



Conservation gap analysis for crop wild relatives

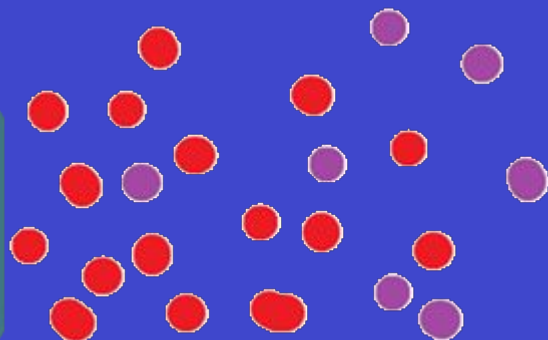
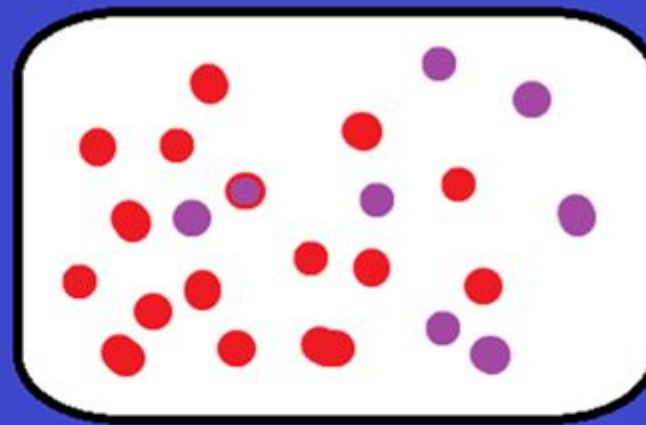
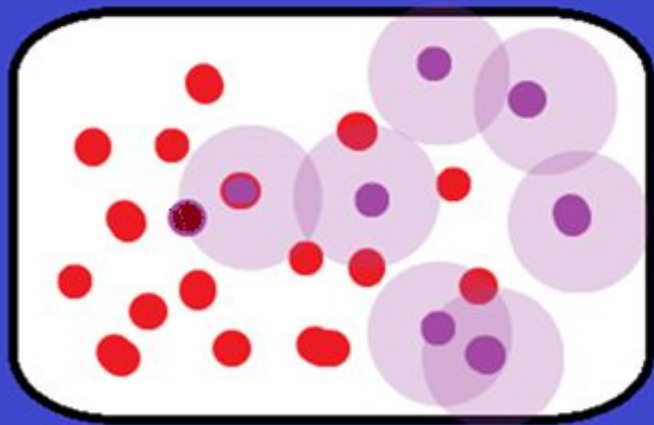
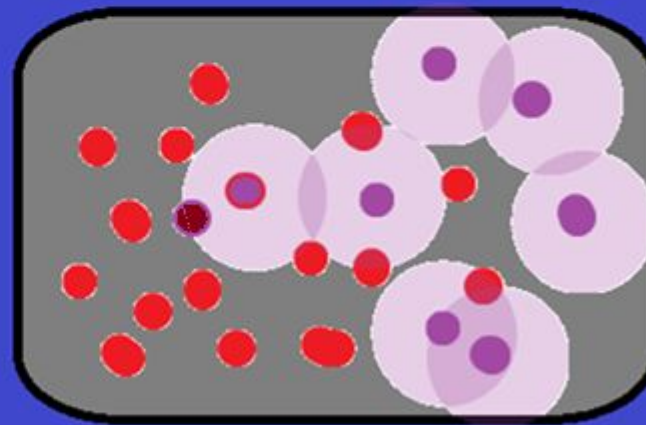
Alliance Bioversity International & CIAT

Outline

- Crop wild relatives and crops
- Use of crop wild relatives
- Importance of preserving crop wild relatives
- Approach and results to assess gaps in CWR collections
- An R package for assessing CWR gaps



The workflow for a gap analysis

A**Species occurrences****B****Realized niche****C****Sampled
germplasm****D****Where to collect****Germplasm****Other coordinates****Collected germplasm
area****Potential area to be
collected**

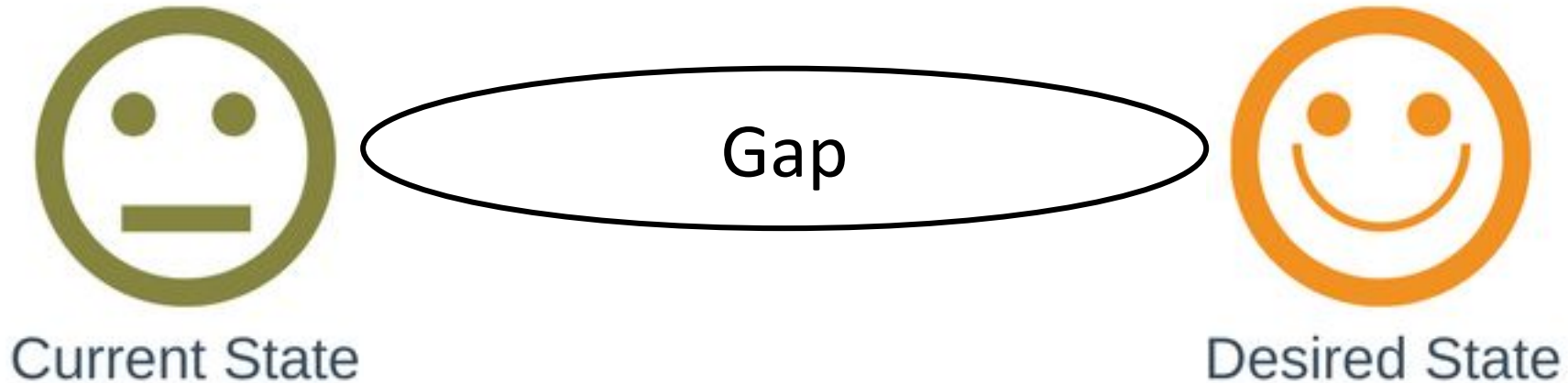


The gap analysis

What is a gap?

Something that is missing

Typically, this "something" takes us from a (current) undesired state to a (future) desired state





