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Recursos Genéticos e Biotecnologia

Germplasm collecting: filling the gaps on crop wild relatives in *ex situ* collections in Brazil

Marcelo Brilhante de Medeiros

Adapting Agriculture to Climate Change: A Global Initiative to Collect, Conserve, and Use Crop Wild Relative –https://www.cwrdiversity.org/

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CIAT International Center for Tropical Agriculture Since 1967 Science to cultivate change

Wild crop relatives (WCR) - Background

- WCR: disease resistance, pests and abiotic stresses tolerances;
- Increasing cultivars containing WCR genes;
- Major gaps in genetic diversity have not been filled in germplasm banks;
- Destruction of natural habitats, invasive species, changes from traditional to industrial agriculture and climate change;

Wild Crop Relatives

* ~ 1000,000 WCR species have high priority for food security
* Prioritization in a resource-constrained and time-limited environment: Which species to collect? Where to collect?
* Gap analysis: database intensive, new computational tools and GIS to generate these responses

Análise de lacunas

OPEN ACCESS Freely available online

PLoS one

A Gap Analysis Methodology for Collecting Crop Genepools: A Case Study with *Phaseolus* Beans

Julián Ramírez-Villegas[1]*, Colin Khoury[2], Andy Jarvis[1,3,4], Daniel Gabriel Debouck[5], Luigi Guarino[2]

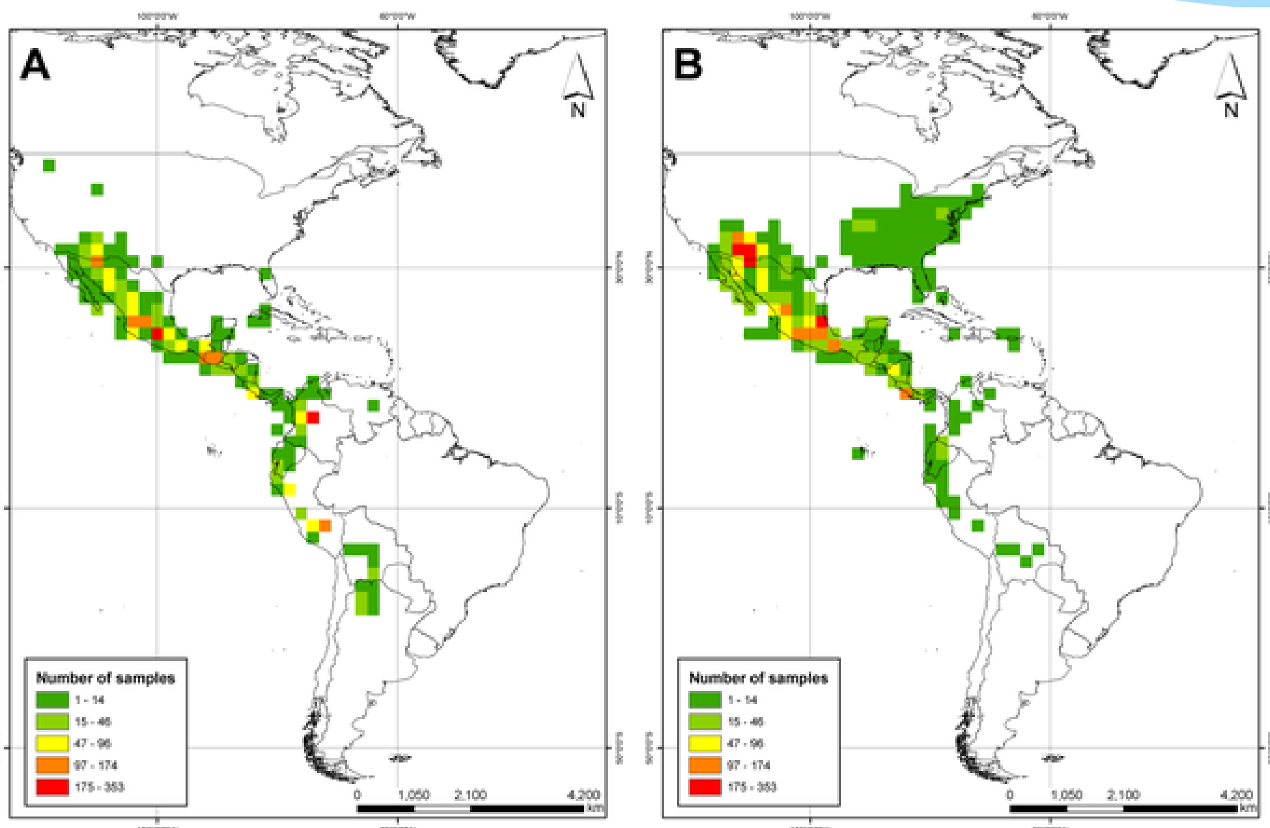


Figure 1. Sampling density (richness records) for (A) herbarium and Germplasm genebanks (B).

