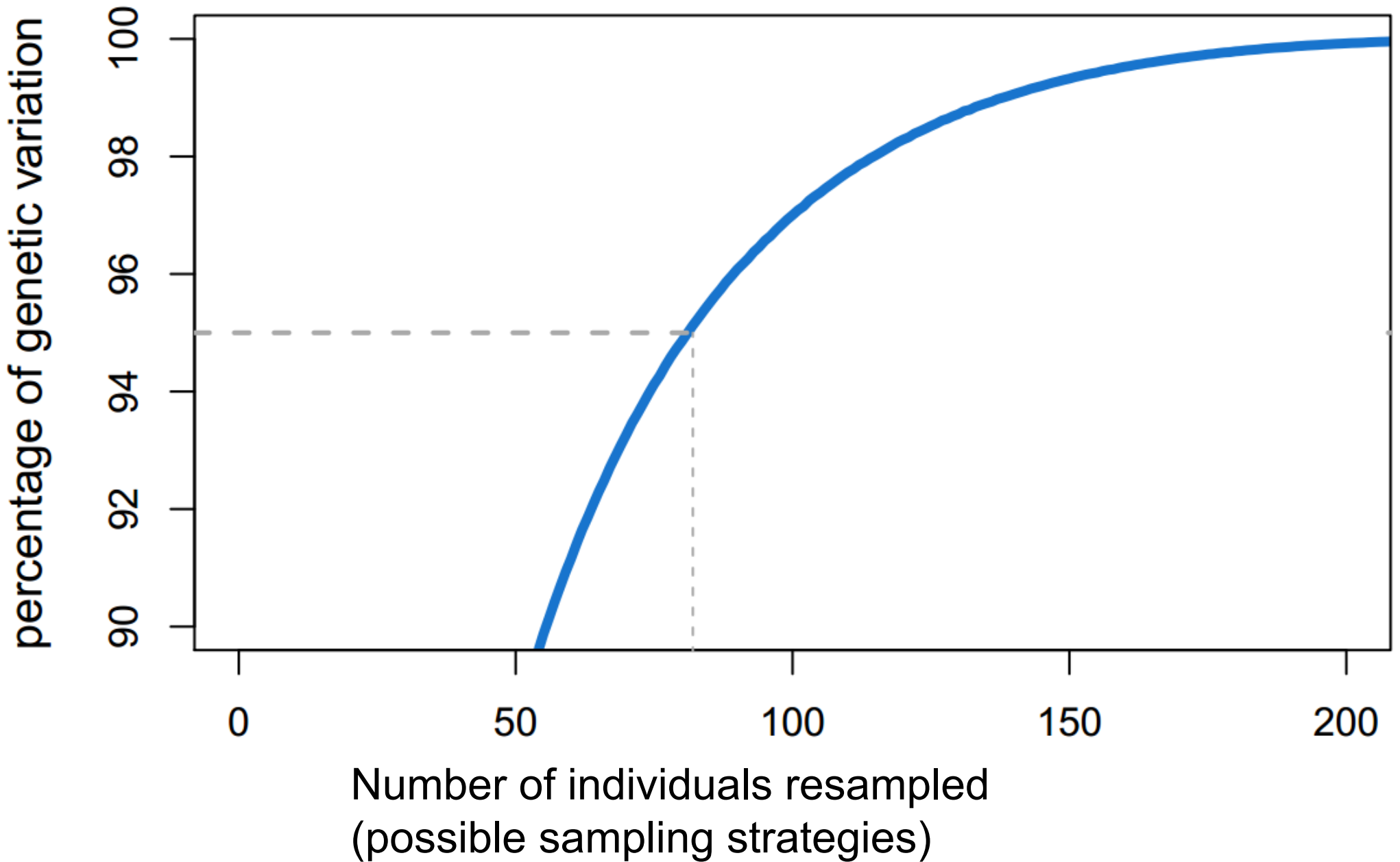


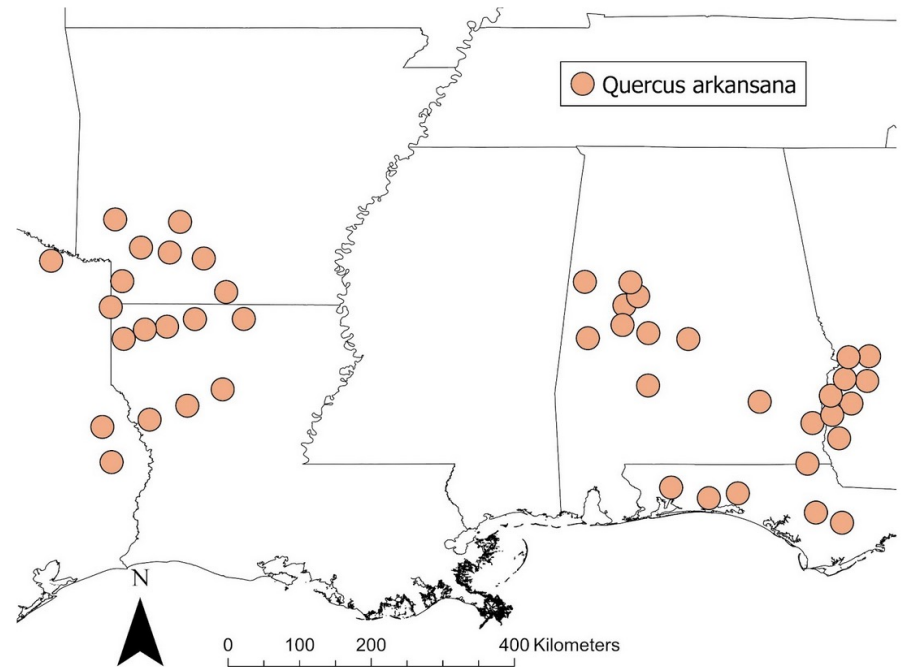
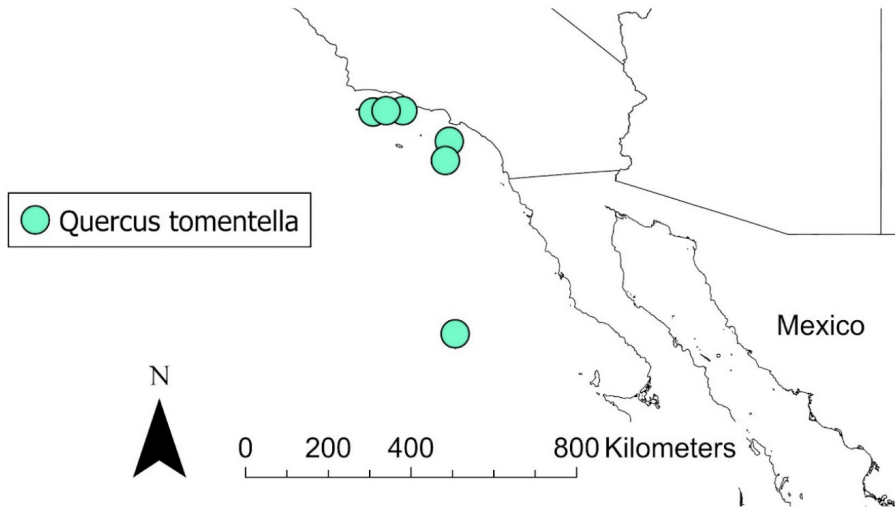
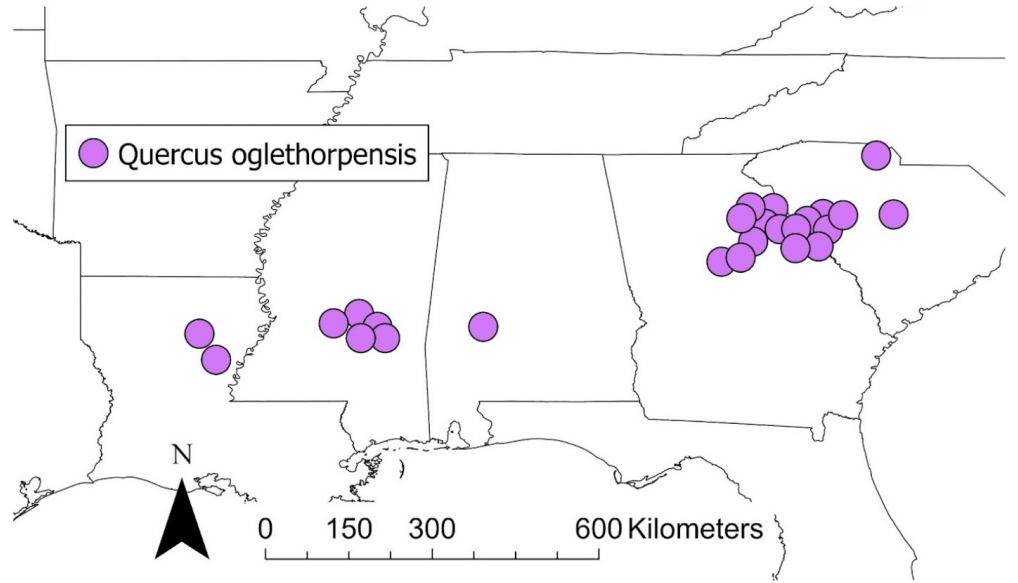
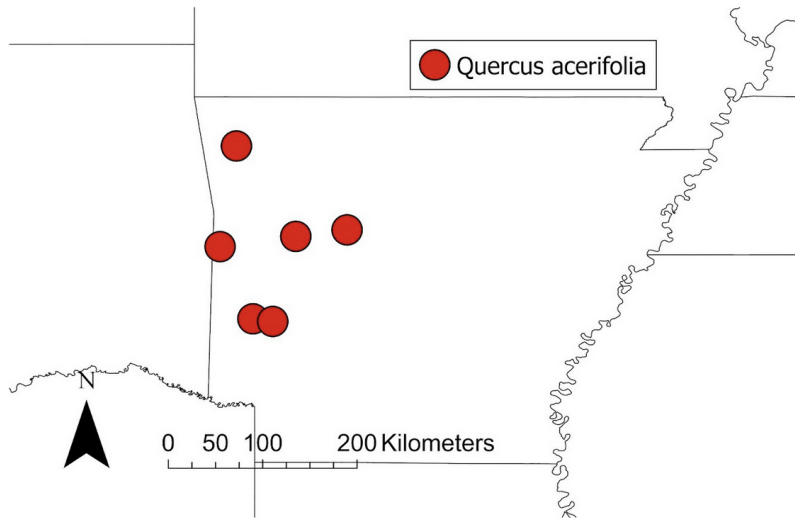
Simulate sampling from the range

Samples	Percent Gen Div in Sample
1	5
2	10
3	13
4	15
...	...
199	94.7
200	95
...	...
500	100

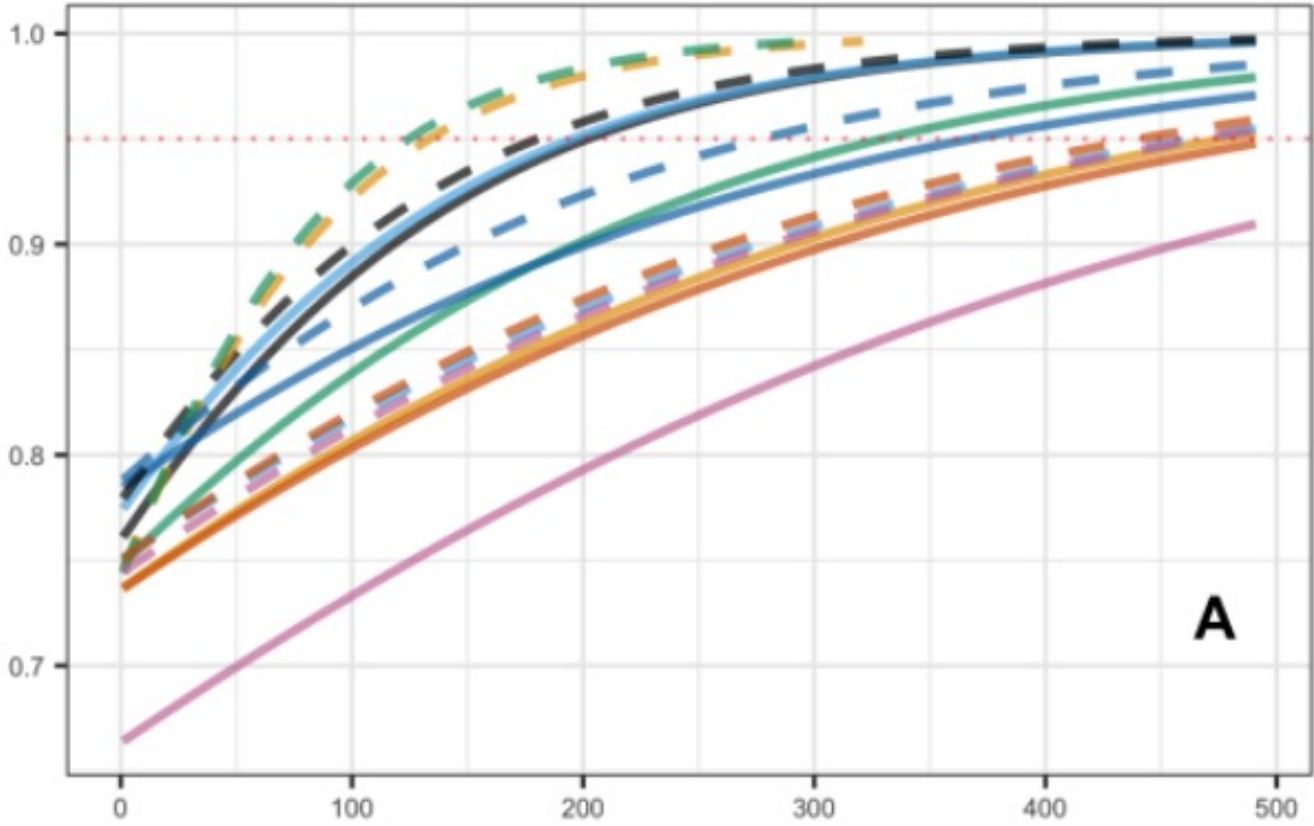
Minimum size →

Improving collections with simulations





Proportion of genetic diversity (alleles)