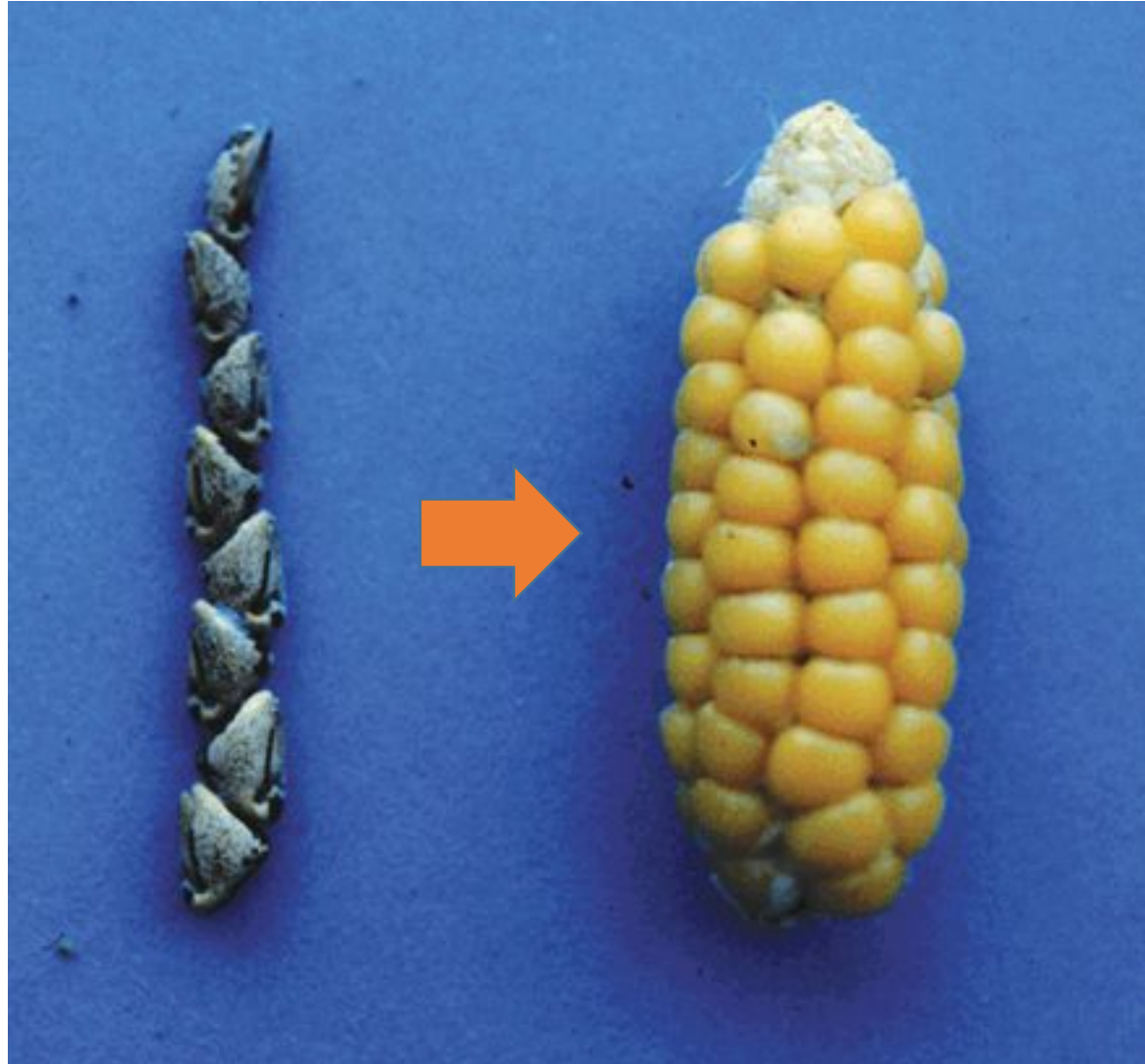
Use of crop wild relatives

Crop wild relatives



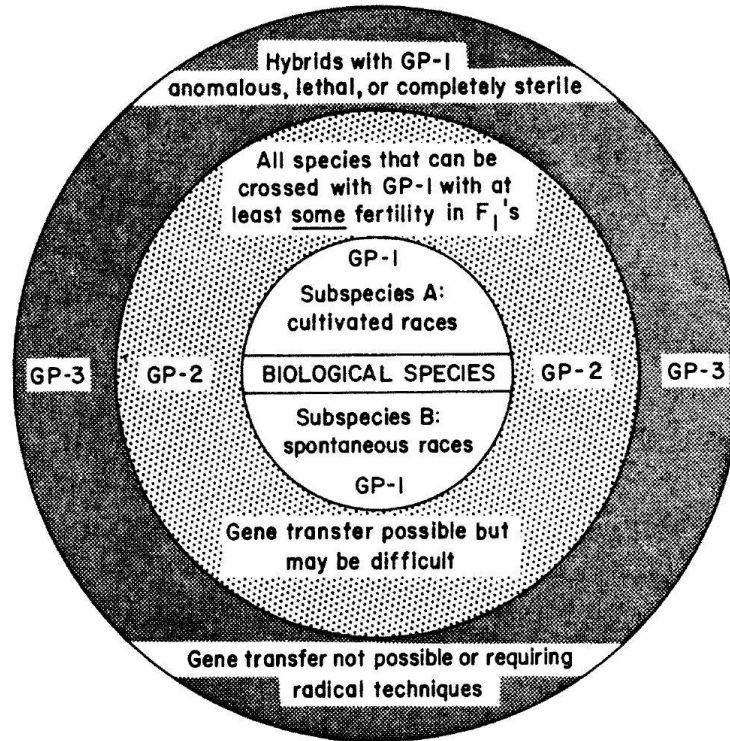
Left: *Solanum galapagense*, accession LA0317, collected in 1954 by Alf Kastedalen at Bartolome, Galapagos Islands. Photo credit: H. Teppner
Right: Cultivated tomato. Photo credit: Softeis, Wikimedia commons

Crop wild relatives

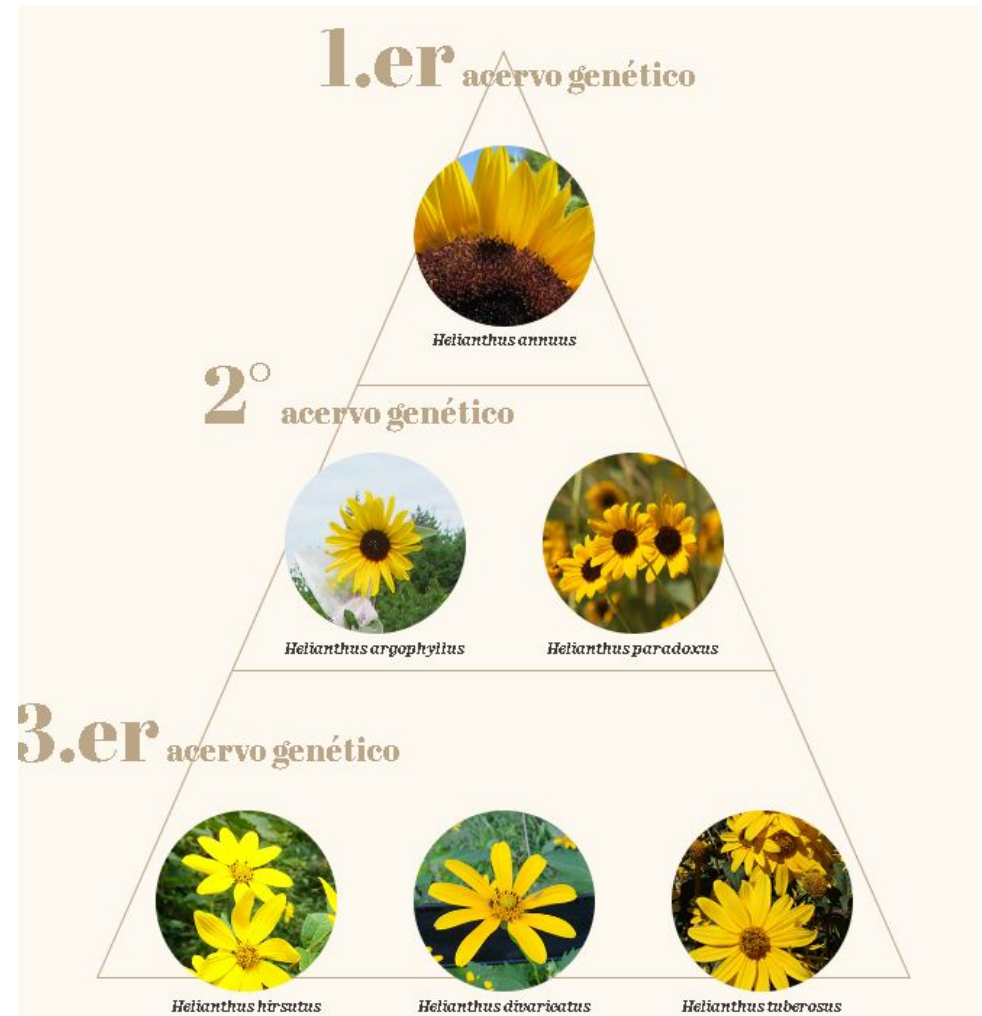


Crop wild what?

Wild plants related to domesticated



Harlan & de Wet (1971) *Taxon* 20(4): 509.



Global database for genetic relative assignments:

<https://npgsweb.ars-grin.gov/gringlobal/taxon/taxonomysearchcwr>

Global targets for agrobiodiversity conservation



United Nations Sustainable Development Goals SDG 2: End hunger, achieve food security and improved nutrition, and promote sustainable agriculture

Goal 2.5: “By 2020 maintain genetic diversity of seeds, cultivated plants, farmed and domesticated animals and their **related wild species**, including through soundly managed and diversified seed and plant banks at national, regional and international levels, and ensure access to and fair and equitable sharing of benefits arising from the utilization of genetic resources and associated traditional knowledge as internationally agreed.”

