



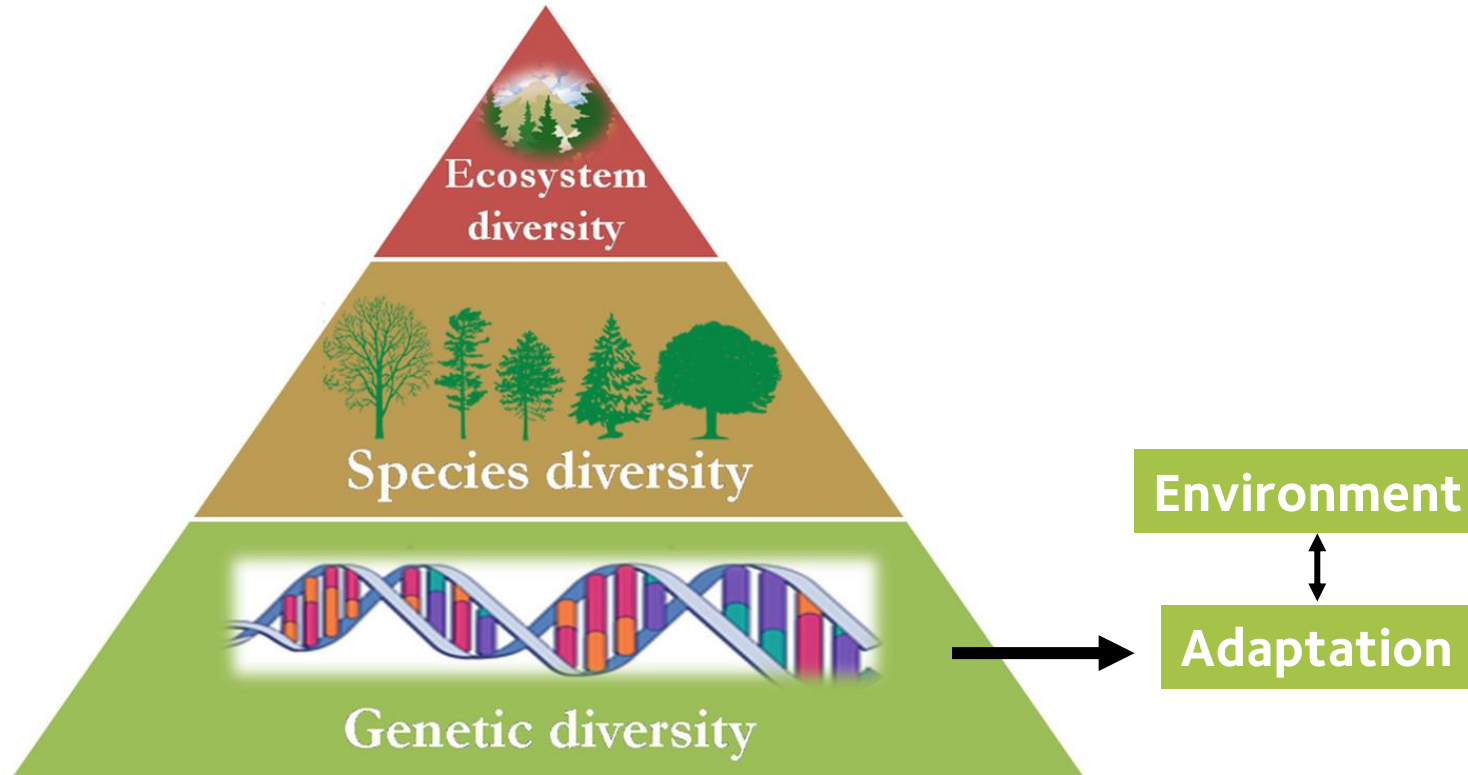
“As you sow, so shall you reap?”: Genomic prediction under climate change for matching germplasm sources to restoration site