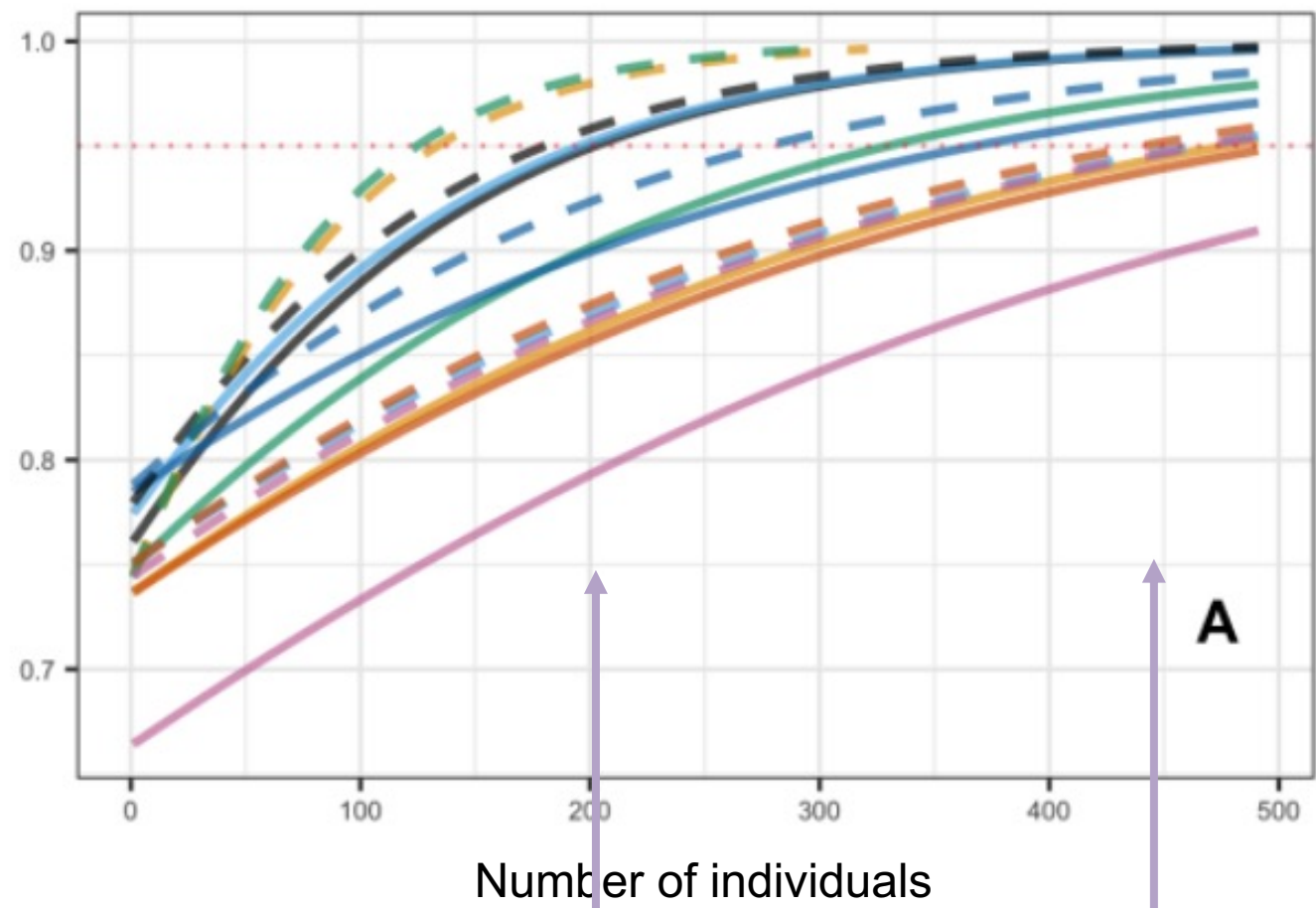
- Species
- Q. acerifolia
 - Q. arksanana
 - Q. austrina
 - Q. boyntonii
 - Q. carmenensis
 - Q. cedrosensis
 - Q. engelmannii
 - Q. georgiana
 - Q. graciliformis
 - Q. havardii
 - Q. hinckleyi
 - Q. oglethorpensis
 - Q. pacifica
 - Q. tomentella

Number of individuals



Rosenberger et al 2022,
Biological Conservation

Proportion of genetic diversity (alleles)



- Species
- Q. acerifolia
 - Q. arksanana
 - Q. austrina
 - Q. boyntonii
 - Q. carmenensis
 - Q. cedrosensis
 - Q. engelmannii
 - - Q. georgiana
 - Q. graciliformis
 - Q. havardii
 - Q. hinckleyi
 - Q. oglethorpensis
 - Q. pacifica
 - Q. tomentella

Most species it is 200 to 450
Minimum size from 125 to >500



Improving collections with simulations

- *Fraxinus excelsior*, European ash
- 2 million ash seed, 60+ sites
- Built a model at large & small scale



Step 1: Build demographic-genetic model on Forest Inventory data and desk study of ash tree biology. Check model parameters to ensure it produces realistic genetic datasets

Step 2: Run model to produce data files of distribution of trees and their genes in 1082 populations

Step 2: Choose 23 populations across the range and use their allele frequencies to start 23 local scale simulations

Step 3: Sample this *large scale dataset* with different spatial strategies (i.e. Fig 2) and number of populations (N_p) and trees (N_t)

Step 4: Calculate the proportion of genetic variation captured by each strategy

Sample	N_p	N_t	Prop GD
A	20	20	90%
B	20	5	70%
...			



Step 3: Sample each *local scale dataset* with different numbers of trees (N_t) and seeds (N_s)

Step 4: Calculate proportion of genetic variation captured by each strategy

Sample	N_t	N_s	Prop GD
A	20	20	90%
B	20	5	70%
...			