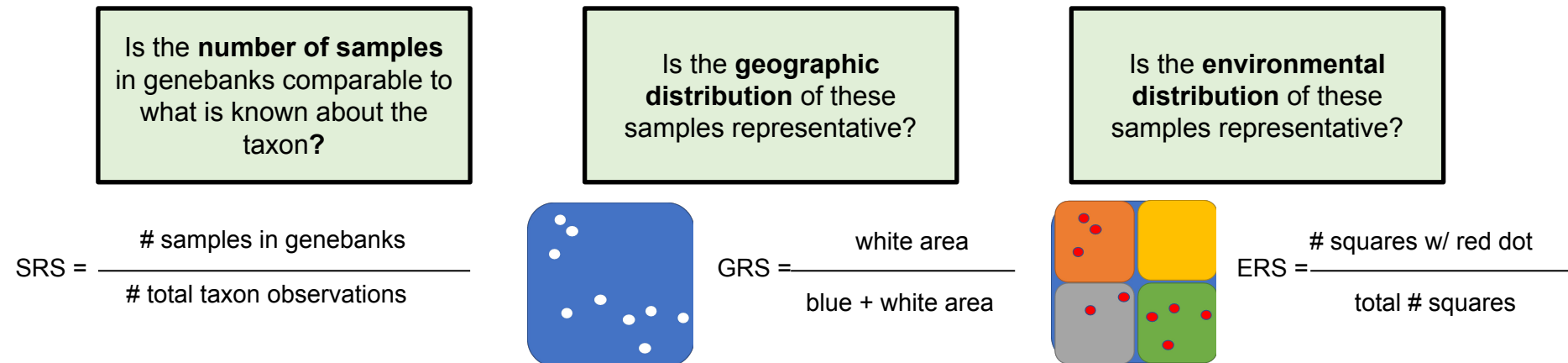


Convention on Biological Diversity Strategic Plan for Biodiversity 2011-2020 Aichi Biodiversity Targets

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.”

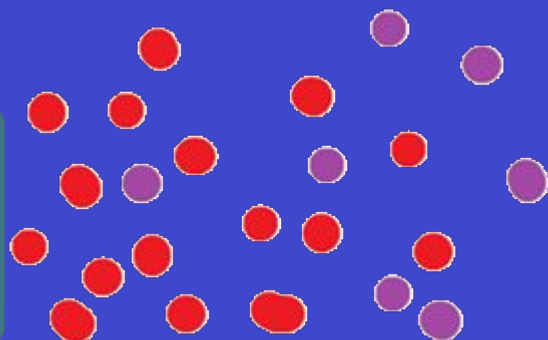
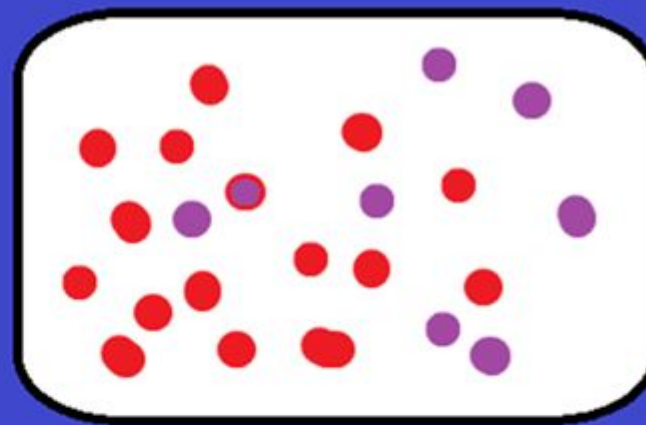
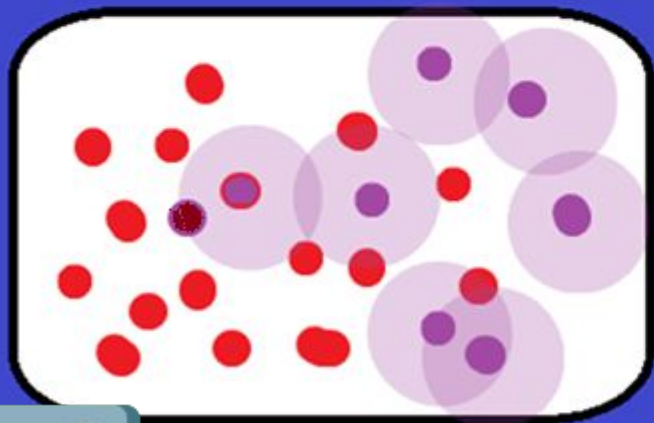
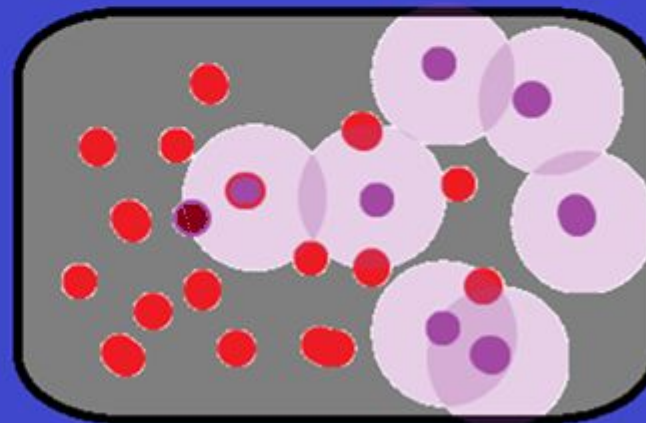
Methods for gap analysis of wild species

First, we want to know which taxa are well sufficiently conserved

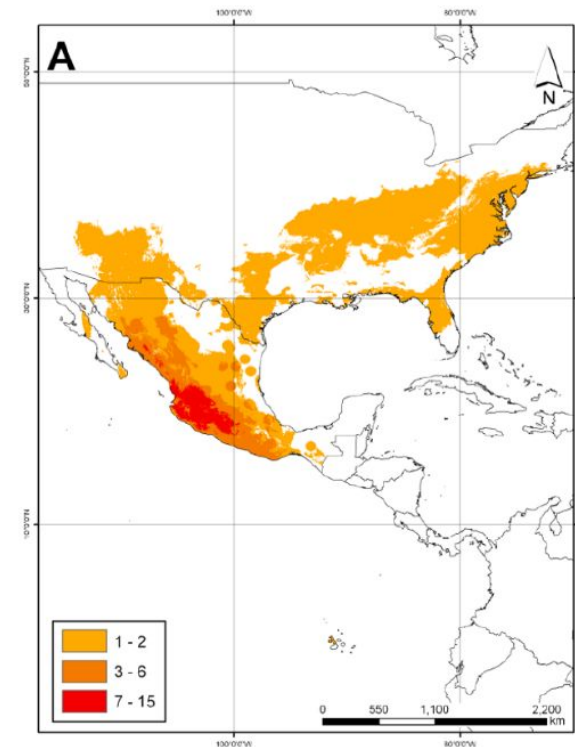
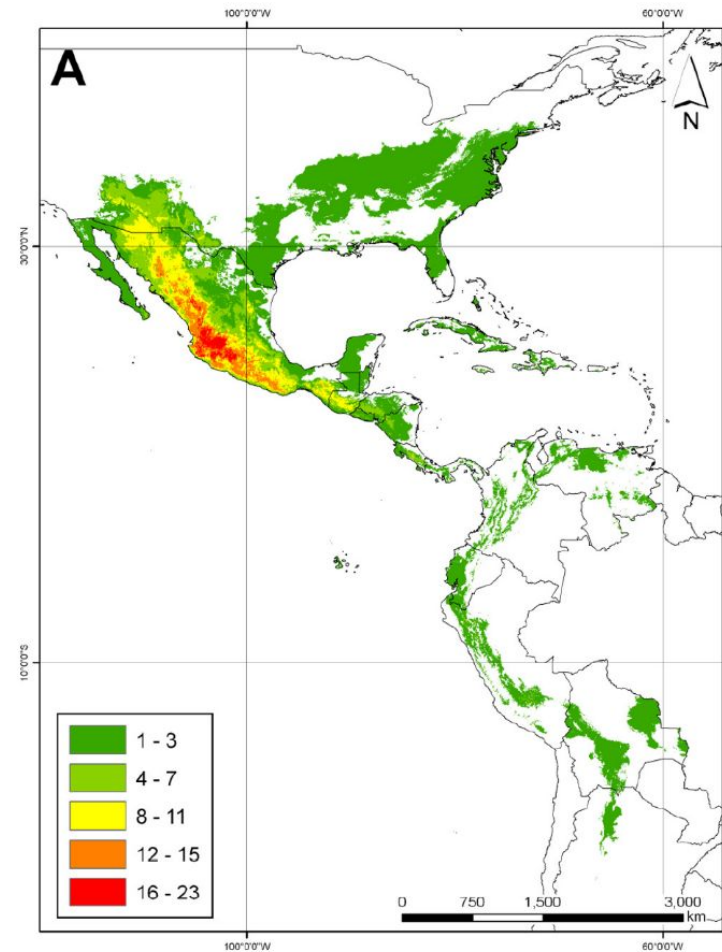