Tin Hang (Henry) Hung, University of Oxford

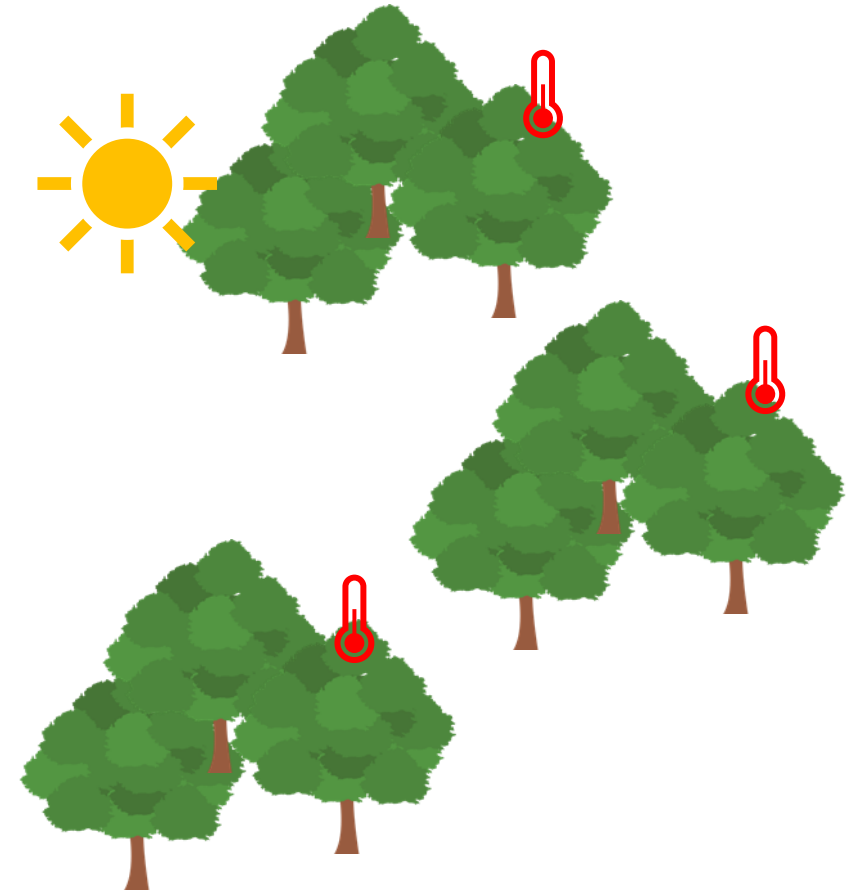
6 December 2021

Final virtual workshop

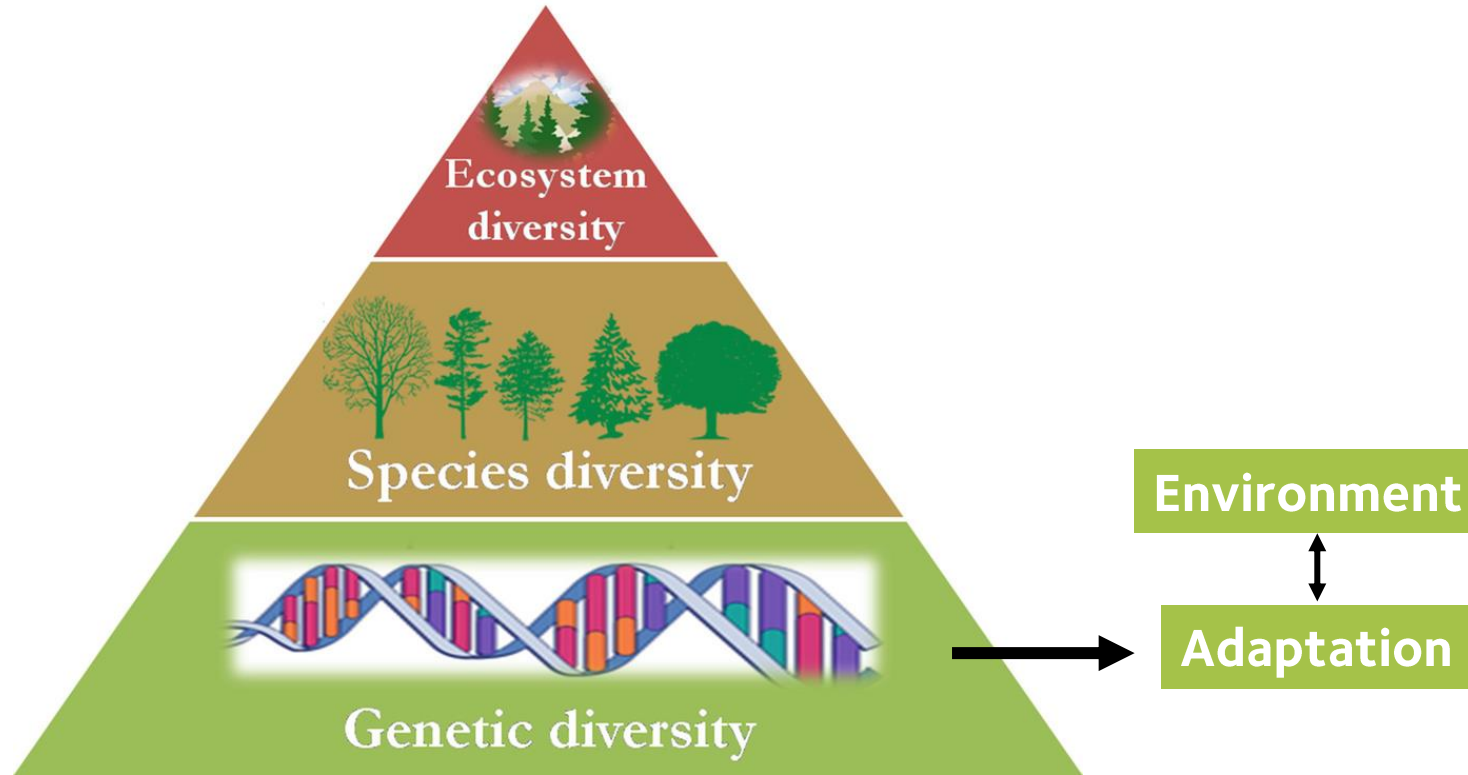
What is genetic diversity?



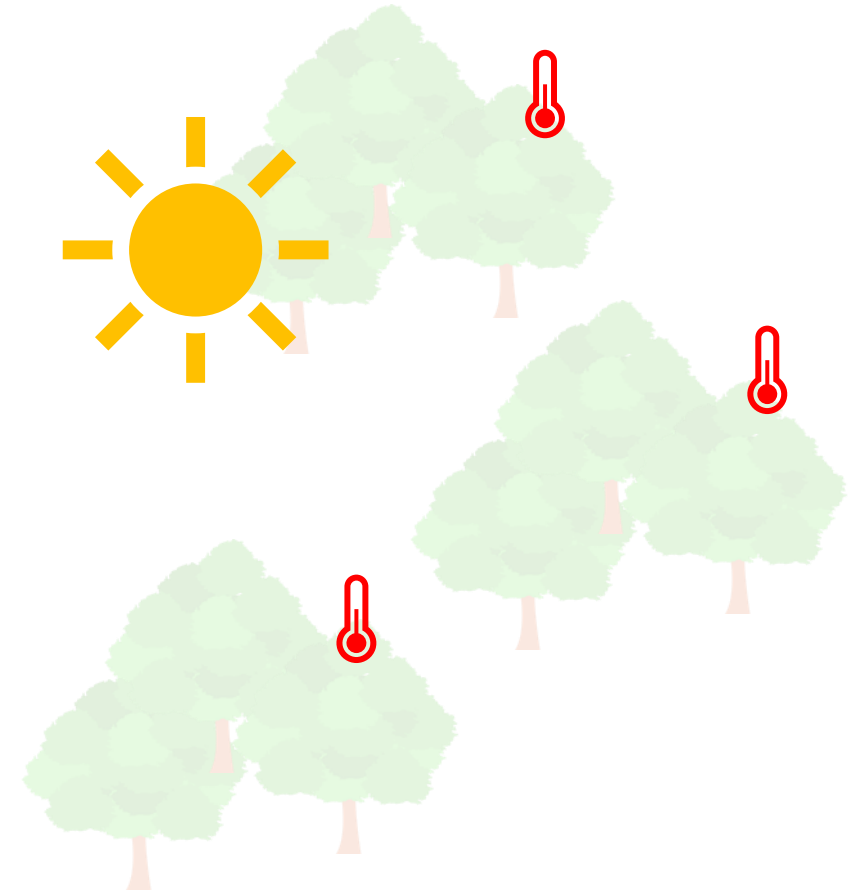
► Nonic & Šijacic-Nikolic. 2021 *Life on Land*