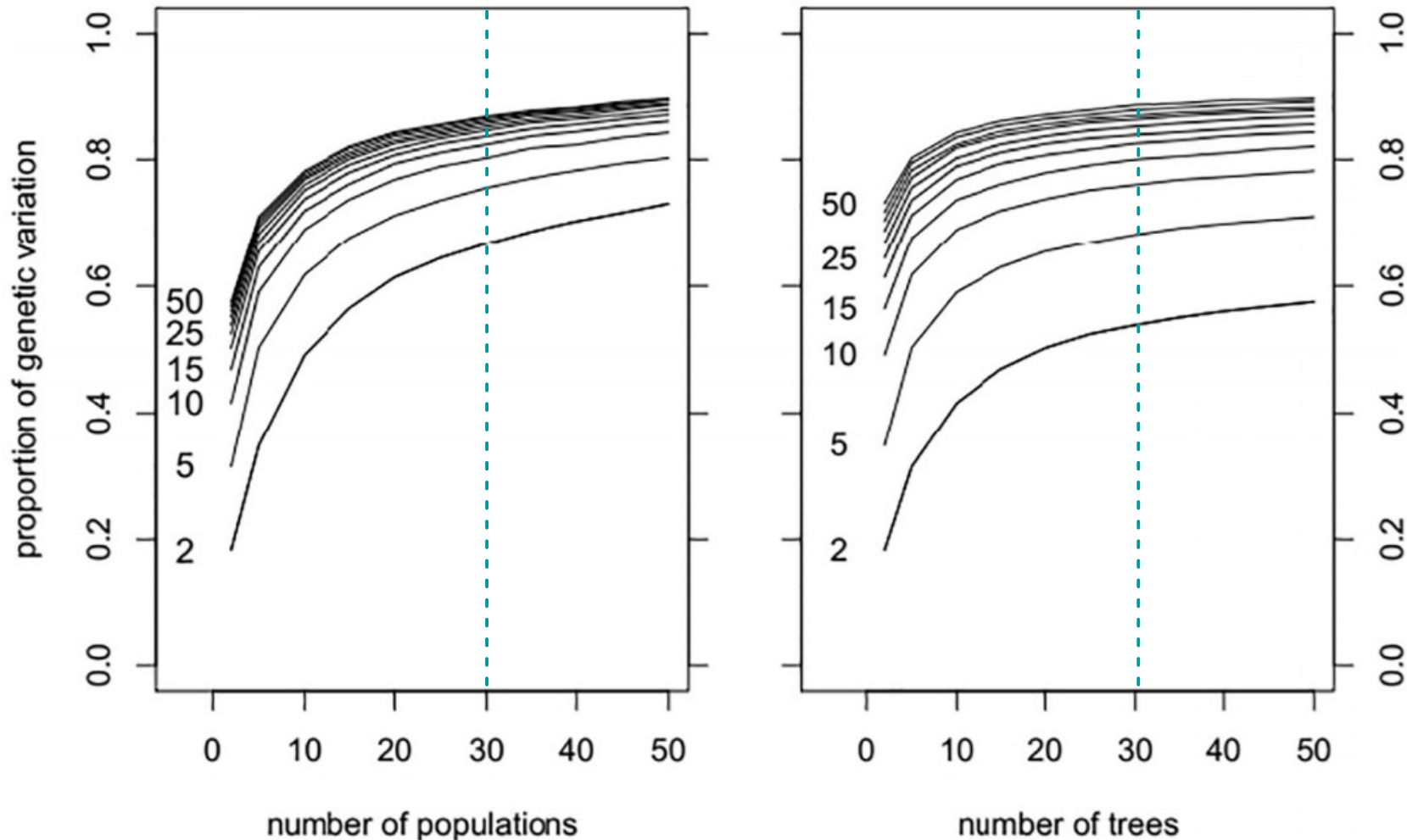


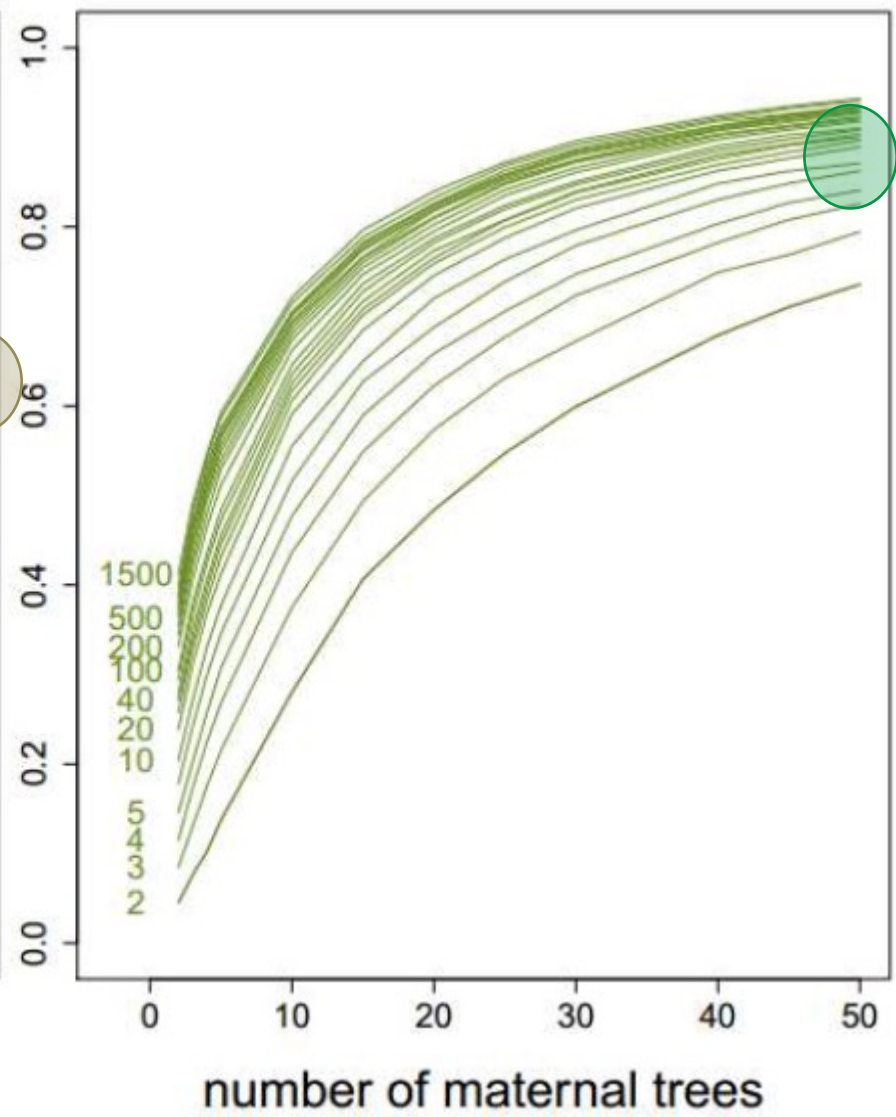
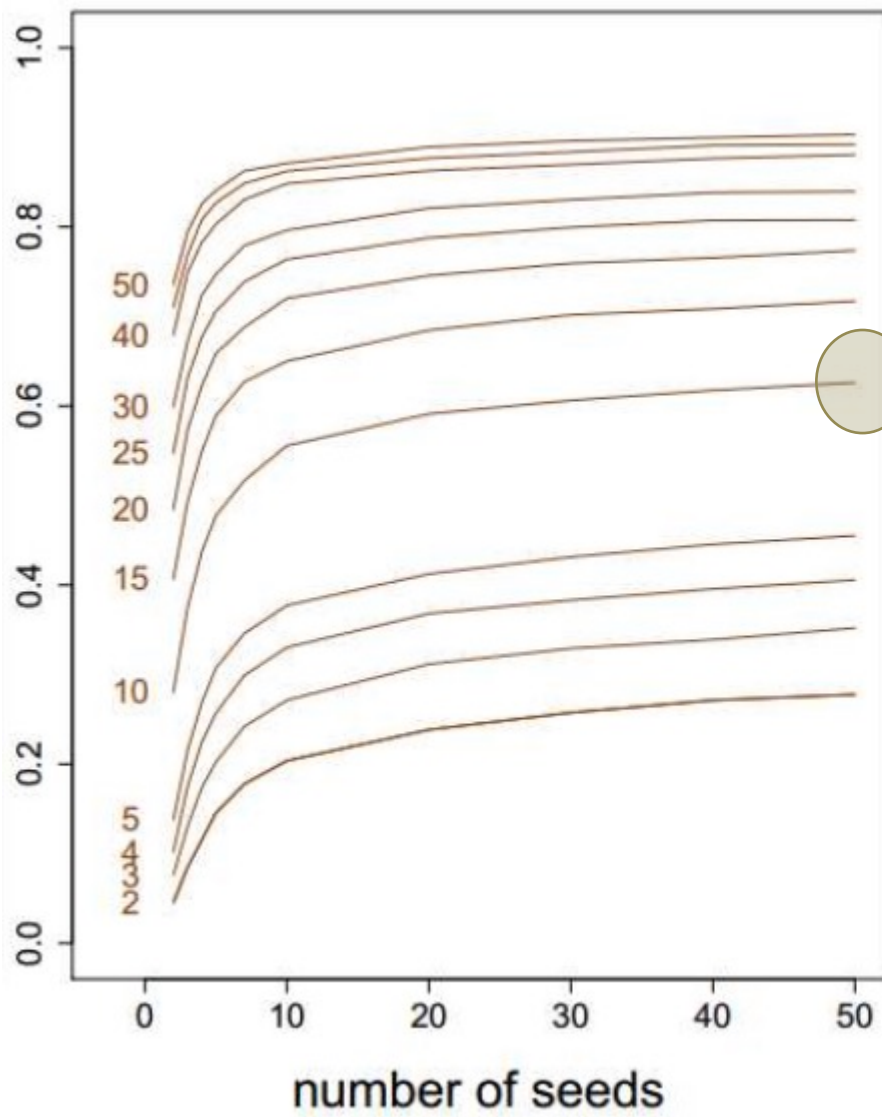
N_p = number populations, N_t = number trees, N_s = number seeds, Prop GD = proportion of genetic diversity (i.e. of number of alleles)

Improving collections with simulations

Optimal stopping point estimate

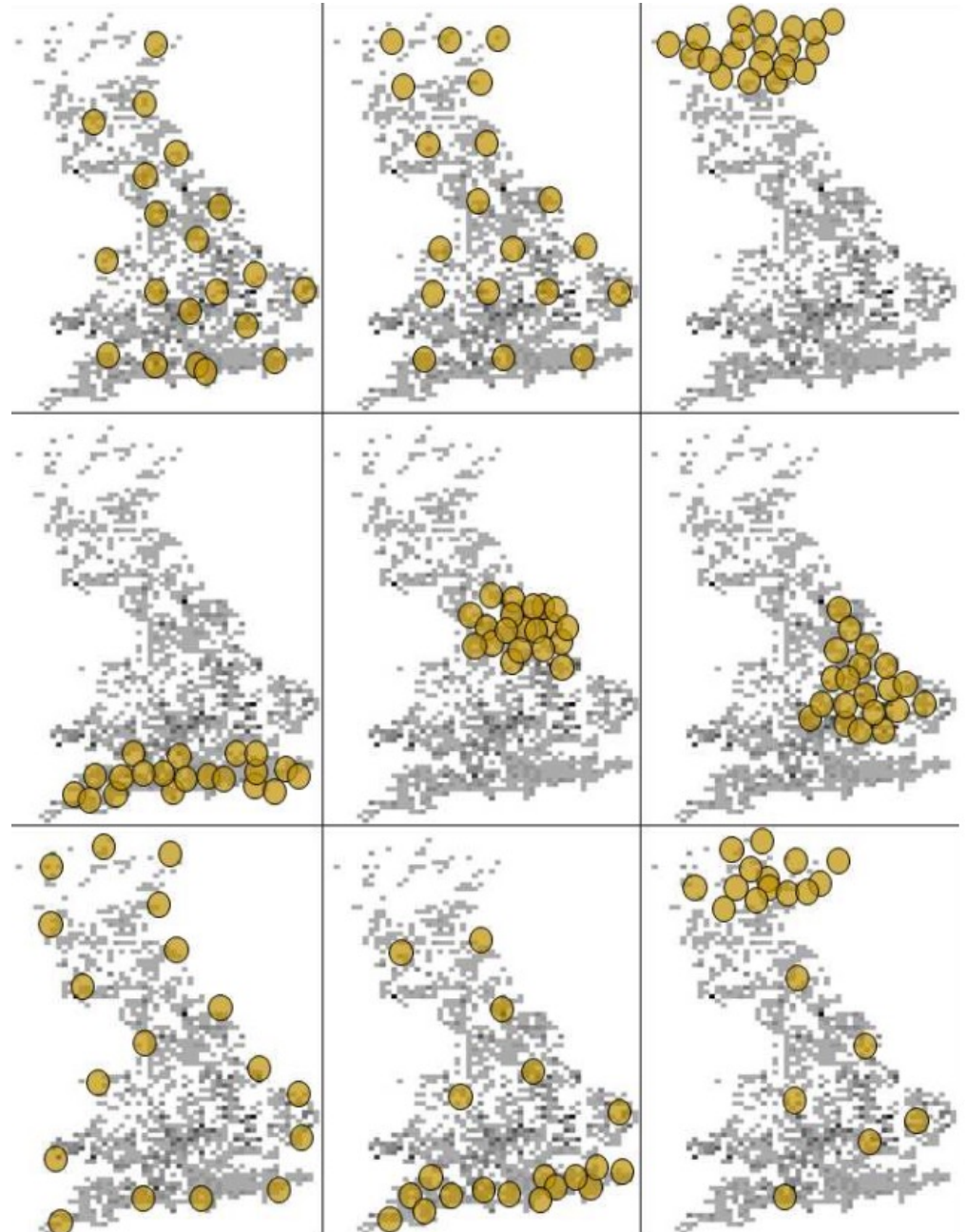
- 30 populations, 30 trees (0.5% improvement)
- Close to a priori advice in sampling manual





Improving collections with simulations

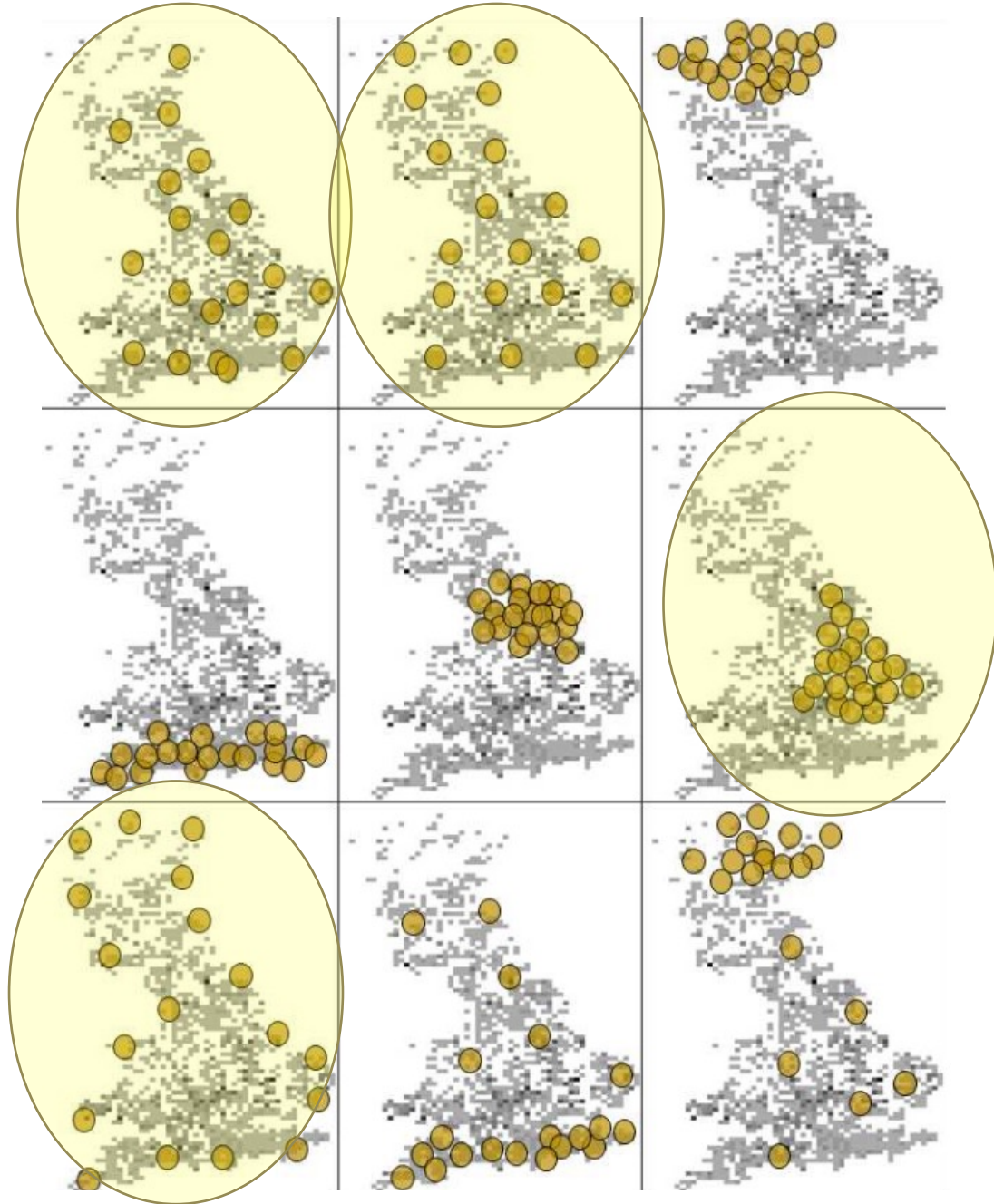
Where to sample across the range? The best strategies were:



Improving collections with simulations

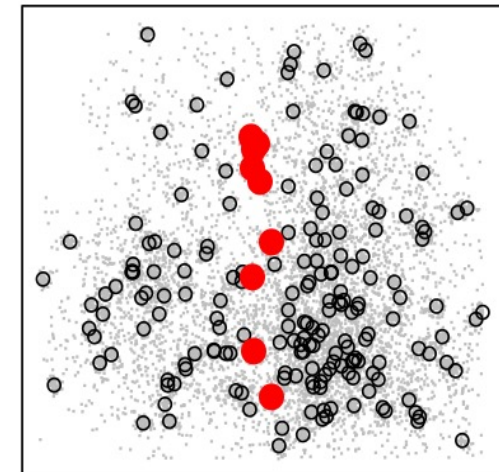
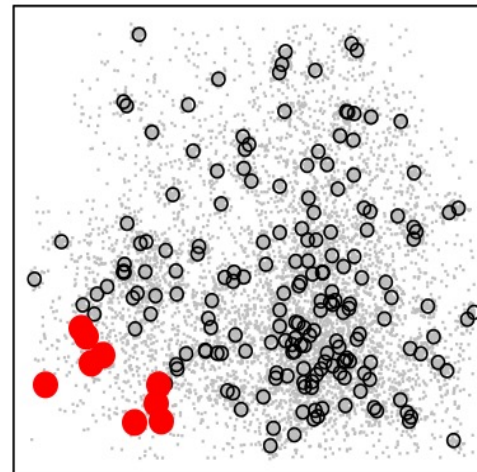
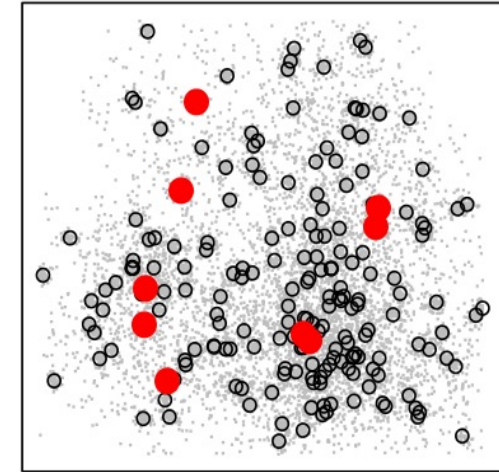
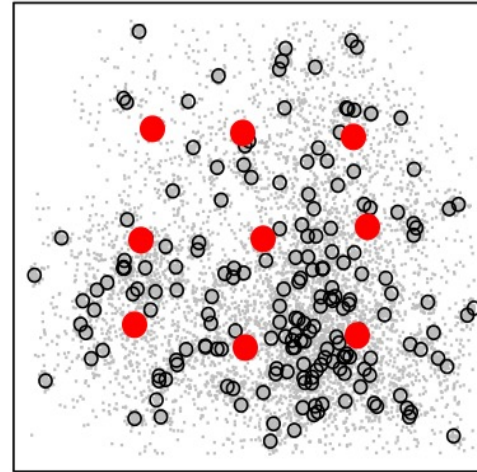
Where to sample across the range? The best strategies were:

- Randomly
- Stratified
- Edge
- Core



Improving collections with simulations

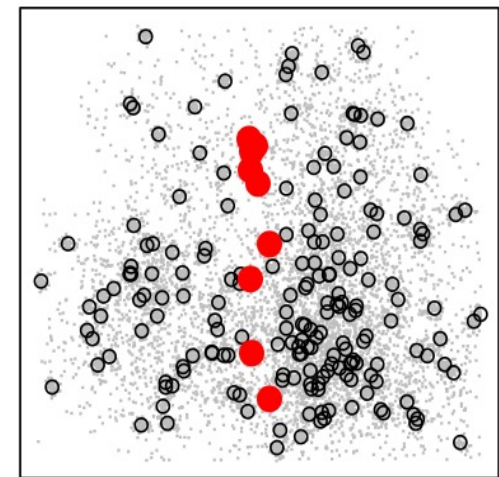
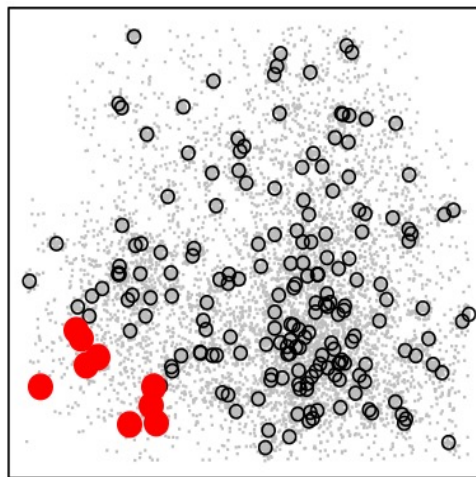
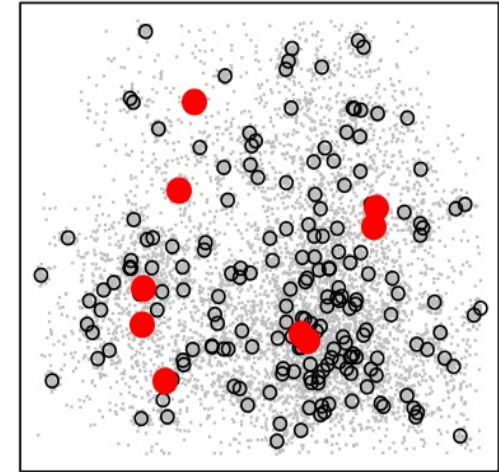
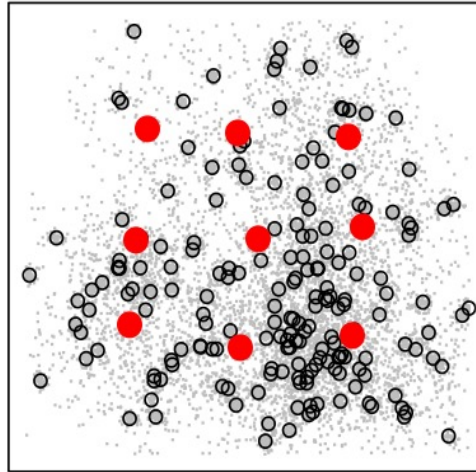
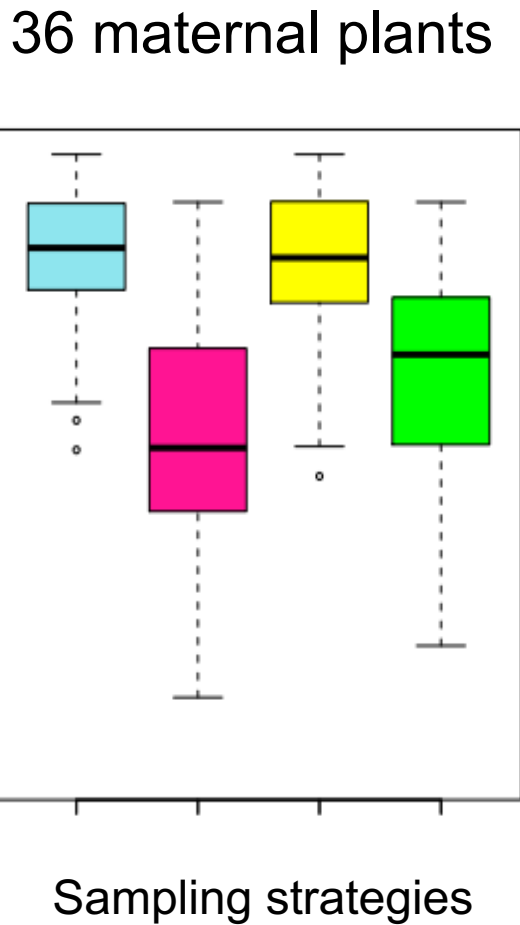
Within a population – how to sample?



Improving collections with simulations

Within a population - **sample widely (randomly or on a grid)**

Proportion of genetic variation captured



Improving collections with simulations

Main message: Simulations complement DNA based studies

They can provide advice on minimum sampling and sampling logistics, both across all species and tailored to each species

Gap analysis of populations and species

Gap analysis of populations and species

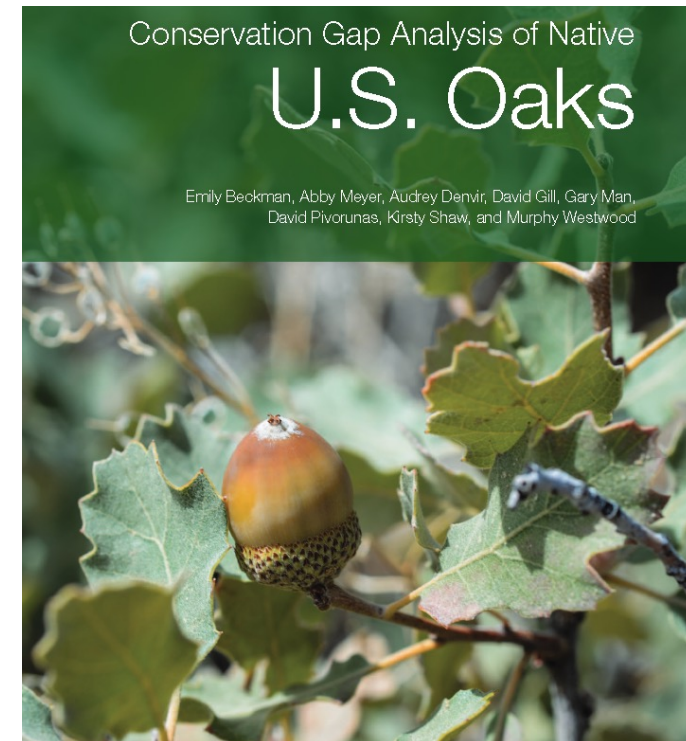
Use GIS tools to estimate which species and populations are the least well conserved

Gap analysis of populations and species

Emily Beckman & Murphy Westwood

Quick method can be applied to many species

- 1) Compile known *wild locations* (herbaria, etc)
- 2) Compile known *ex situ seed source locations*
- 3) Calculate the “coverage” of the *ex situ seed sources* (40%)



An ecogeographic framework for in situ conservation of forest trees in British Columbia

Andreas Hamann, Pia Smets, Alvin D. Yanchuk, and Sally N. Aitken

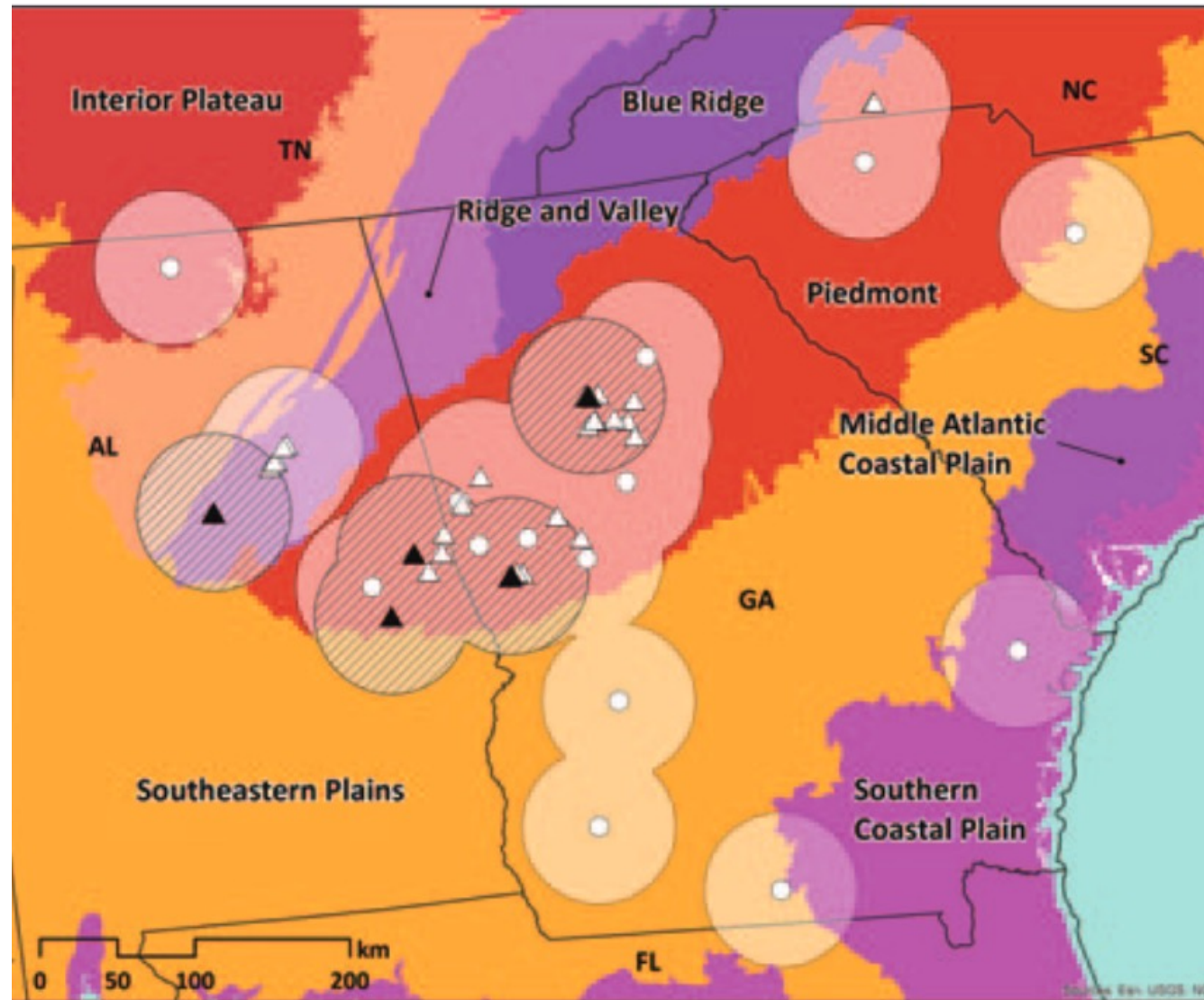
assessments of in situ conservation of forest trees based on basic botanical and ecological data... how well each species is represented in protected areas... under certain conditions this approach can pinpoint gaps at the level of genetically differentiated populations without actually using genetic data.