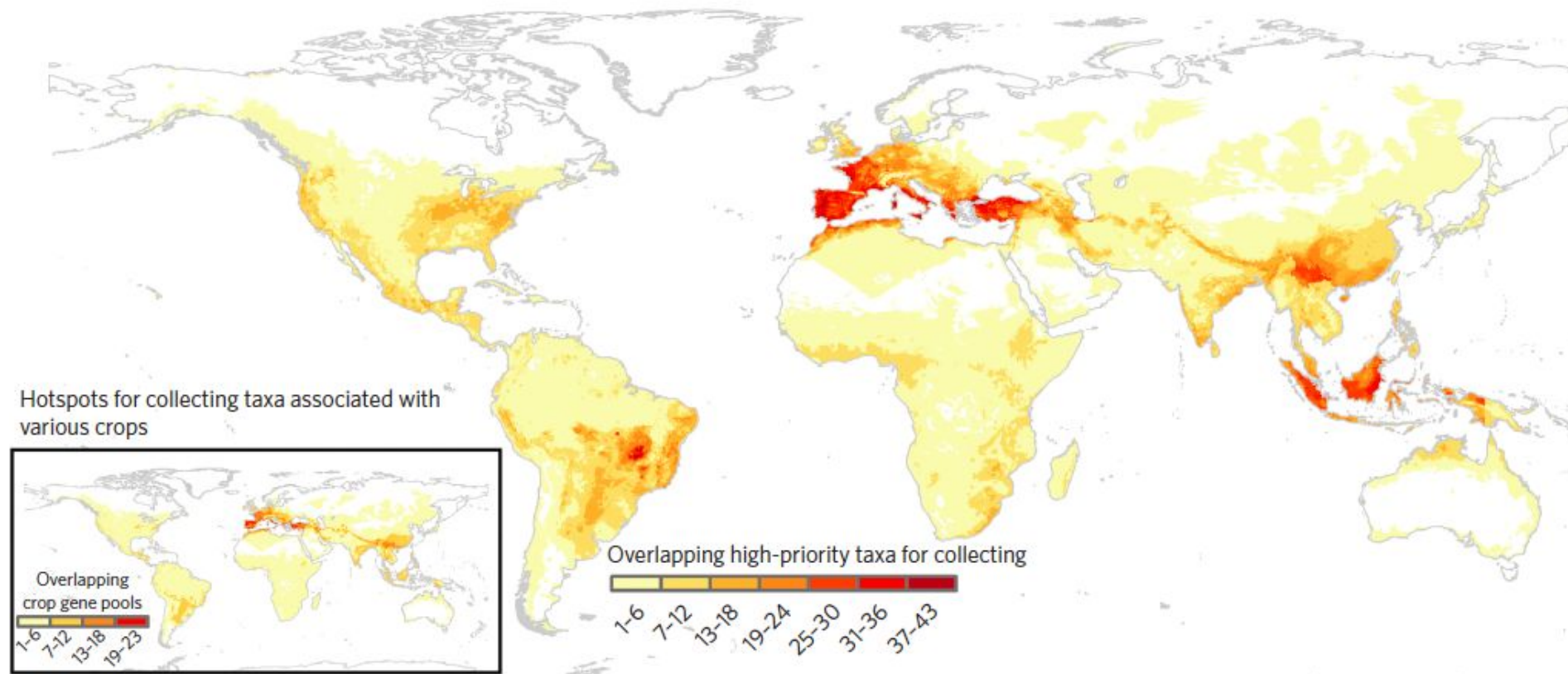
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Ex situ conservation gaps for crop wild relatives



Global *ex situ* conservation priorities for crop wild relatives



www.cwrdiversity.org

CWR priorities for conservation

71.1% (765): High priority for collecting

13.8% (148): Medium priority for collecting

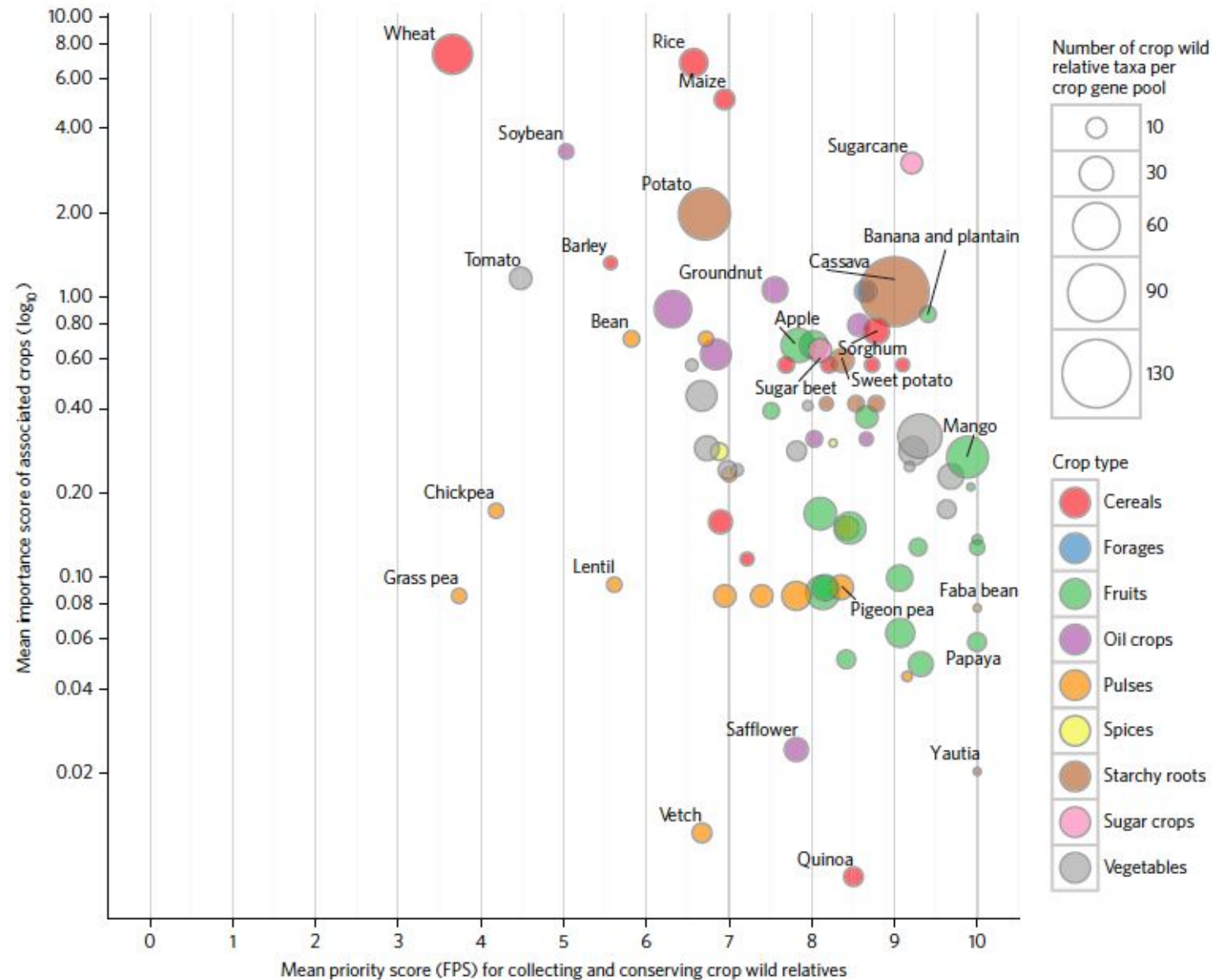
11.0% (118): Low priority for collecting