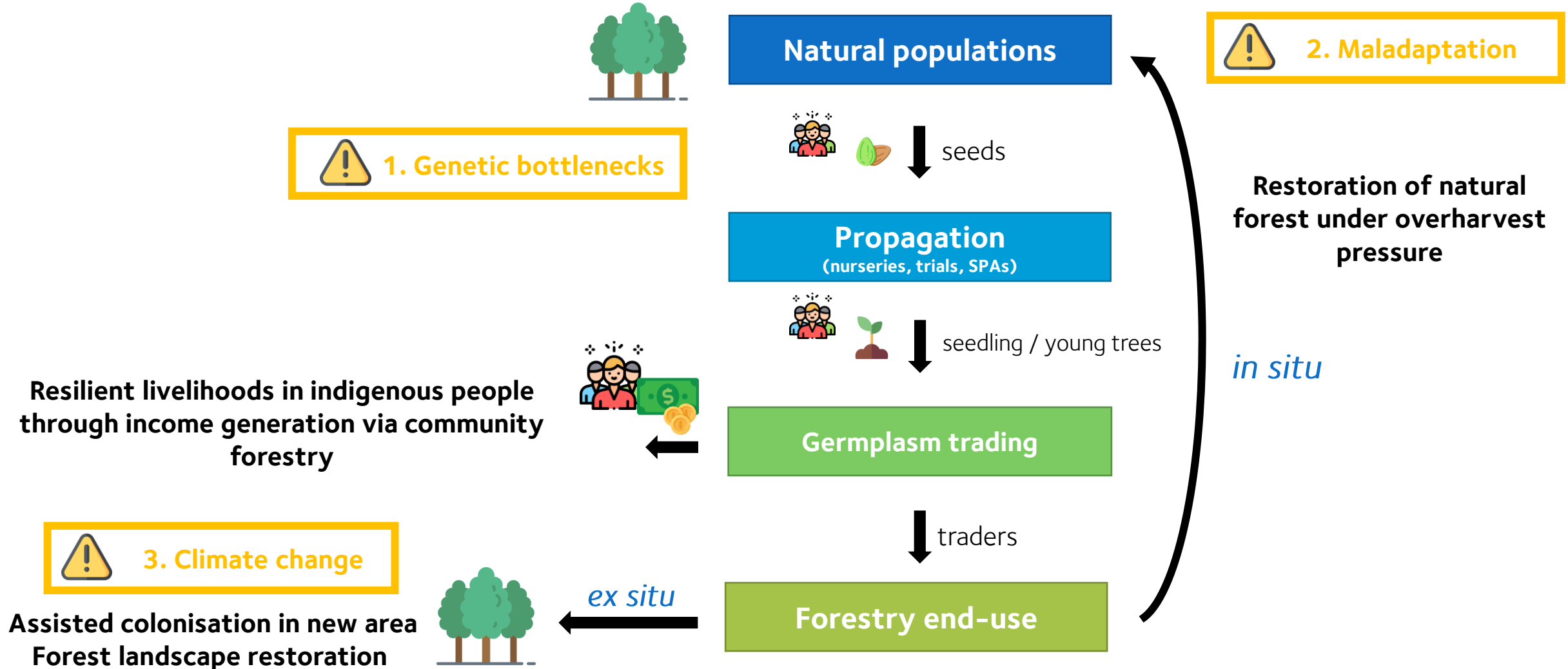
What is genetic diversity?



► Nonic & Šijacic-Nikolic. 2021 *Life on Land*



Where are the genetic risks?