Gap analysis

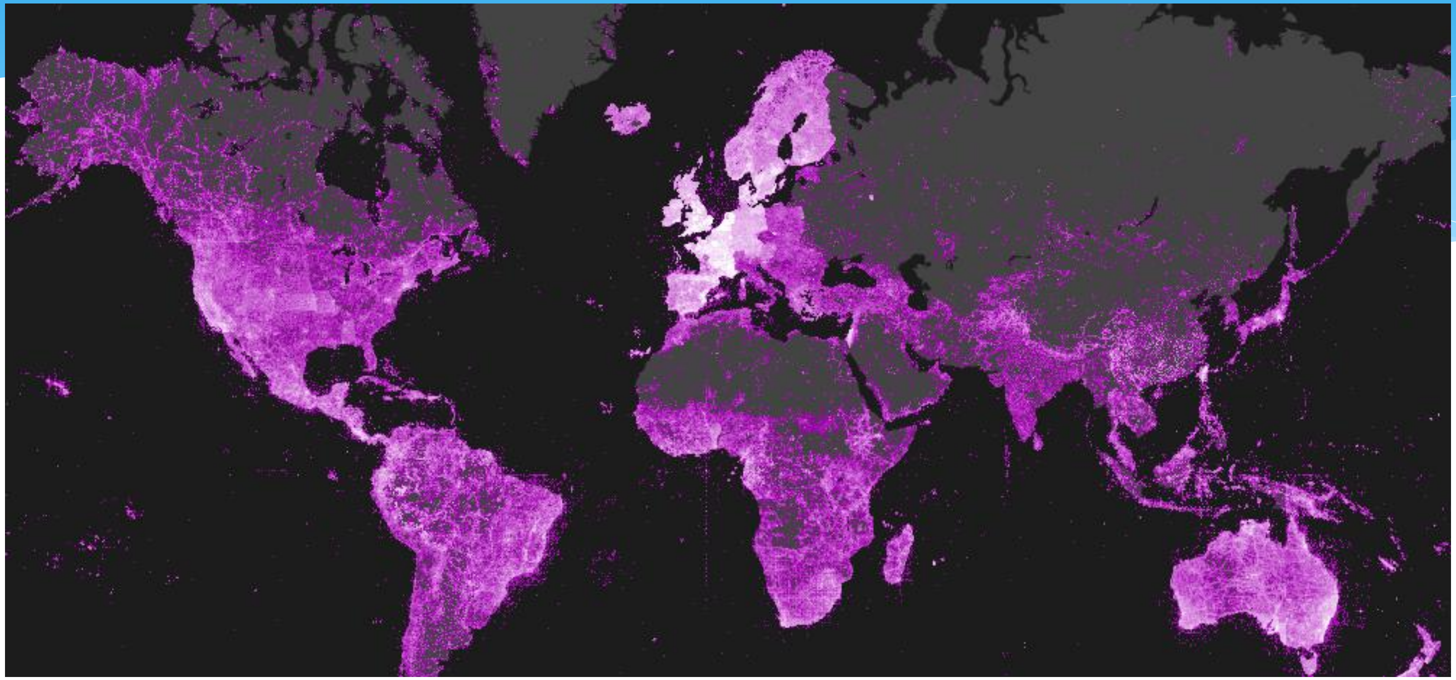
* Sampling representativity = germplasm accessions in relation to herbarium records
* Geographic representativeness = geographic distribution of taxax and spatial distribution of genebanks samples
* Environmental representativeness = environmental coverage of genebank samples and potential environmental areas

Gap analysis

* species rarity = number of populations in rare environments and total number of populations