(2005)

Gap analysis of populations and species

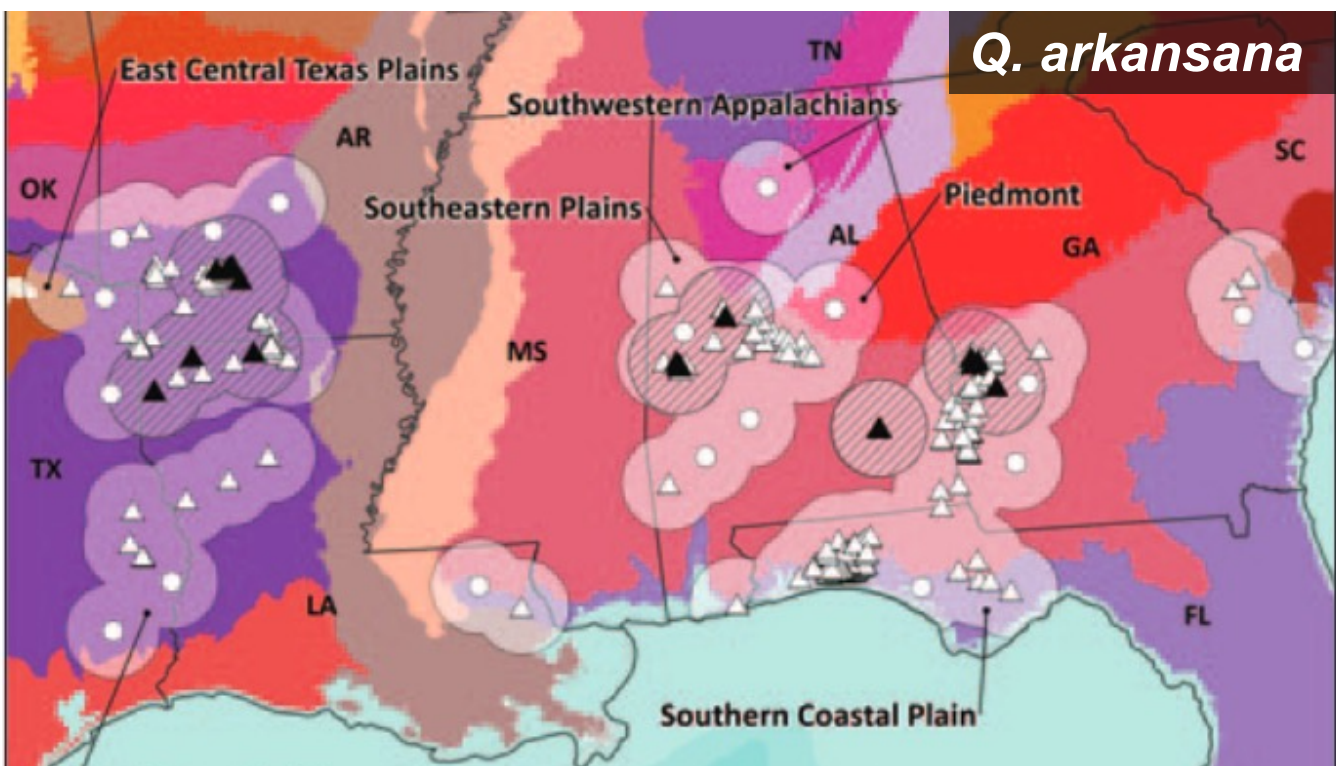
Quercus georgiana- Georgia oak

- 29% geographic coverage
- 41% ecological coverage

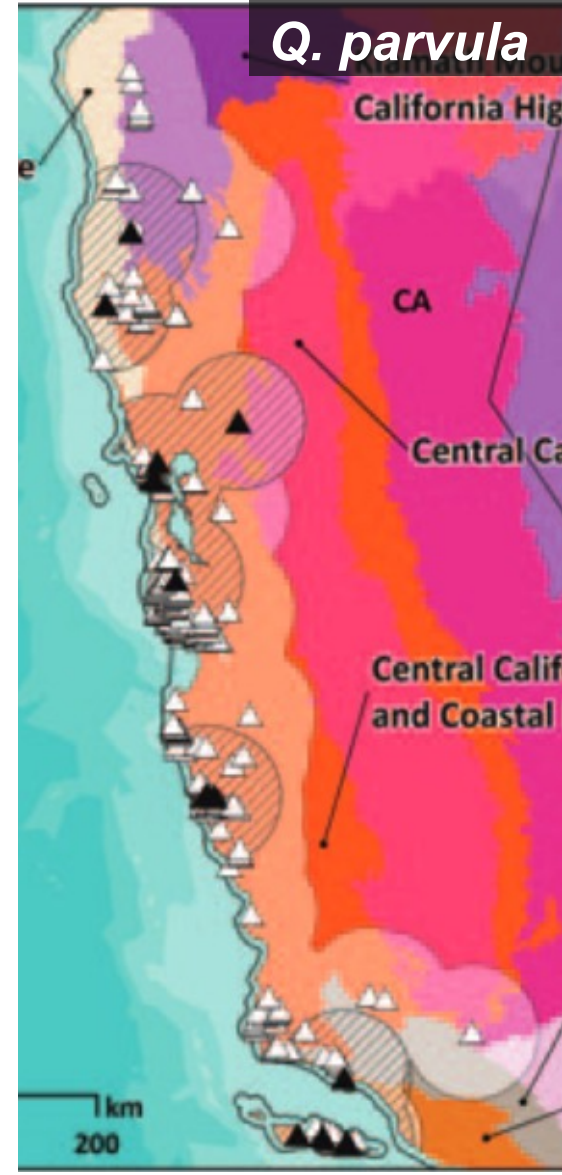


- ▲ Wild provenance source of ex situ living specimen
- △ Geolocated native occurrence record
- County centroid native occurrence record

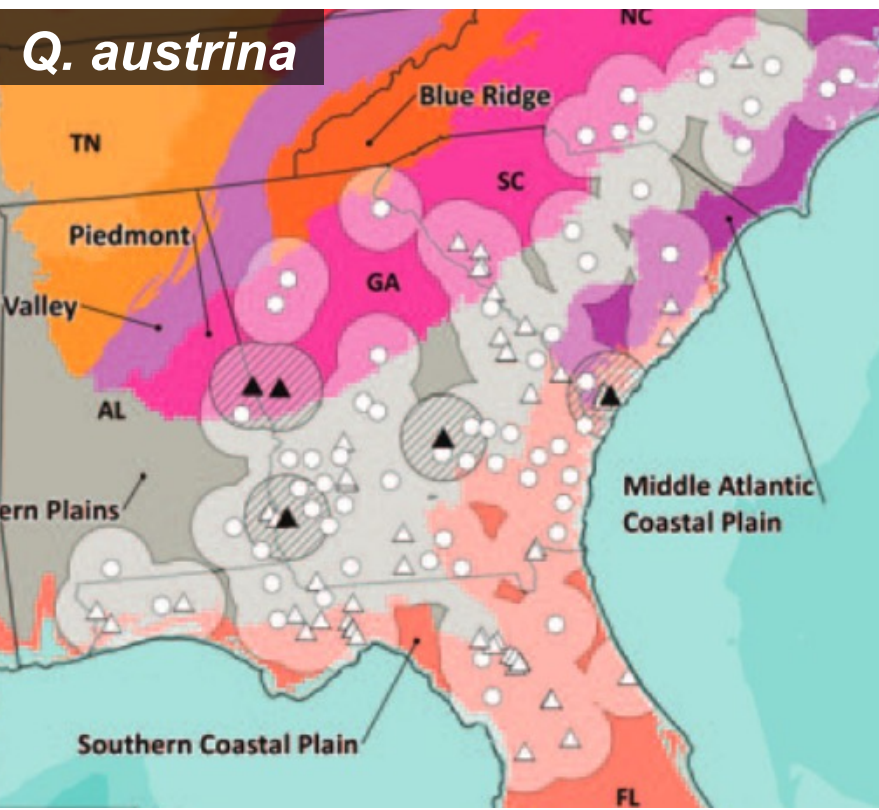
Q. arkansana



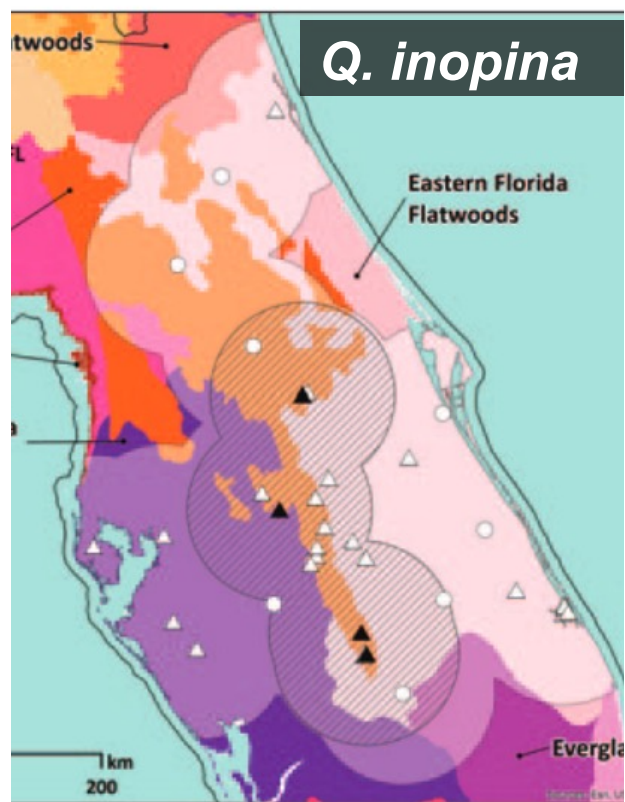
Q. parvula



Q. austrina

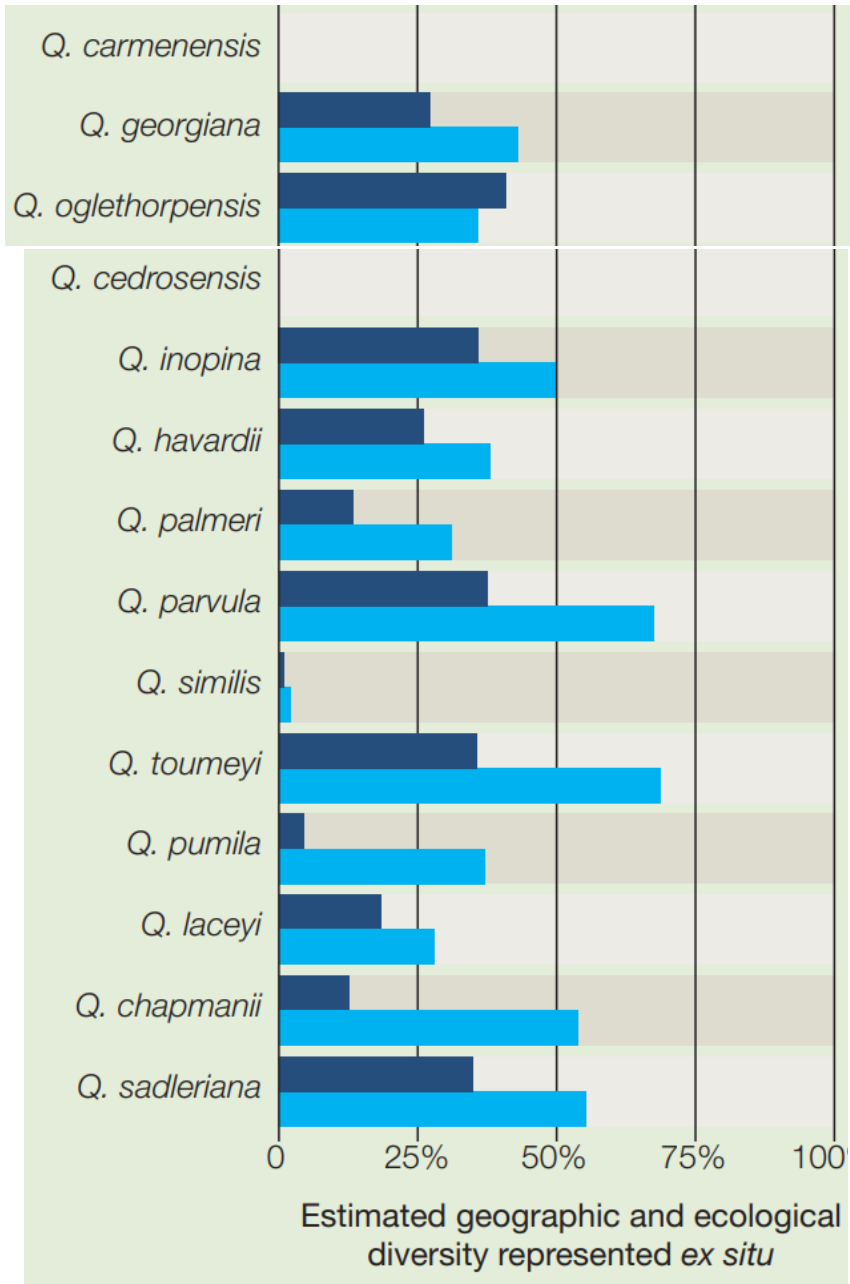


Q. inopina



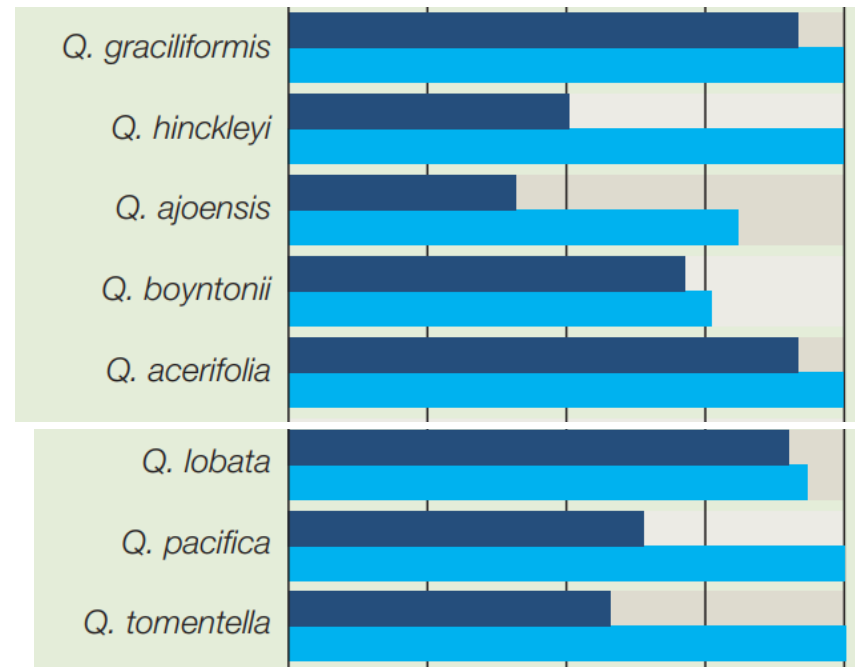
Gap analysis of populations and species

Can be used to prioritize-
which species need more?
(and when are we done?)