5 main conservation units were delineated using ~10 genetic markers

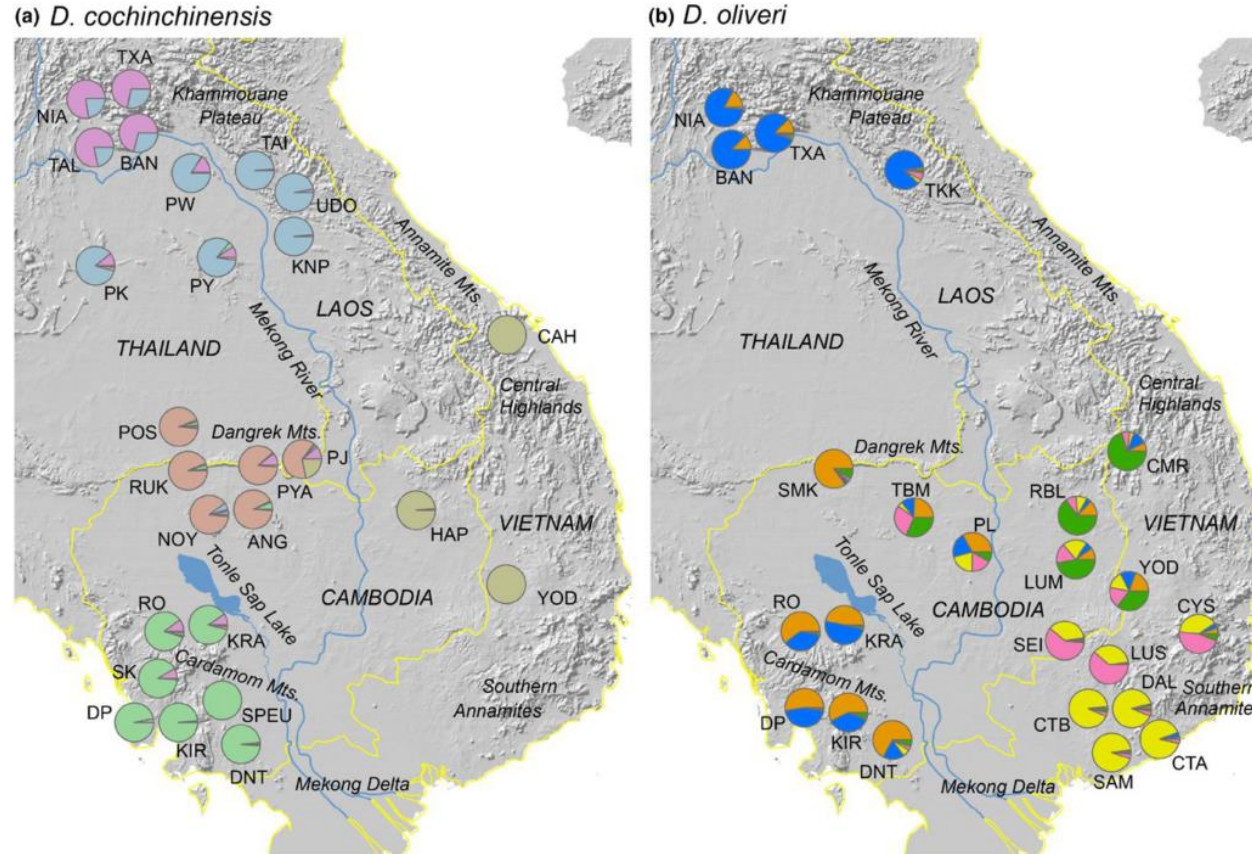


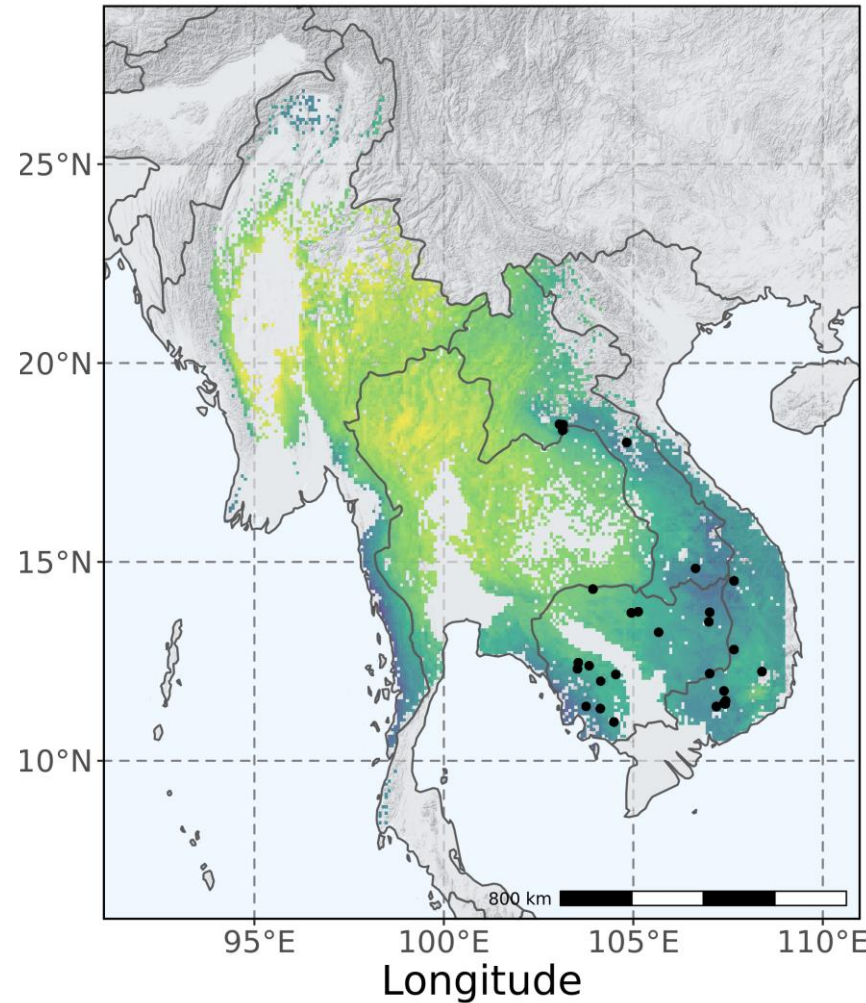
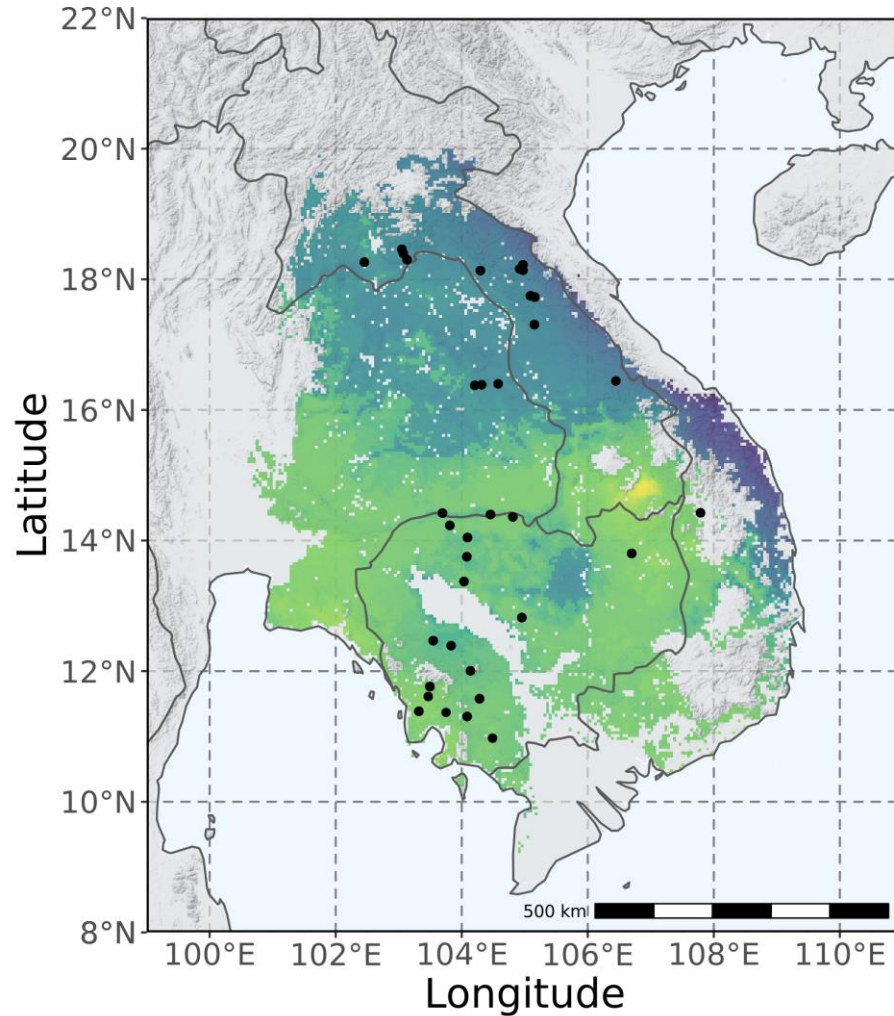
FIGURE 3 Structure results for $K = 5$ for (a) *Dalbergia cochinchinensis* and (b) *Dalbergia oliveri*. The allocation of individuals within each population to the five identified clusters for each species is shown in different colors

► Hartvig et al. 2017 *Ecol Evol*

Variation across the range



1. Genetic bottlenecks





- ~200,000 genetic markers
- Adaptive variation across the species range
- *D. cochinchinensis*: temperature-driven
- *D. oliveri*: precipitation-driven

► Hung et al. in preparation

Differences found in greenhouse experiment

Seedlings were drought-treated in a greenhouse experiment and compared with a control group