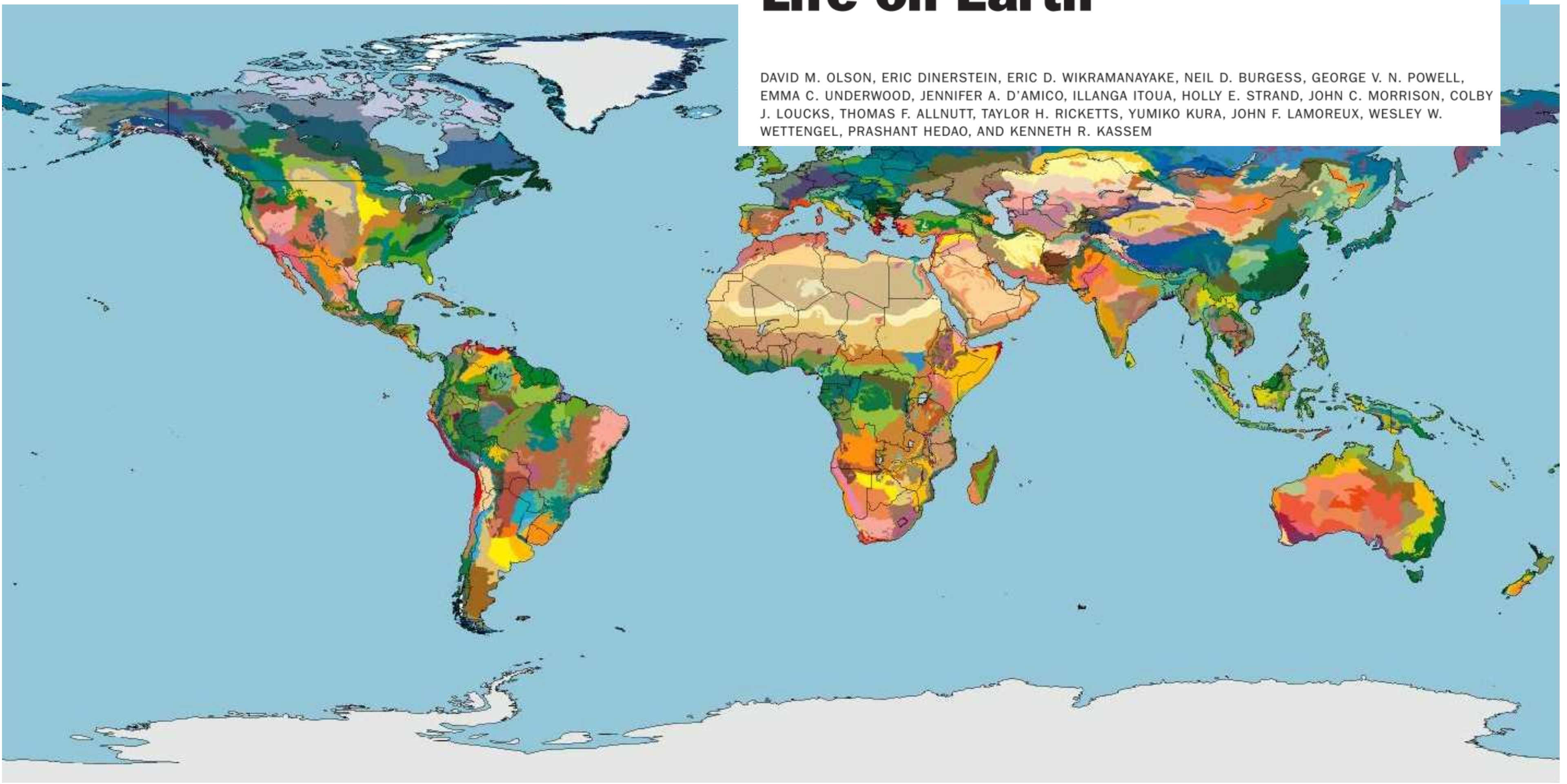
* Final score = sampling, geographical, environmental and rarity representativity scores