KEY

- Estimated geographic coverage
- Estimated ecological coverage



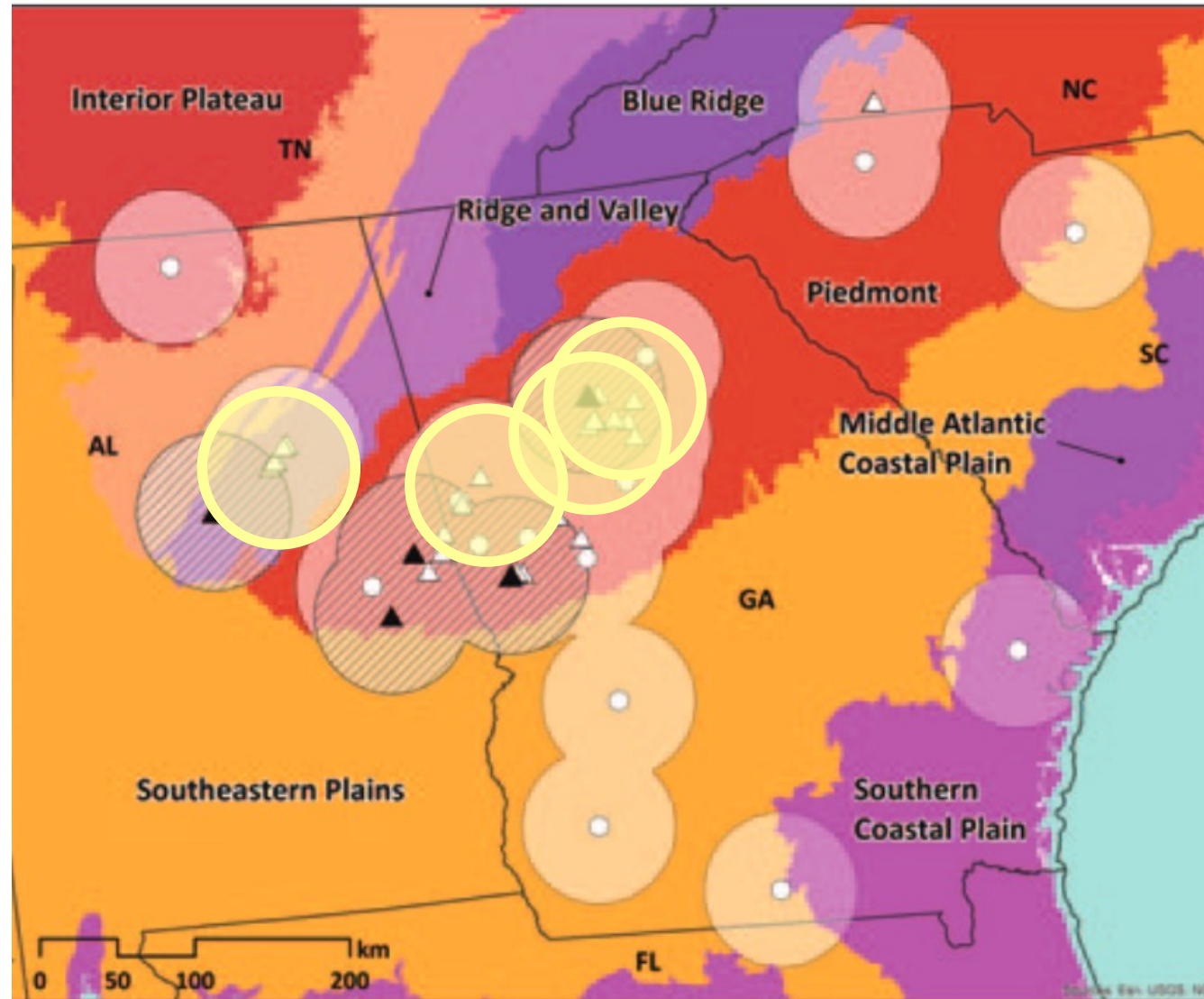
Gap analysis of populations and species

Closing the gaps! New sites,
100s of new seedlings



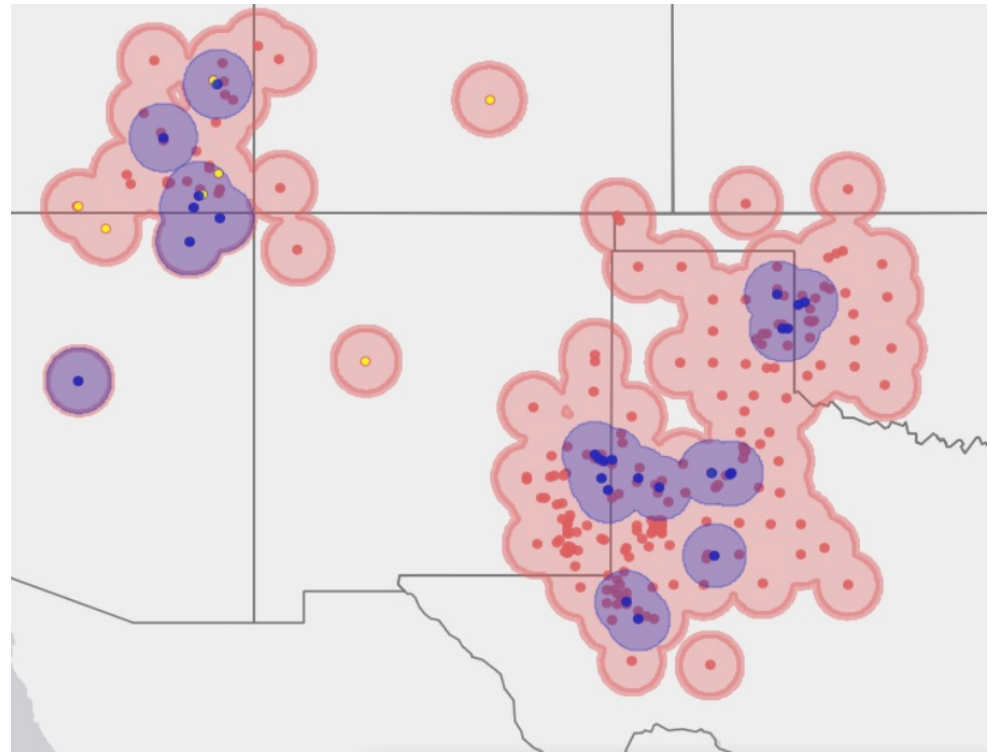
American
Public Gardens
Association

PublicGardens.org



Range wide collection of the desert-adapted oak *Quercus havardii*

- previously present in only one botanic garden!
- shared hundreds of seeds with nine botanic gardens



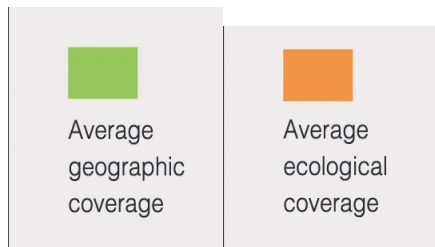
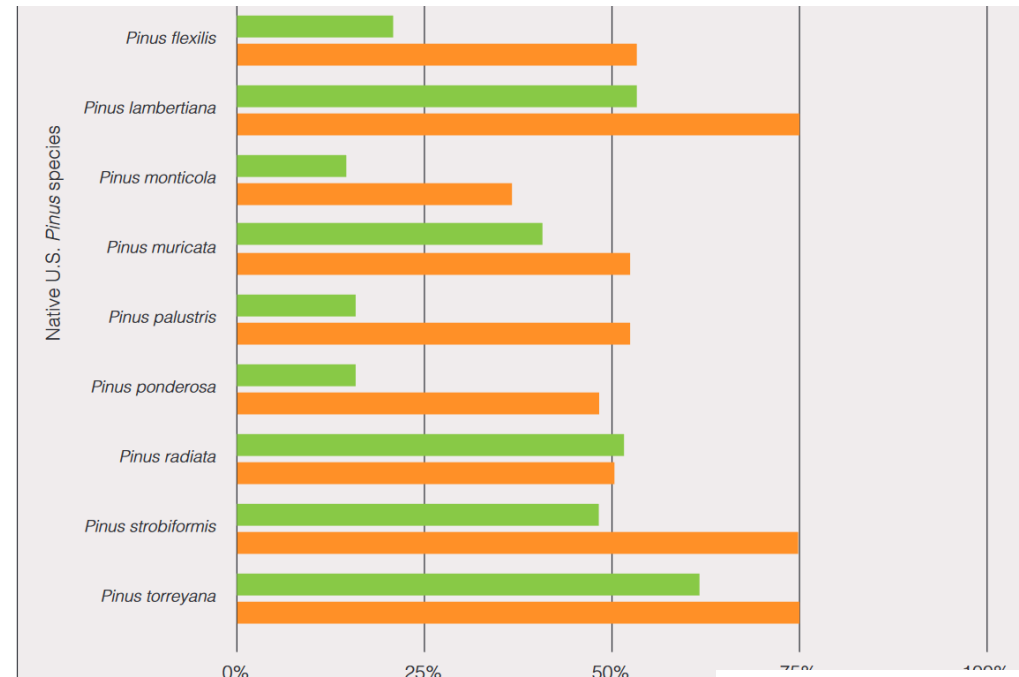
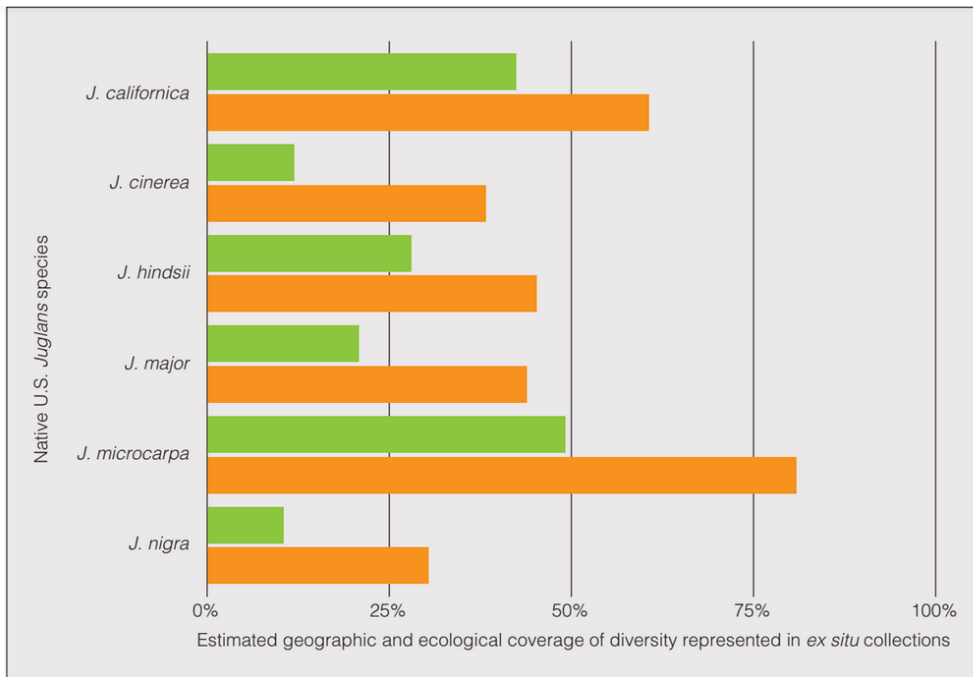
Zumwalde et al 2022, *Evolutionary Applications* “Assessing ex situ genetic and ecogeographic conservation”