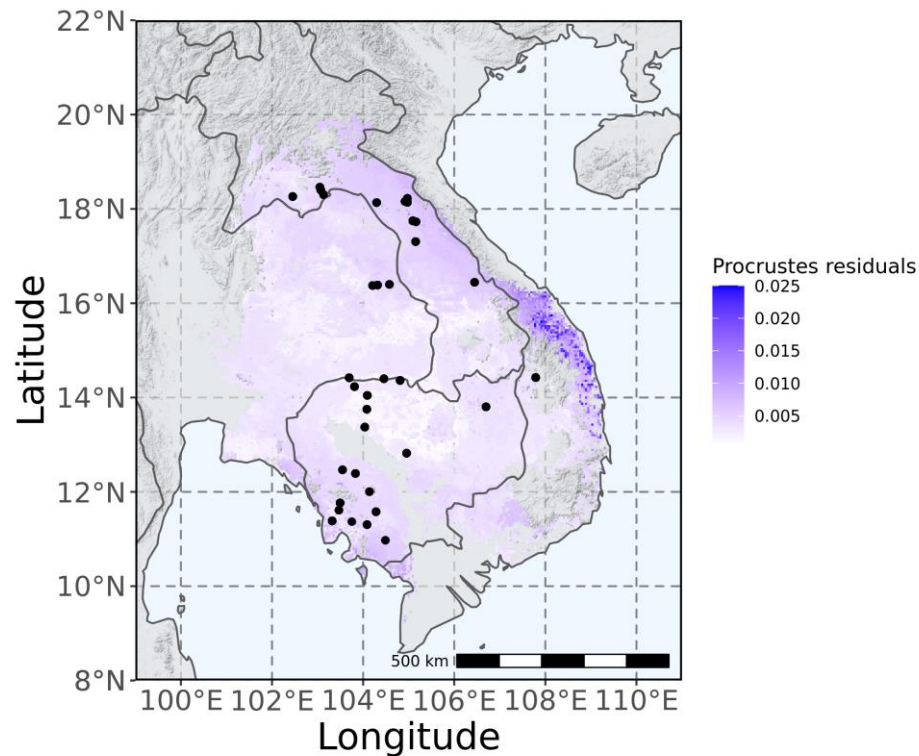
	<i>D. cochinchinensis</i>	<i>D. oliveri</i>
water relation 	Decreasing water potential	More stable water potential
carbon assimilation 	Higher sugar content	Lower sugar content
	Drought tolerance Pioneering species Shade-intolerant	Drought avoidance Climax species



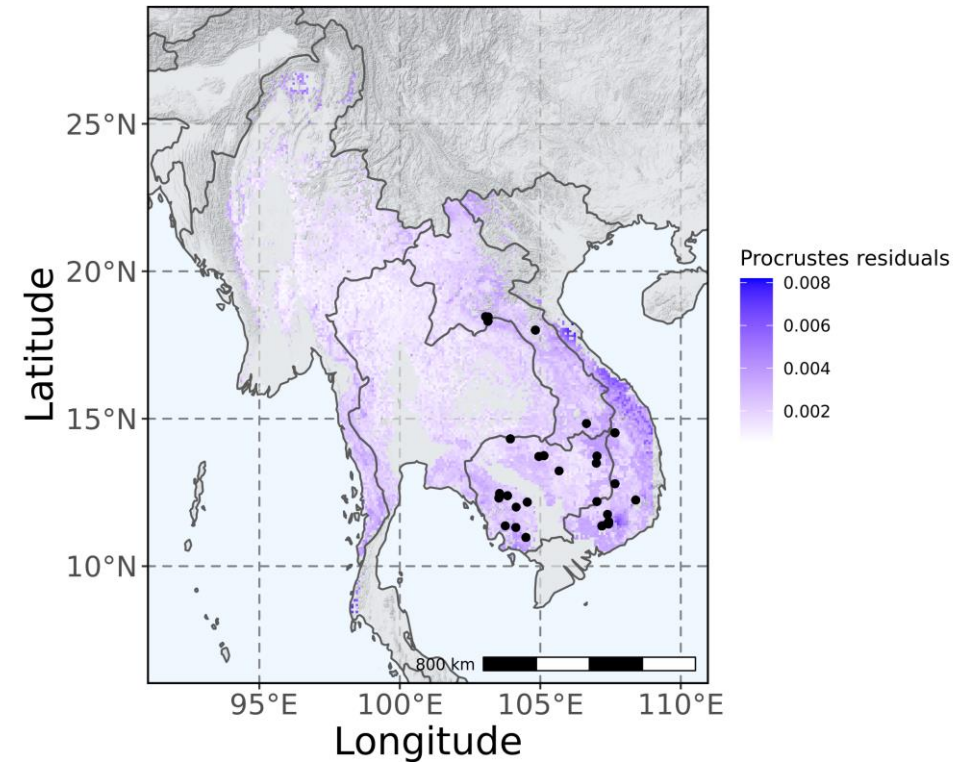
► Hung et al. 2020 *Ecol Evol*



Strong gene–environment association in coastal areas: recommended for *in situ* conservation at a high priority



D. cochinchinensis



D. oliveri

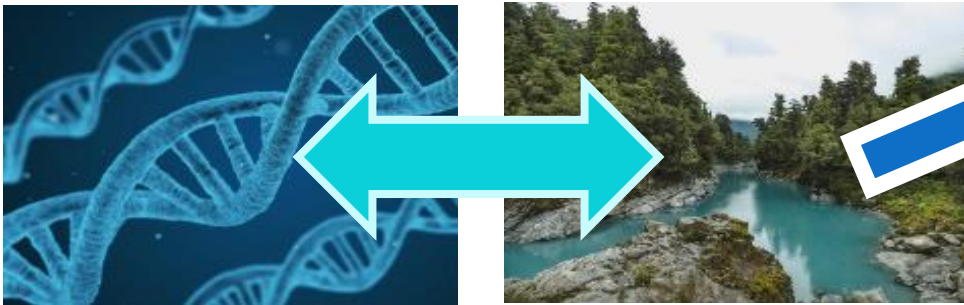
“As you sow, so shall you reap”?