4.2% (45): Sufficiently represented

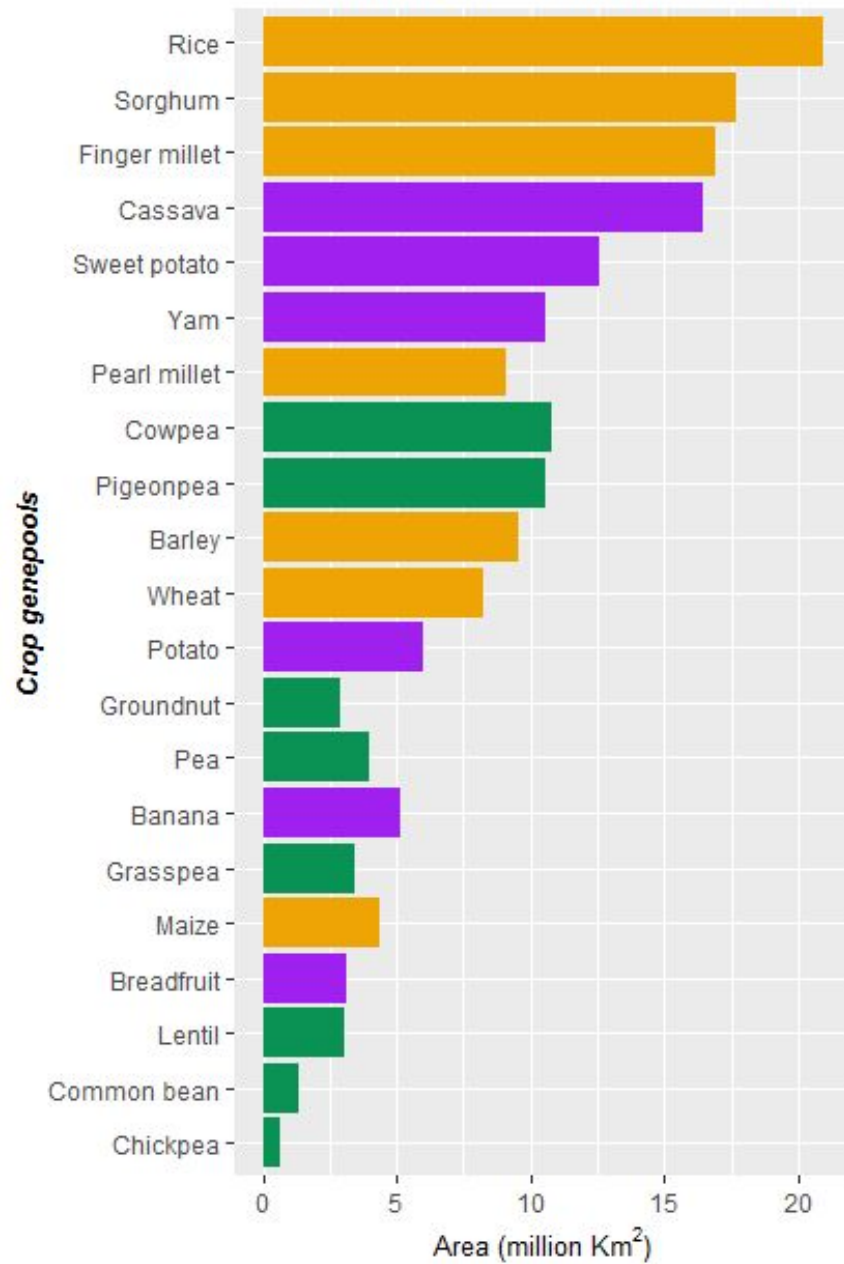
1,076

CWR taxa
analyzed

CWR priorities for conservation

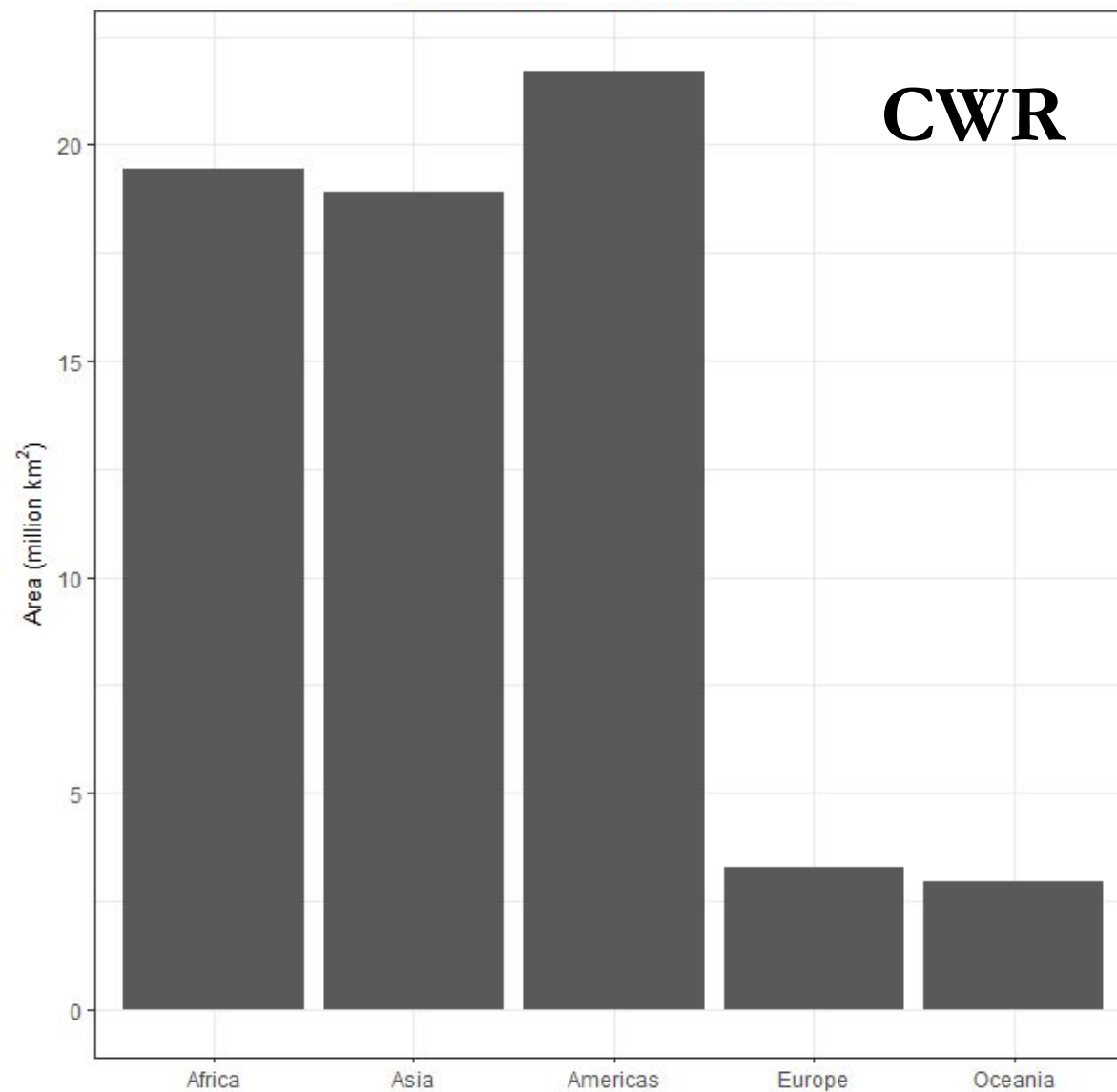


CWR priorities for conservation