Conservation Gap Analysis of Native U.S. Walnuts



Conservation Gap Analysis of Native U.S. Pines

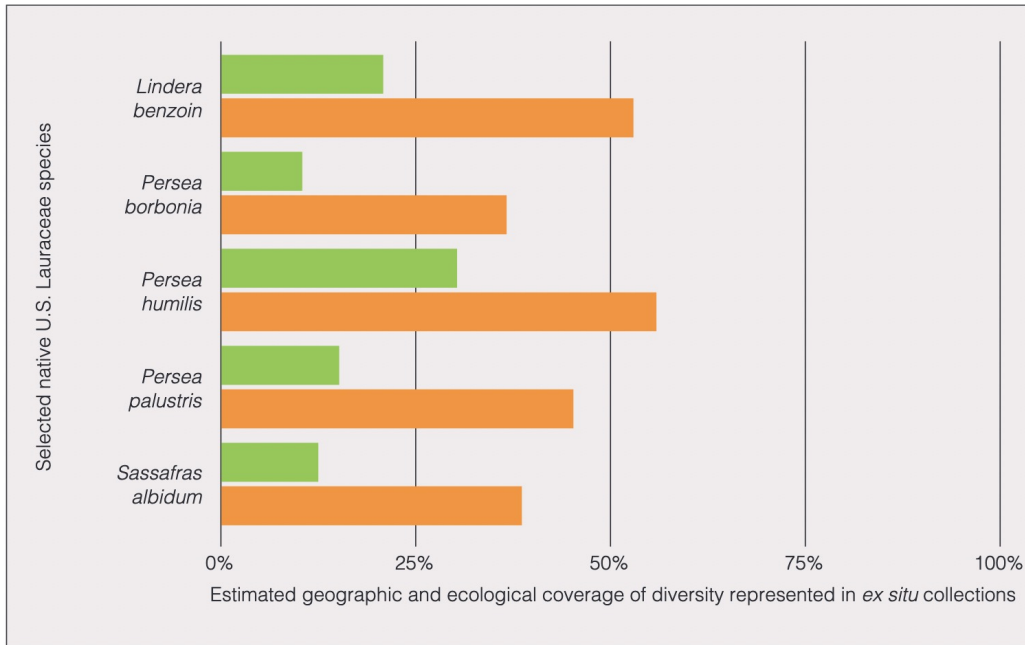


E Beckman et al 2021, BGCI





Conservation Gap Analysis of Selected Native U.S. Laurels

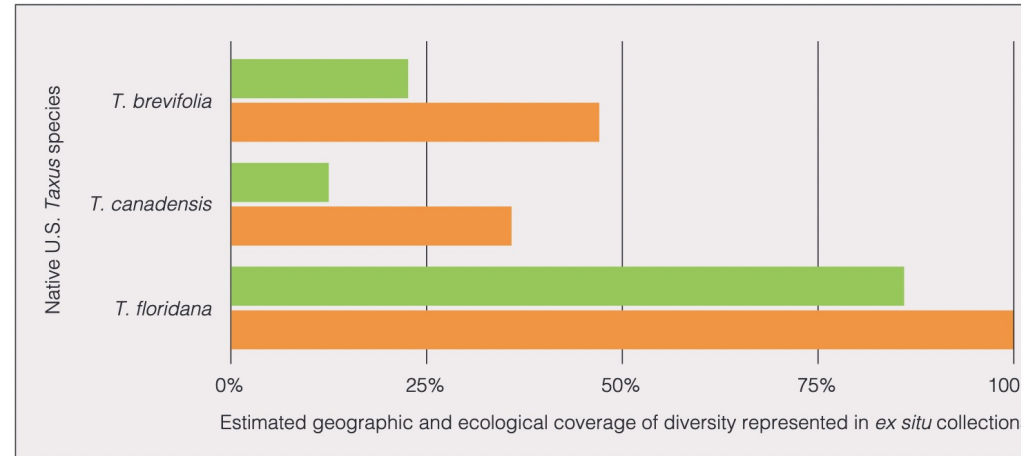


 Average geographic coverage

 Average ecological coverage



Conservation Gap Analysis of Native U.S. Yews

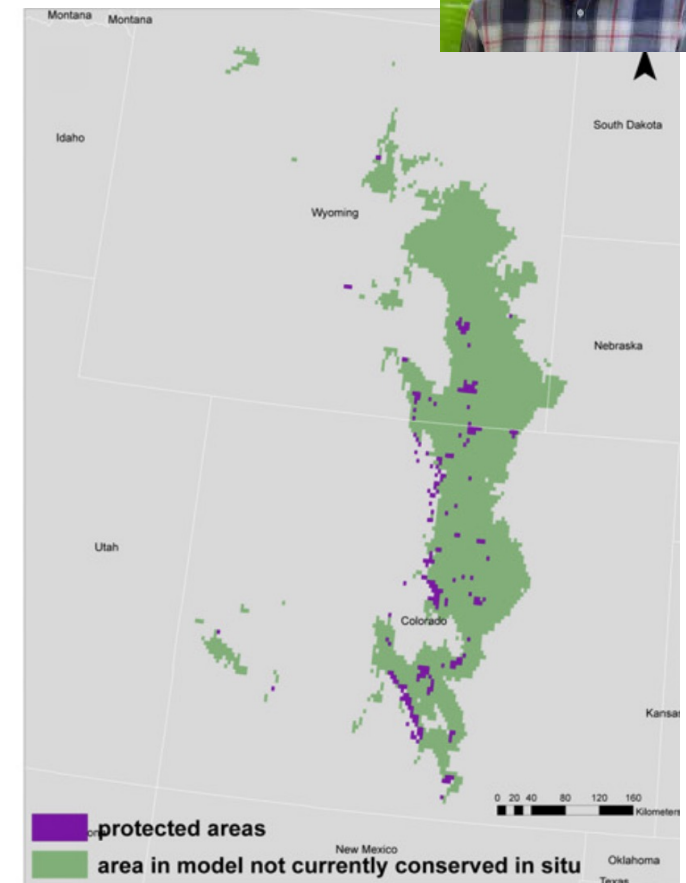
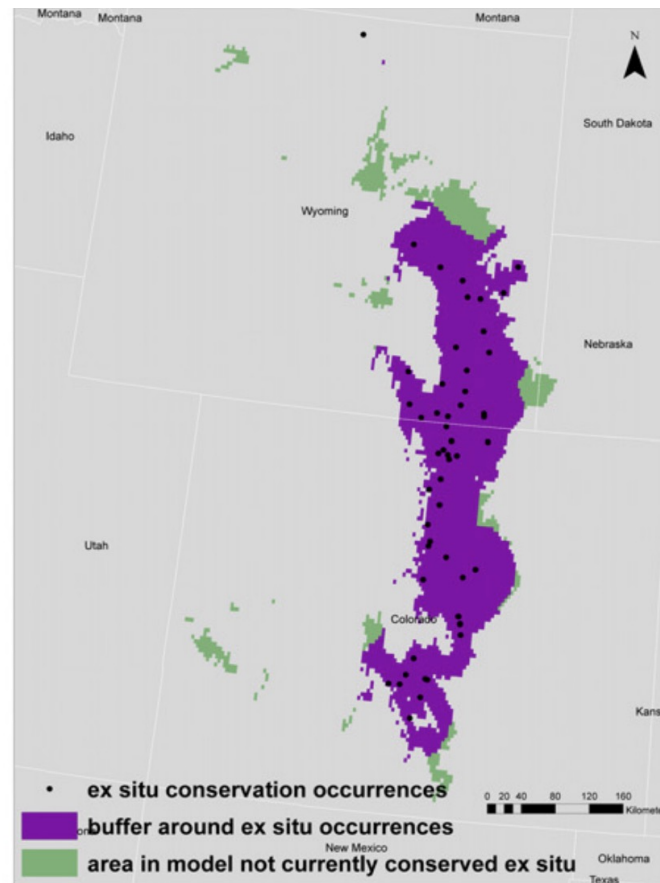
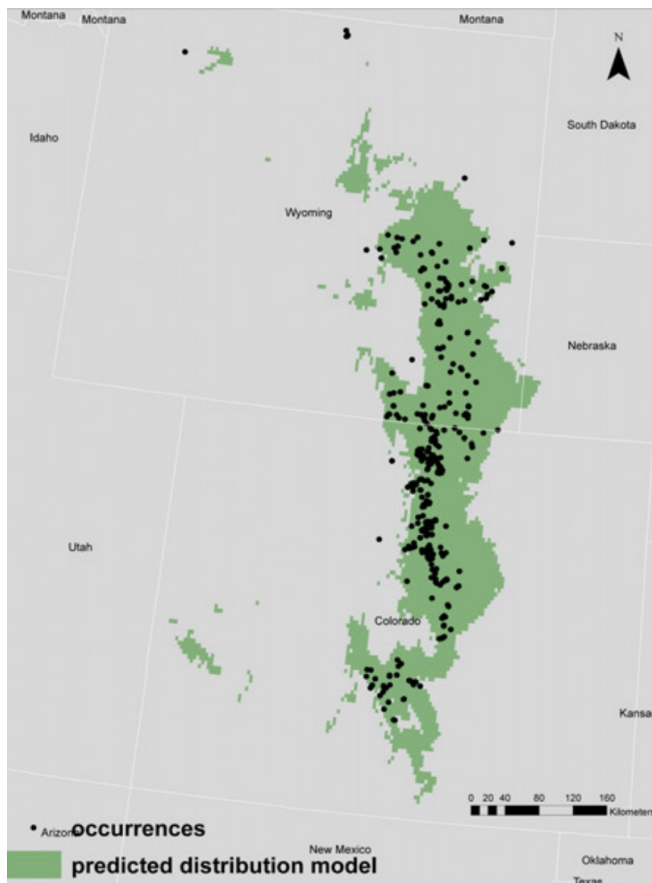


E Beckman et al 2021, BGCI






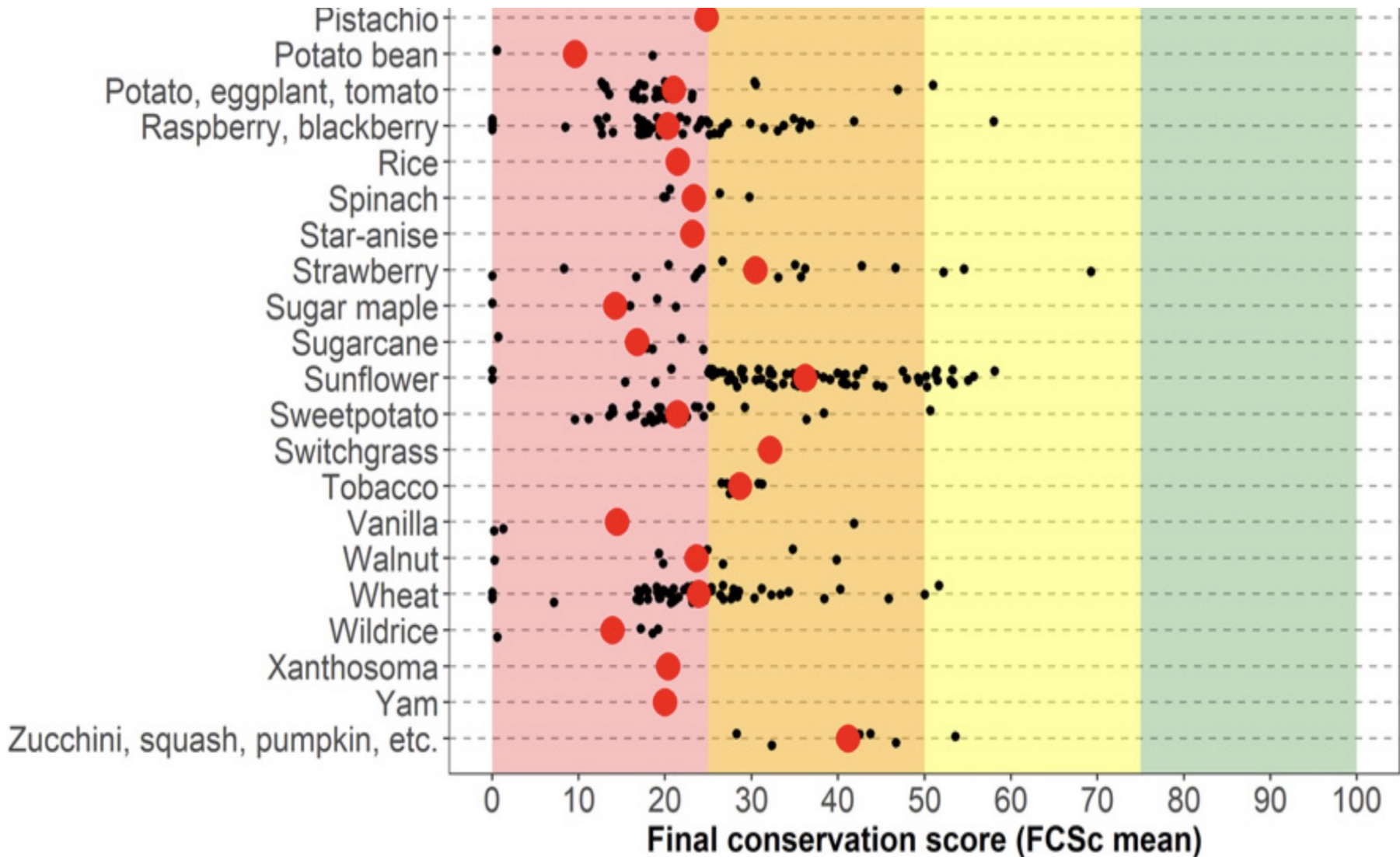
Gap analysis of populations and species

- 600 Crop Wild Relatives of the US (cereal, fruit, nut, oil, pulse, roots, tubers, vegetables)
- 7000 species globally