Gap analysis – data



GBIF
Global Biodiversity
Information Facility

Gap analysis



Terrestrial Ecoregions of the World: A New Map of Life on Earth

DAVID M. OLSON, ERIC DINERSTEIN, ERIC D. WIKRAMANAYAKE, NEIL D. BURGESS, GEORGE V. N. POWELL, EMMA C. UNDERWOOD, JENNIFER A. D'AMICO, ILLANGA ITOUA, HOLLY E. STRAND, JOHN C. MORRISON, COLBY J. LOUCKS, THOMAS F. ALLNUTT, TAYLOR H. RICKETTS, YUMIKO KURA, JOHN F. LAMOREUX, WESLEY W. WETTENGEL, PRASHANT HEDAO, AND KENNETH R. KASSEM

WorldClim - Global Climate Data

Free climate data for ecological modeling and GIS

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WorldClim

WorldClim is a set of global climate layers (climate grids) with a spatial resolution of about 1 square kilometer. The data can be used for mapping and spatial modeling in a GIS or with other computer programs. If you are not familiar with such programs, you can try DIVA-GIS or the *R* raster package.

The current version is Version 1.4 (release 3). Please write us if you find any problems.

WorldClim 1.4: Current conditions (~1960-1990)

If you need the highest resolution (**30 arc-seconds (~1 km)**) then you can **download by tile**. See the Methods page for more info on how these data were generated, and this page for info on details about the data (such as units).

Generic grid format

variable	10 minutes	5 minutes	2.5 minutes	30 seconds
minimum temperature (°C * 10)	tmin 10m	tmin 5m	tmin 2.5m	tmin 30s
maximum temperature (°C * 10)	tmax 10m	tmax 5m	tmax 2.5m	tmax 30s
average temperature (°C * 10)	tavg 10m	tavg 5m	tavg 2.5m	tavg 30s
precipitation (mm)	prec 10m	prec 5m	prec 2.5m	prec 30s
bioclimatic variables	bio 10m	bio 5m	bio 2.5m	bio1-9, 10-19

ESRI grids

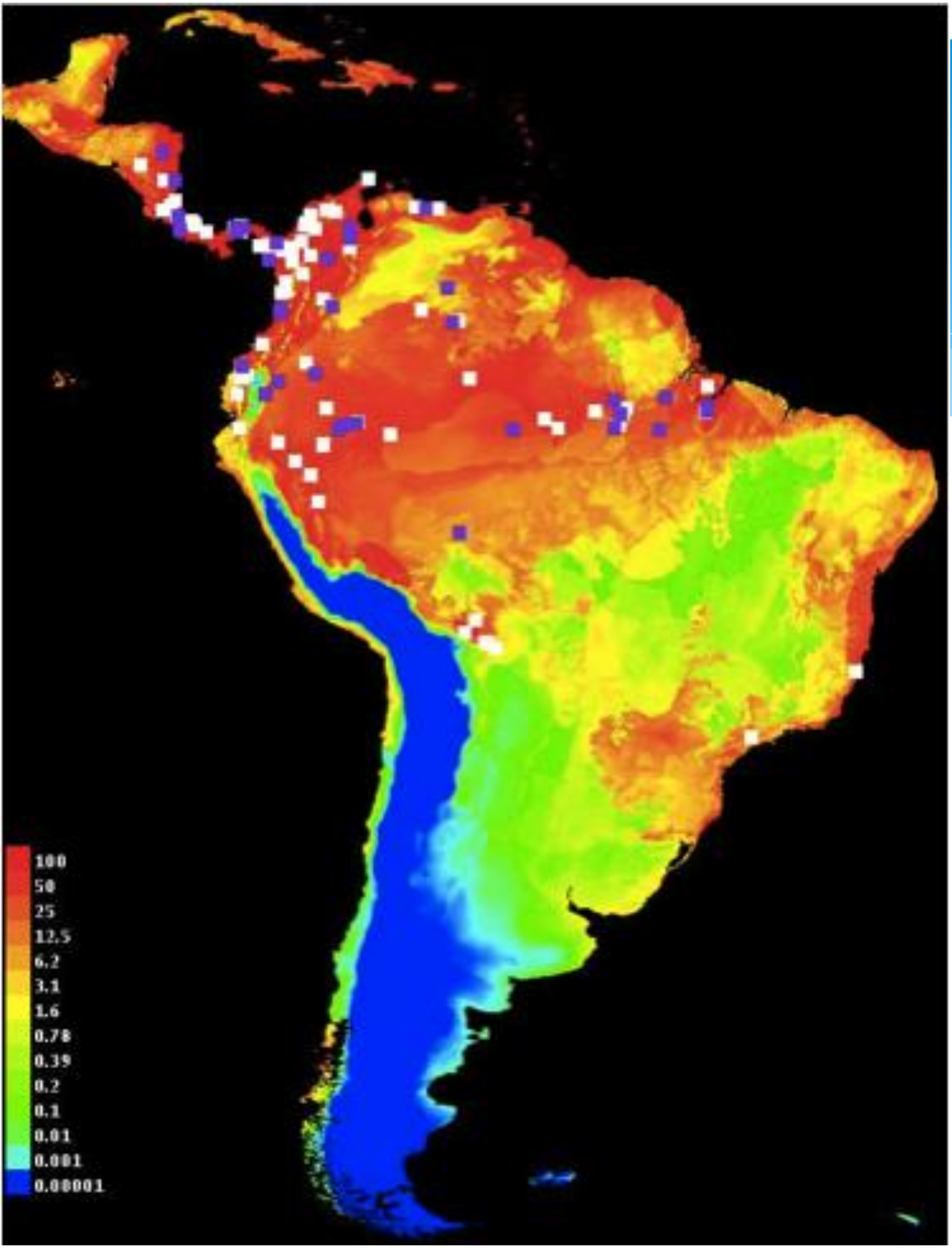
variable	10 minutes	5 minutes	2.5 minutes	30 seconds
minimum temperature (°C * 10)	tmin 10m	tmin 5m	tmin 2.5m	tmin 30s
maximum temperature (°C * 10)	tmax 10m	tmax 5m	tmax 2.5m	tmax 30s
average temperature (°C * 10)	tavg 10m	tavg 5m	tavg 2.5m	tavg 30s
precipitation (mm)	prec 10m	prec 5m	prec 2.5m	prec 30s
bioclimatic variables	bio 10m	bio 5m	bio 2.5m	bio 30s