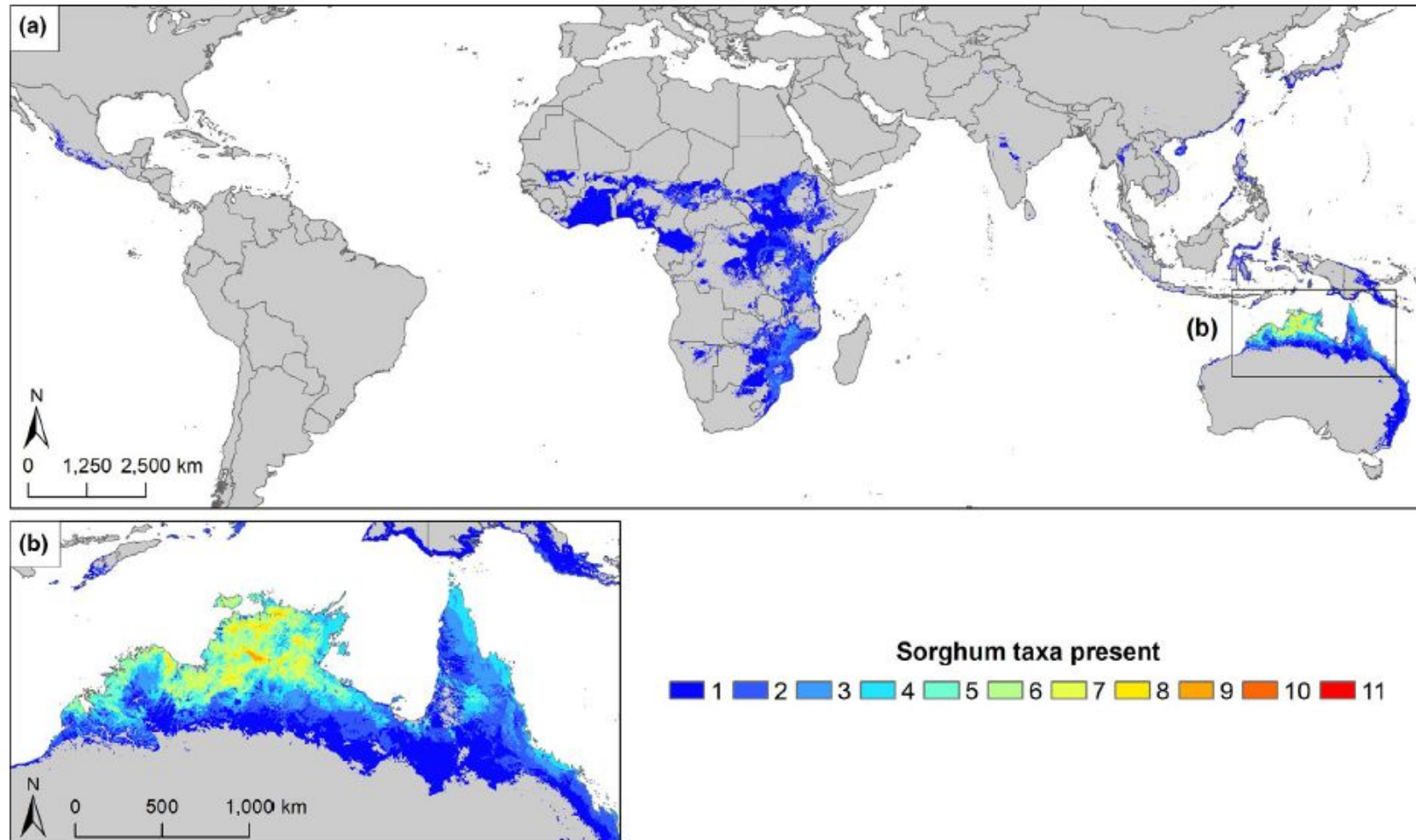
**Total global physical area
considered a gap**

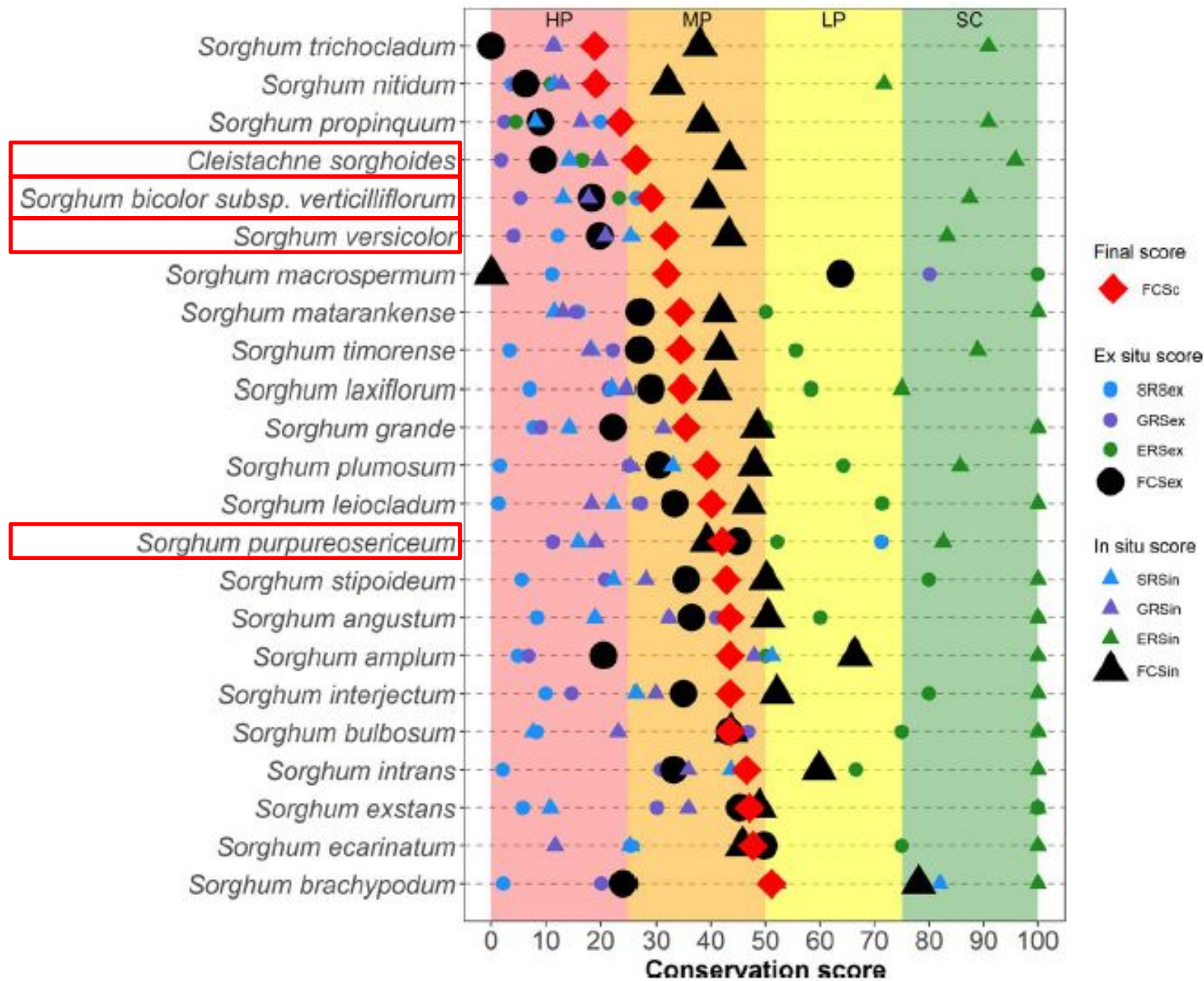
Regional CWR priorities for conservation



Castañeda-Álvarez and Khoury *et al.* (2016) *Nature Plants* 2(4): 16022.