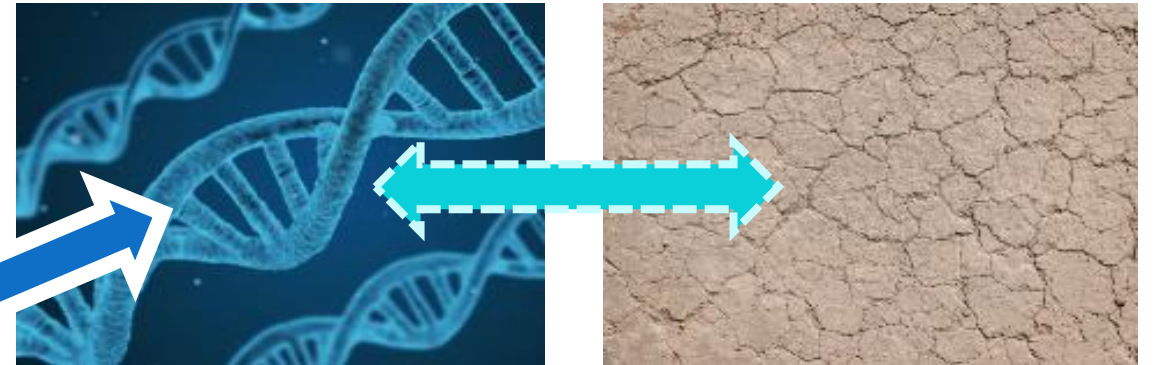
3. Climate change



Trees have long generation time which is **outpaced** by the climate change



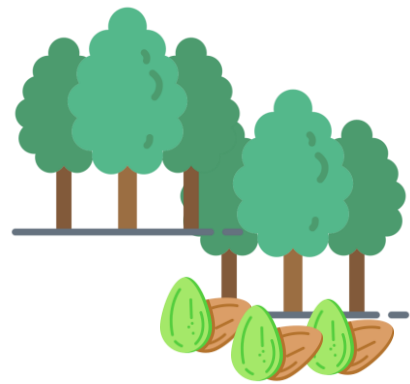
Populations may be adapted to their current climate



Populations may not keep track of changing climate

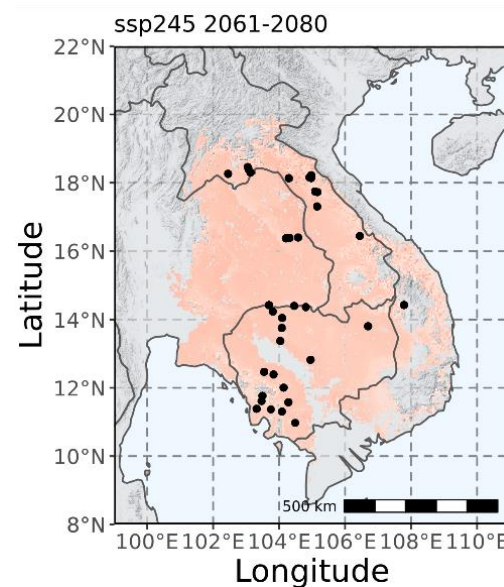
Implication of genomic vulnerability

Genomic vulnerability measures how likely the population will become **genetically maladapted** in the future



in situ populations
(seed sources)