Bioclimatic variables

Bioclimatic variables are derived from the monthly temperature and rainfall values in order to generate more biologically meaningful variables. These are often used in species distribution modeling and related ecological modeling techniques. The bioclimatic variables represent annual trends (e.g., mean annual temperature, annual precipitation) seasonality (e.g., annual range in temperature and precipitation) and extreme or limiting environmental factors (e.g., temperature of the coldest and warmest month, and precipitation of the wet and dry quarters). A quarter is a period of three months (1/4 of the year).

They are coded as follows:

BIO1 = Annual Mean Temperature
BIO2 = Mean Diurnal Range (Mean of monthly (max temp - min temp))
BIO3 = Isothermality (BIO2/BIO7) (* 100)
BIO4 = Temperature Seasonality (standard deviation *100)
BIO5 = Max Temperature of Warmest Month
BIO6 = Min Temperature of Coldest Month
BIO7 = Temperature Annual Range (BIO5-BIO6)
BIO8 = Mean Temperature of Wettest Quarter
BIO9 = Mean Temperature of Driest Quarter
BIO10 = Mean Temperature of Warmest Quarter
BIO11 = Mean Temperature of Coldest Quarter
BIO12 = Annual Precipitation
BIO13 = Precipitation of Wettest Month
BIO14 = Precipitation of Driest Month
BIO15 = Precipitation Seasonality (Coefficient of Variation)
BIO16 = Precipitation of Wettest Quarter
BIO17 = Precipitation of Driest Quarter
BIO18 = Precipitation of Warmest Quarter
BIO19 = Precipitation of Coldest Quarter