An example with an African crop







R code for gap analysis



A JOURNAL OF SPACE
AND TIME IN ECOLOGY

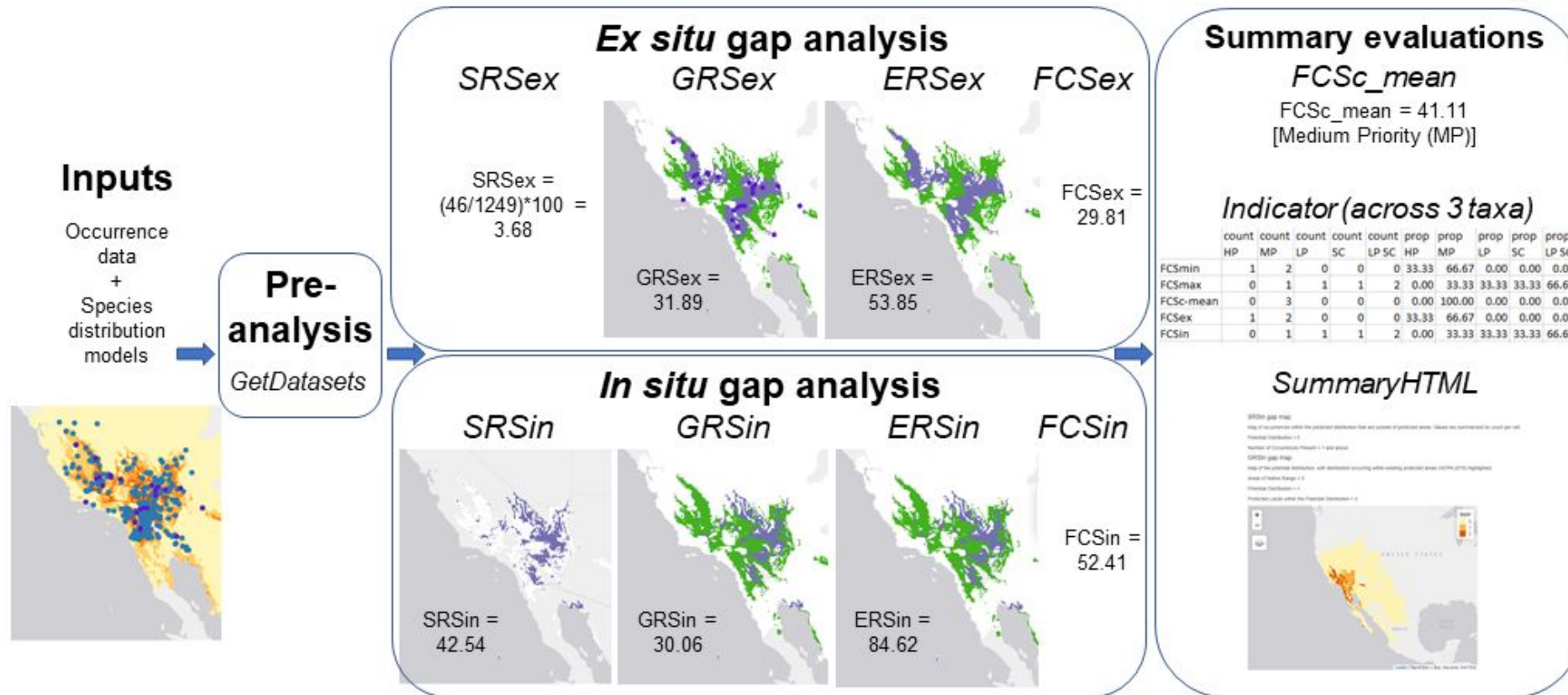
Software notes |  Open Access |  

GapAnalysis: an R package to calculate conservation indicators using spatial information

Daniel Carver, Chrystian C. Sosa, Colin K. Khoury, Harold A. Achicanoy, Maria Victoria Diaz, Steven Sotelo, Nora P. Castañeda-Álvarez, Julian Ramirez-Villegas 

First published: 04 May 2021 | <https://doi.org/10.1111/ecog.05430> | Citations: 18

An R code for conservation gap analysis



An R code for conservation gap analysis

Function family	Brief description	Input data	Outputs	Functions
Pre-analysis	Downloads input datasets required for the ex situ and in situ conservation gap analyses	No input is required, but an internet connection is needed	Files stored in the package installation folder	<i>GetDatasets</i>
Ex situ conservation gap analysis	Produces metrics that estimate the degree of representation in ex situ conservation repositories and identifies gaps in conservation	Occurrence data (data.frame), species distribution models (raster), G buffers (sp, sf), ecoregions layer (sp)	data.frame of evaluation metrics, GRSex and ERSex gap maps	<i>SRSex; GRSex; ERSex; FCSEX</i>
In situ conservation gap analysis	Produces metrics that estimate the degree of representation in protected natural areas and identifies gaps in conservation	Occurrence data (data.frame), species distribution models (raster), WDPA protected areas layer (raster), ecoregions layer (sp)	data.frame of evaluation metrics, SRSin, GRSin and ERSin gap maps	<i>SRSin; GRSin; ERSin; FCSin</i>
Summary evaluations	Combines conservation analyses, calculates indicator and produces taxon-level summary information	Output data.frame from ex situ and in situ gap analysis, gap maps (raster)	Data.frame of summary combined evaluation metrics, and indicator, across taxa. Html document per taxon	<i>FCSc_mean; indicator; SummaryHTML</i>

An R code for conservation gap analysis

Map of ex situ geographical representativeness (GRSex)

Map of the potential distribution, with previous germplasm collection points surrounded by a 50 km buffer overlaid. Only germplasm points are displayed on the map.

Native area (ecoregions within countries where species has been observed in the field) = 0

Potential distribution not conserved ex situ = 1

Potential distribution conserved ex situ (within G buffer) = 2






Lets try an example:
The true challenge














Install package: Version 2.0

- `remotes::install_github("CIAT-DAPA/GapAnalysis")`

Exercise

- Use *Cucurbita cordata*, *Cucurbita digitata*, and *Cucurbita palmata*
- Perform a gap analysis
- Prioritize where to collect those CWR species