GPS



Priority

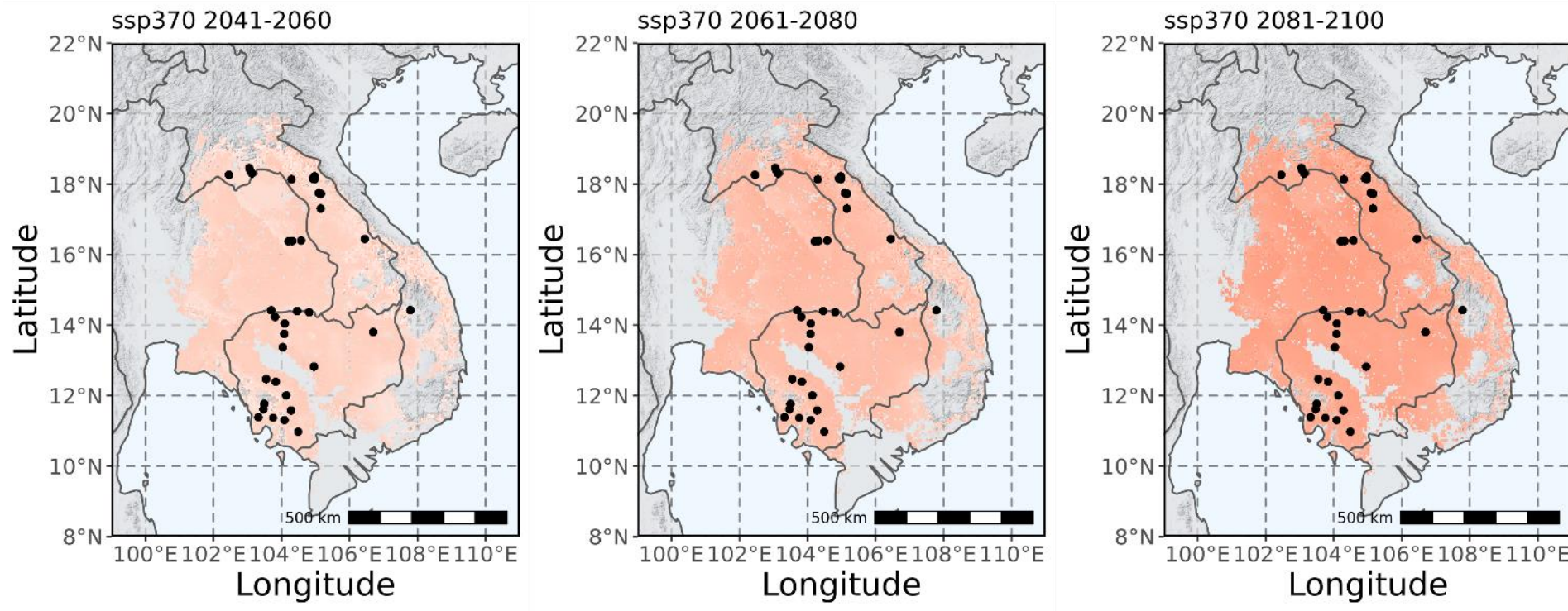
Genomic vulnerability prediction



3. Climate change



Highly vulnerable populations should be conserved with higher priority



D. cochinchinensis

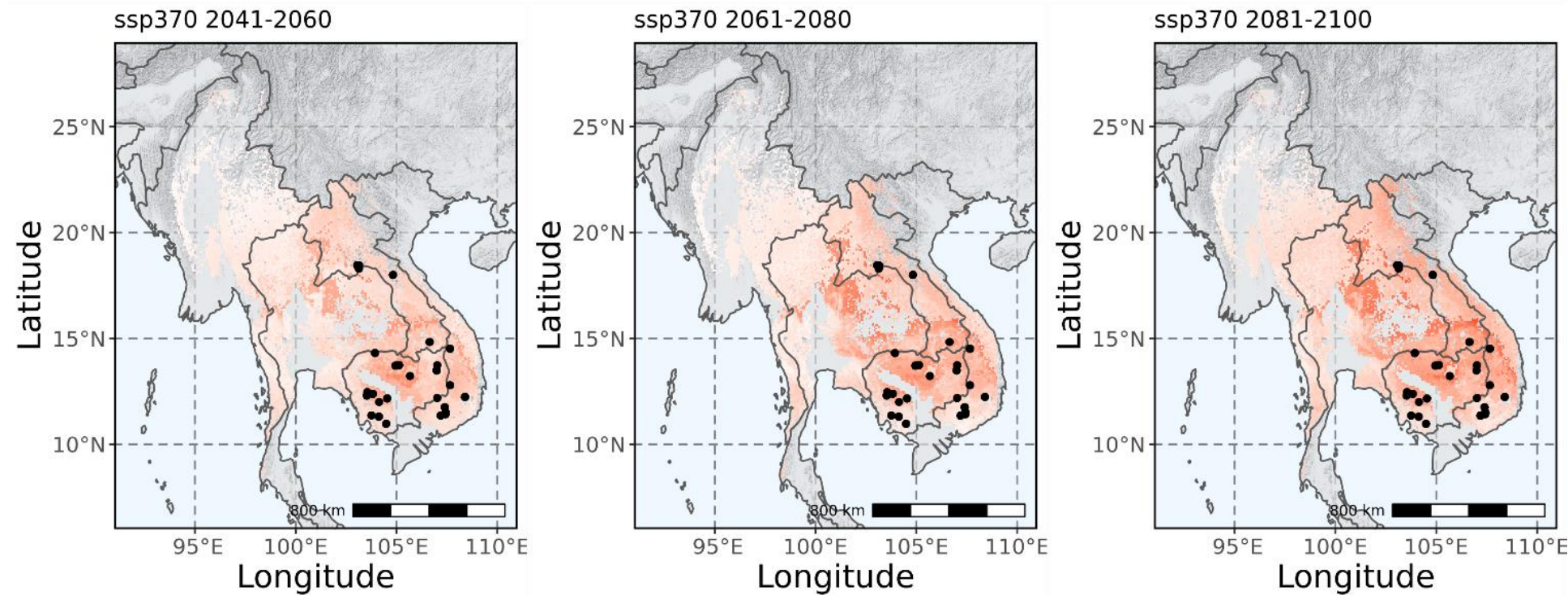
Genomic vulnerability prediction



3. Climate change



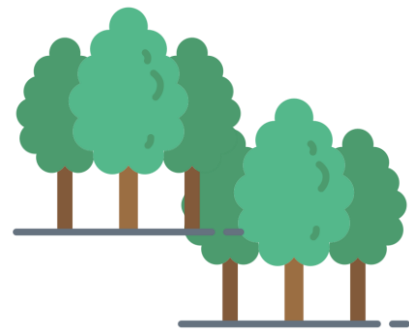
Highly vulnerable populations should be conserved with higher priority



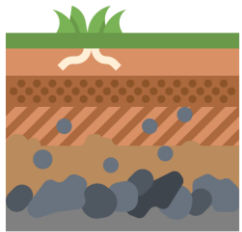
D. oliveri

Implication of genomic similarity

Genomic match measures where the **current** seed sources are most likely to adapt to a **future** restoration site