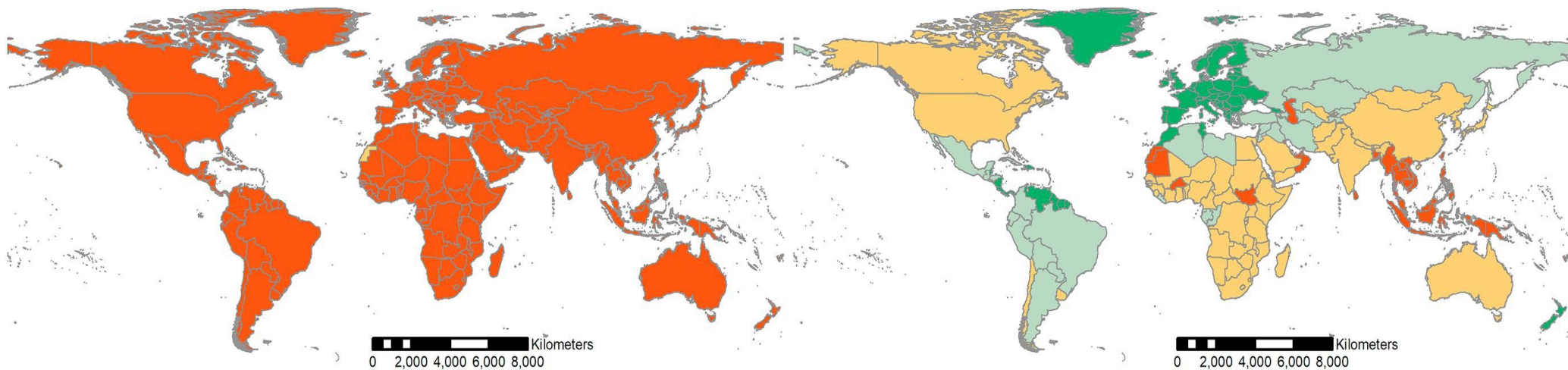
Crop wild relatives of the United States require urgent conservation action

Colin K. Khoury^{a,b,c,1,2} , Daniel Carver^{a,d,1} , Stephanie L. Greene^a , Karen A. Williams^e , Harold A. Achicanoy^b , Melanie Schori^e , Blanca León^{f,9} , John H. Wiersema^h , and Anne Francesⁱ 



Gap analysis of populations and species

- Overall 3% of species range protected ex situ
- Overall 40% of species range protected in situ
- Conclusion: we have *very little* of species' geographic ranges protected ex situ



Indicator  < 25  25 - 50  50 - 75  > 75



Gap analysis of populations and species

Main message: Gap analyses can identify which species have much of their ecogeographic range covered, and which do not

What about effective population size?

What about effective population size?

What other tools can we use to quickly assess genetic diversity status ex situ?

What about effective population size?

- Proportion of populations with an effective population size (N_e) above 500
- Proportion of distinct populations maintained

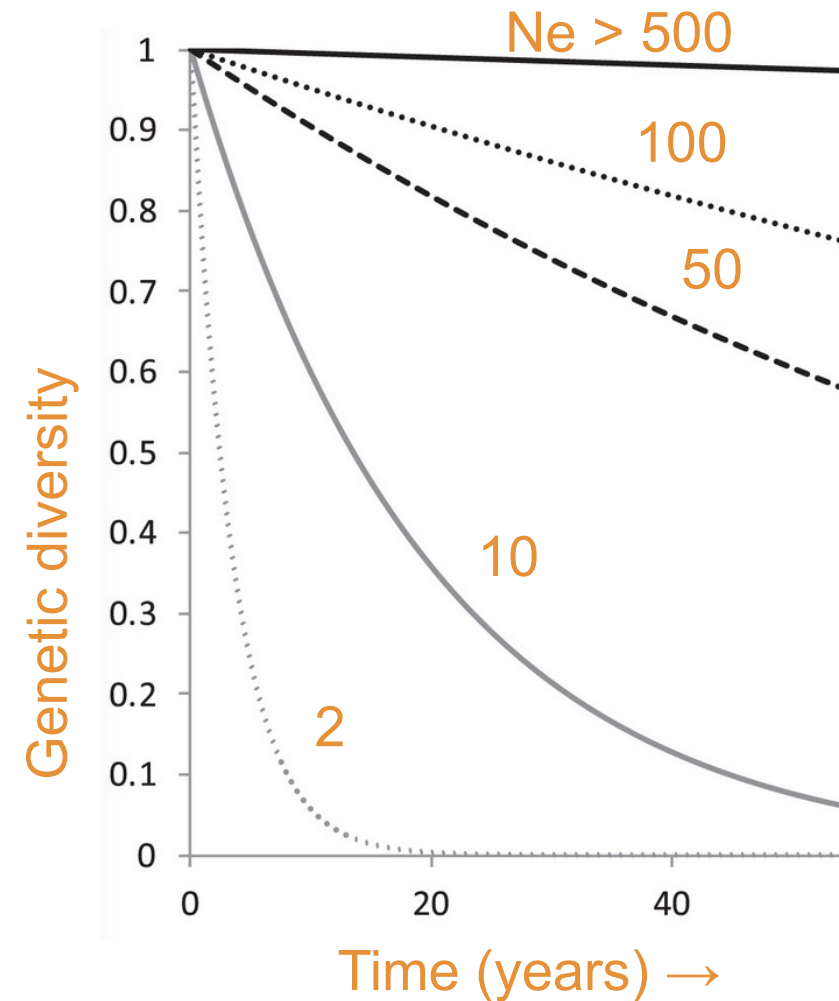


2020 UN BIODIVERSITY CONFERENCE
COP 15 / CP-MOP 10 / NP-MOP 4
Ecological Civilization-Building a Shared Future for All Life on Earth
KUNMING – MONTREAL

What about effective population size?

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

Understandable: Long been used in forestry, agriculture, fisheries, conservation biology

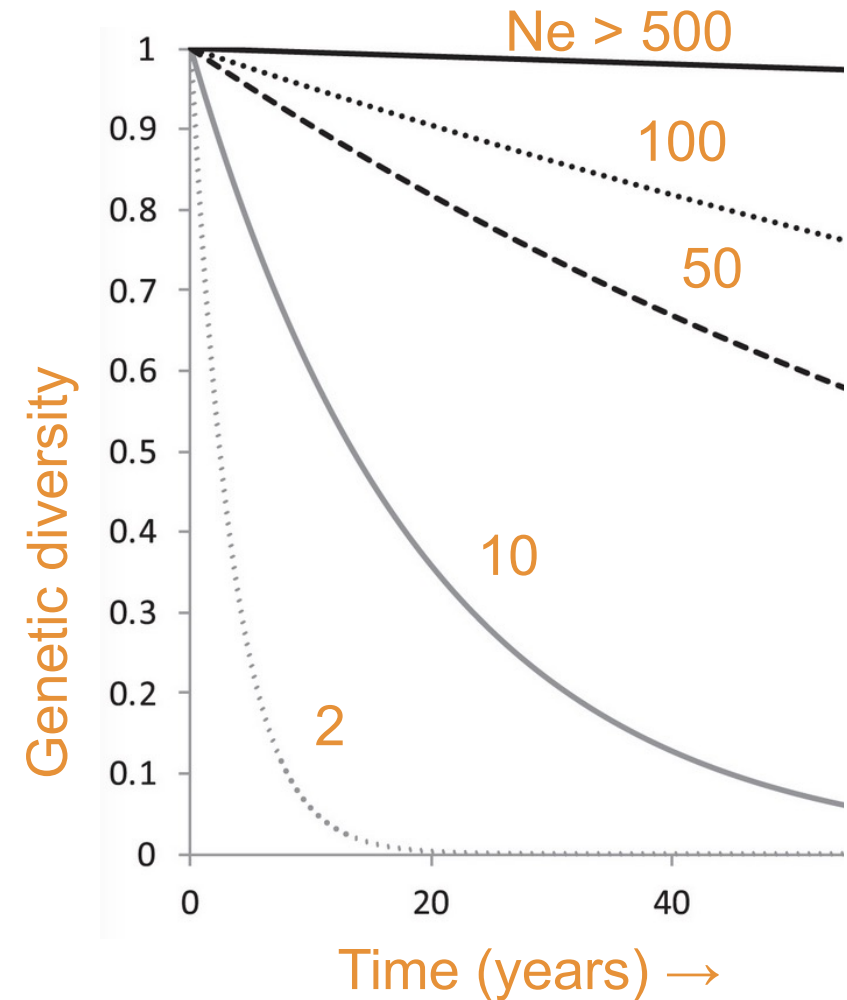


What about effective population size?

Measurable- data available?

Use 1/10th of census size (N_c)

Or for gene banks, number of maternal plants sampled



What about effective population size?

- 8 countries: South Africa, Mexico, Sweden, Belgium, France, Japan, Australia, Columbia
- Diversity of sources (Red List, management reports, databases, expert consultations)



Hoban et al 2023. Monitoring status and trends in genetic diversity for the Convention on Biological Diversity: An ongoing assessment... *Cons Lett*



CONABIO
COMISIÓN NACIONAL PARA
EL CONOCIMIENTO Y USO
DE LA BIODIVERSIDAD

SANBI

Biodiversity for Life

South African National Biodiversity Institute



環境省

Ministry of the Environment

NATUR
VÅRDS
VERKET

SWEDISH
ENVIRONMENTAL
PROTECTION
AGENCY

How to maintain genetic diversity in situ?

(Mostly) resolved issues

- Repeatable methodology
- Standard data storage
- Reflecting uncertainty/ disagreements
- Allowing even scant information

Hoban et al. Too simple, too complex, or just right? Advantages, challenges & resolutions for indicators of genetic diversity
-ecoevorxiv



How to maintain genetic diversity in situ?

Opportunity to assess genetic diversity status of 100s of species in a semi-standard way, without genetic data

Can be used for:

- prioritizing species under greatest genetic threat
- quantify progress over time, nationally
- identifying populations for management measures
- connect genetic diversity concerns to the public and policy people → increase concern and funding

Hoban et al. Too simple, too complex, or just right? Advantages, challenges & resolutions for indicators of genetic diversity
-ecoevorxiv



Faster and more meaningful than change in DNA summary stats

How to maintain genetic diversity in situ?

Could we measure effective population size in ex situ collections, including gene banks?

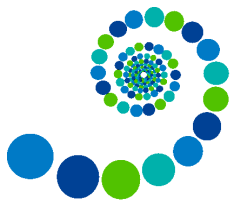
- Essentially, related to number of maternal plants sampled
- Botanic Gardens Conservation International
PlantSearch

Big question- what diversity do we need?

What amount and type of diversity is needed to survive?

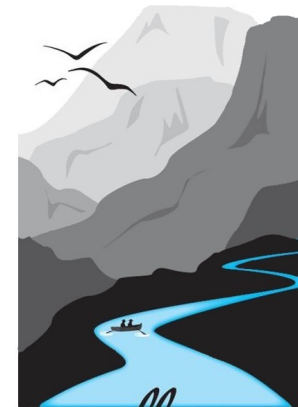
Depends on the type of selection pressure and the standing variation for selection

Pest/ disease resistance may occur in 1 of 100 plants, or 1 in a million plants



NIMBioS

National Institute for Mathematical
and Biological Synthesis



Powell Center



THE
CHAMPION
of TREES



American
Public Gardens
Association



INSTITUTE of
Museum and Library
SERVICES



UNITED STATES
BOTANIC GARDEN



- Genetic diversity is a big part of the CBD Kunming Montreal Global Biodiversity Framework
- We've learned lessons about better reporting of genetic diversity to the CBD
- There are different tools to assess genetic diversity, with different advantages:
 - DNA based studies
 - Simulations
 - Gap analysis
 - Effective size



We can and are:
quantifying progress,
producing practical advice,
guiding prioritization,
and leveraging diverse data

We envision and are working towards
well-documented, diverse,
representative, backed-up
collections of plant biodiversity

hobanlab.com | evbio.uchicago.edu

Graduate students: NSF INTERN program

Undergraduate students: REU & RAMP

shoban@mortonarb.org



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