Nombre 

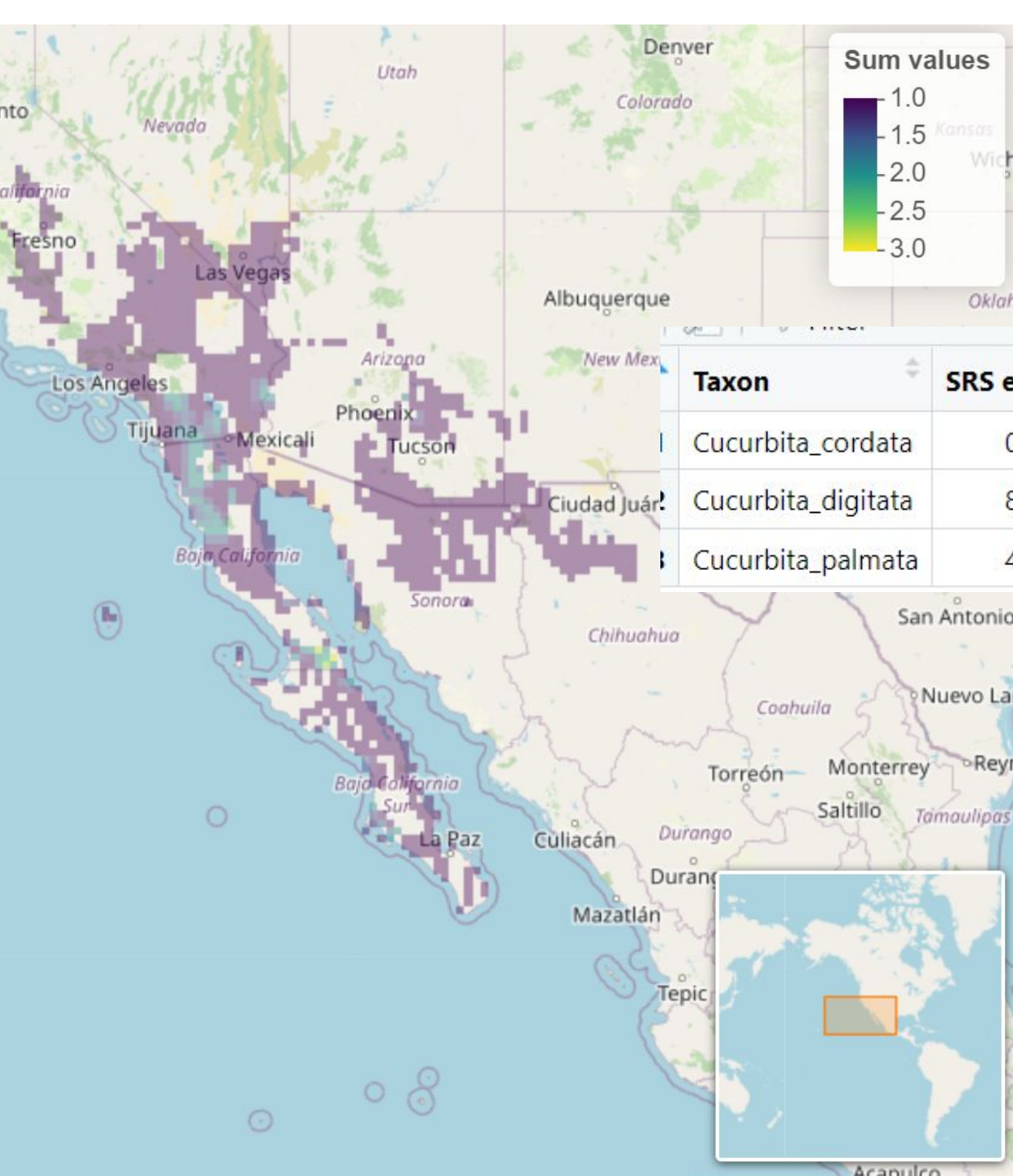
	SUMMARY_GAP_files	
	SUMMARY_GAP.html	
	occurrences.csv	
	Day_4_SDM.pptx	
	CWR_GAPANALYSIS.R	
	CWR_GAPANALYSIS_SUMMARY.R	
	Bactris_gasipaes_fc.LQHP_rm.1.5_p10.tif	



Time to interpret outcomes

- URGENT PRIORITY
- HIGH PRIORITY
- MEDIUM PRIORITY
- LOW PRIORITY

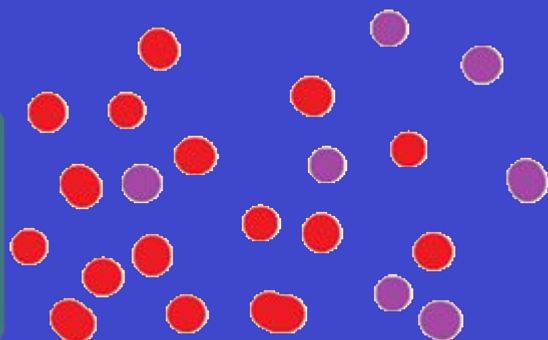
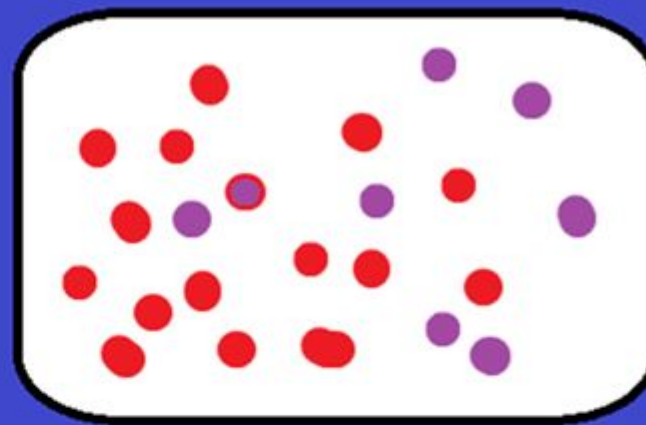
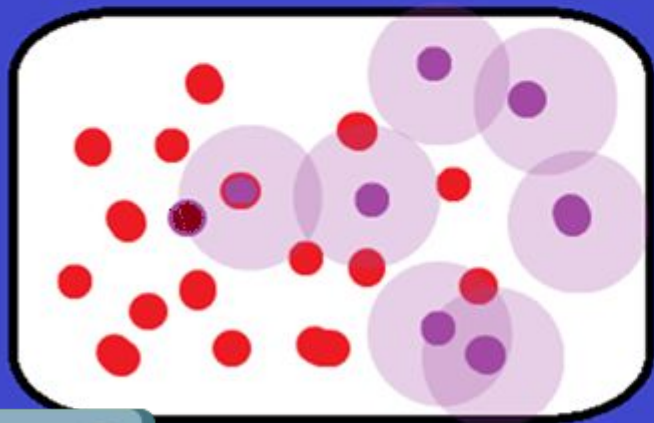
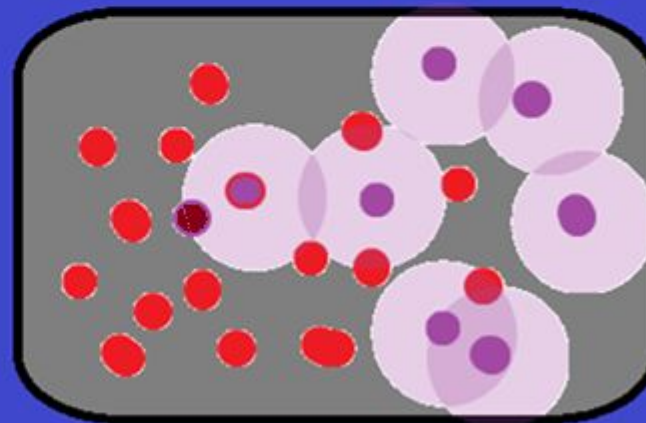
```
if (sp_fcs < 25) {  
  score <- "UP"  
}  
else if (sp_fcs >= 25 & sp_fcs < 50) {  
  score <- "HP"  
}  
else if (sp_fcs >= 50 & sp_fcs < 75) {  
  score <- "MP"  
}  
else {  
  score <- "LP"  
}
```

Taxon	SRS exsitu	GRS exsitu	ERS exsitu	FCS exsitu	FCS existu score
Cucurbita_cordata	0.7246377	9.749187	25.00000	11.82461	UP
Cucurbita_digitata	8.1196581	26.208536	70.00000	34.77606	HP
Cucurbita_palmata	4.1078306	20.597421	71.42857	32.04461	HP



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Resources

Blog about history of gap analysis with links to all papers and resources:

<https://agro.biodiver.se/2021/06/the-making-of-gapanalysis-r/>

Gapanalysis.R codesites:

<https://github.com/CIAT-DAPA/GapAnalysis>

<https://cran.r-project.org/web/packages/GapAnalysis/index.html>

Some key papers:

Castañeda-Álvarez and Khoury et al. (2016) Global conservation priorities for crop wild relatives. *Nature Plants* 2(4): 16022.

Ramírez-Villegas et al. (2010) A gap analysis methodology for collecting crop genepools: a case study with *Phaseolus* beans. *PLoS One* 5(10): e13497.

Carver et al. (2021) GapAnalysis: an R package to calculate conservation indicators using spatial information. *Ecography* 44(7): 1000-1009.

Khoury et al. (2021) Crop genetic erosion: understanding and responding to loss of crop diversity. *New Phytologist* 233(1): 84-118.



Questions?