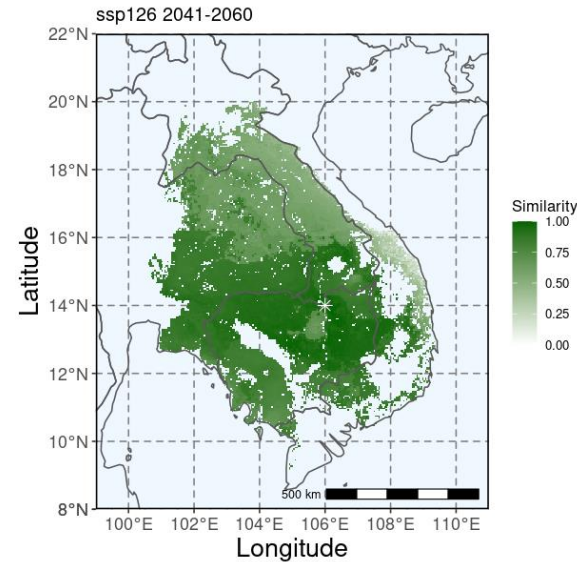


ex situ populations



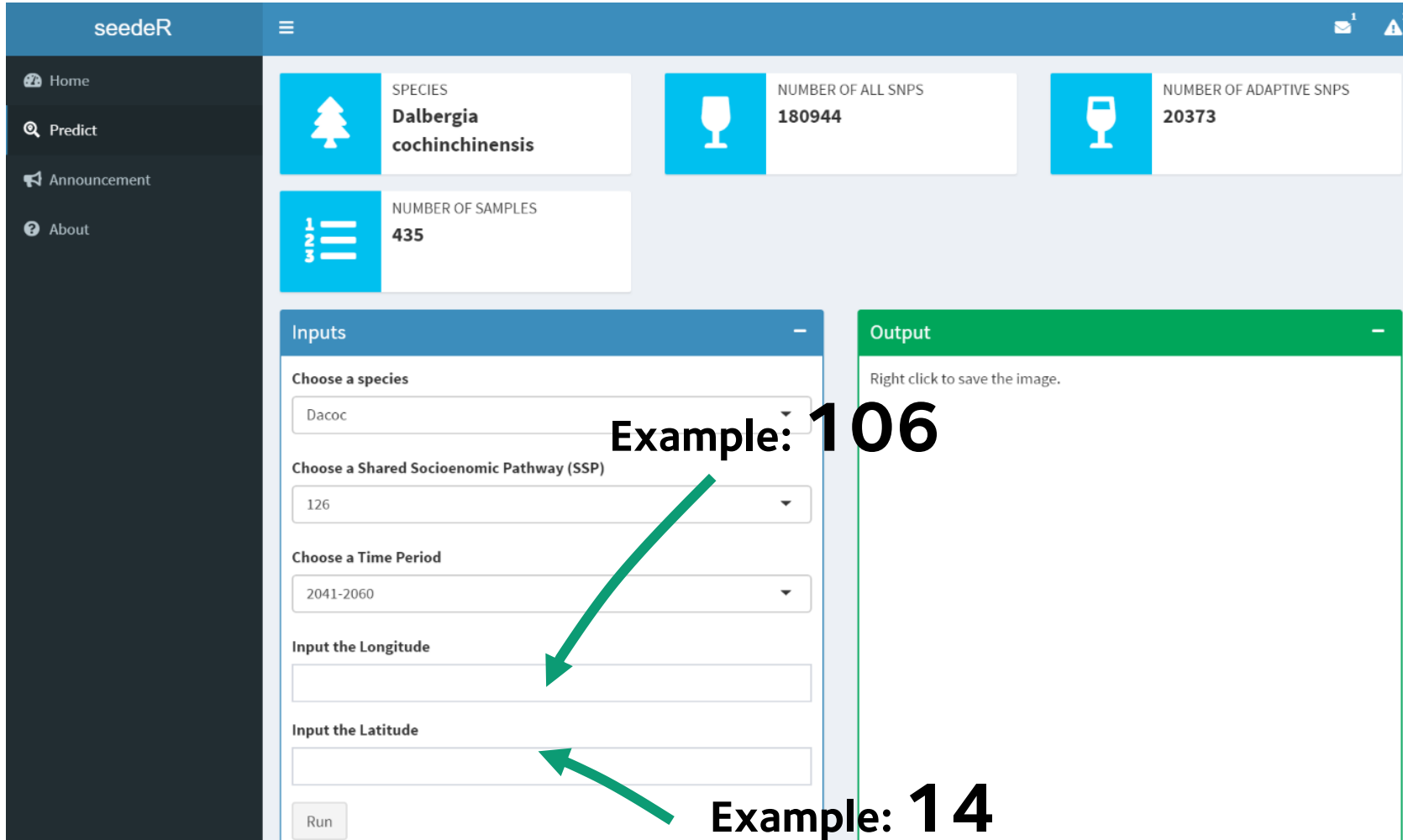
uncolonised sites

GPS



**Assisted
migration**

seedeR: an online app for genomic prediction



The screenshot shows the seedeR web application interface. At the top, there's a header with the 'seedeR' logo and navigation icons. A sidebar on the left contains links for Home, Predict, Announcement, and About. The main content area displays summary statistics for a selected species, *Dalbergia cochinchinensis*: 180,944 total SNPs and 20,373 adaptive SNPs, based on 435 samples. Below this is an 'Inputs' section with dropdown menus for species (Dacoc), Shared Socioeconomic Pathway (126), and Time Period (2041-2060), along with text boxes for longitude and latitude. A 'Run' button is at the bottom of the input section. To the right is an 'Output' section, currently empty, with a prompt to right-click to save the image. Two green arrows point from the 'Example: 106' text to the SSP dropdown and from 'Example: 14' to the latitude input field.

seedeR

Home Predict Announcement About

SPECIES
Dalbergia cochinchinensis

NUMBER OF ALL SNPS
180944

NUMBER OF ADAPTIVE SNPS
20373

NUMBER OF SAMPLES
435

Inputs

Choose a species
Dacoc

Choose a Shared Socioeconomic Pathway (SSP)
126

Choose a Time Period
2041-2060

Input the Longitude

Input the Latitude

Run

Output

Right click to save the image.

Example: 106

Example: 14

Supported by

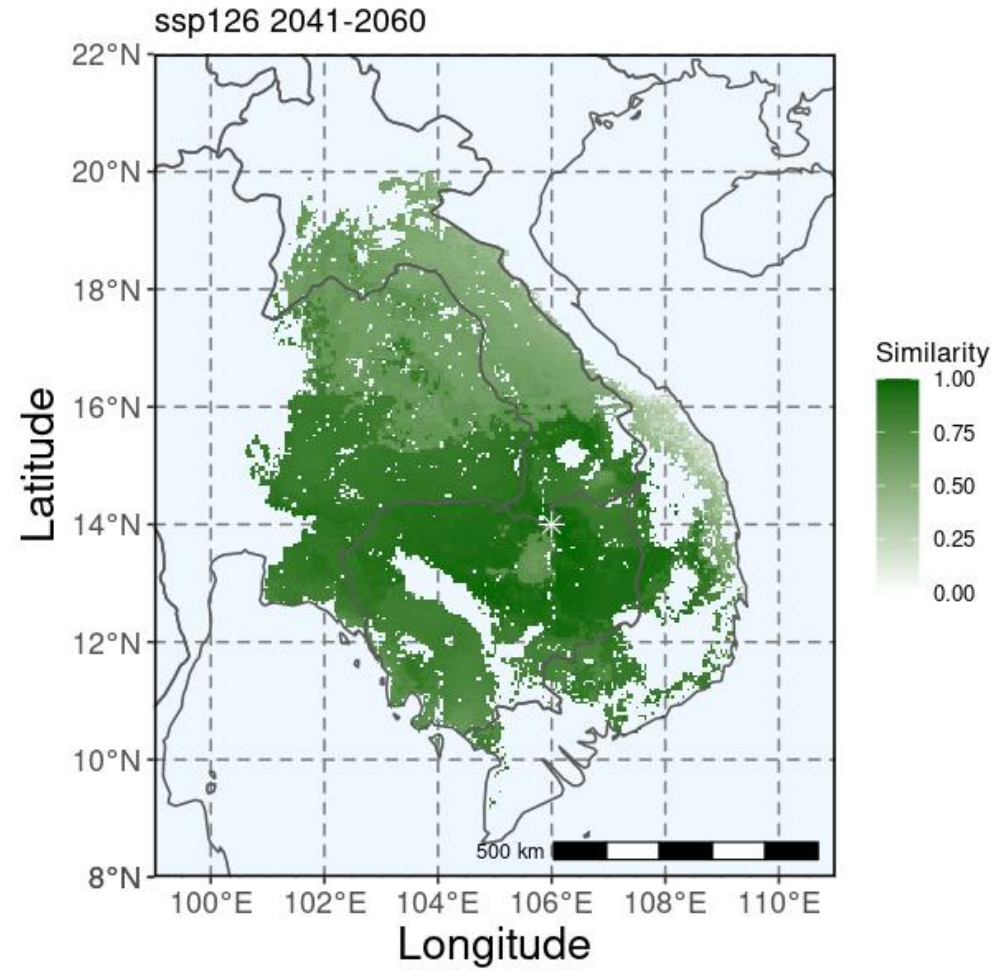


Interactive Data
Network

Developed in



seedeR: an online app for genomic prediction





1. Genetic bottlenecks

- Make sure the adaptive variation of the populations is well-represented in germplasm



2. Maladaptation

- Germplasms with strong local adaptation are recommended to conserve *in situ*



3. Climate change

- Populations with high genomic vulnerability are recommended to conserve *ex situ*
- Assisted migration, by matching current germplasm and future restoration site, can help the species pre-adapt the changing environment

Thank you

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Alliance



RESEARCH
PROGRAM ON
Forests, Trees and
Agroforestry