Gap analysis - processing

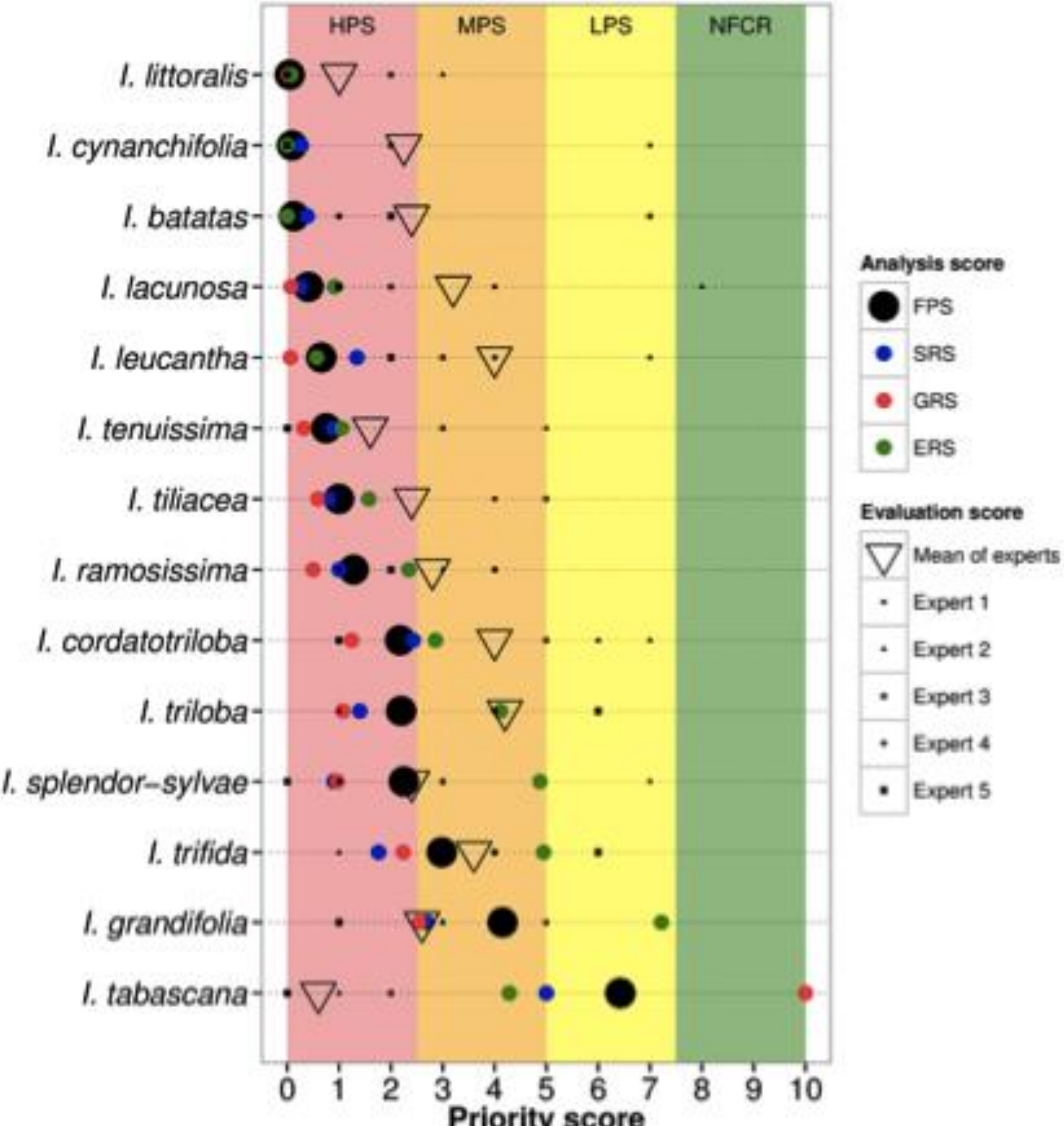
Maxent: niche modelling

WCR - priorities

Ex situ conservation priotities for *Ipomoea* – Khoury et al. 2015. Frontiers in Plant Science

Taxon	Gene pool	Ploidy	Germplasm accessions	Gap analysis priority	Mean expert priority	Eco geographic cluster	Potential adaptation to
Ipomoea batatas	2	4x = 60	4 (0)	HPS	HPS	2	Heat, high precipitation, drought, precipitation seasonality, clay soils
I. cordatotriloba	3	2x, 4x	103 (67)	HPS	MPS	1	Cold, temperature variation, clay soils, sandy soils
I. cynanchifolia	3	2x = 30	1 (0)	HPS	HPS	1,2	Drought, precipitation seasonality, sandy soils
I. grandifolia	3	2x = 30	124 (83)	MPS	MPS	1	Cold, temperature variation, clay soils, sandy soils
I. lacunosa	3	2x = 30	10 (1)	HPS	MPS	1	Cold, temperature variation, drought
I. leucantha	3	2x = 30	18 (15)	HPS	MPS	1,2	Heat, drought, precipitation seasonality, sandy soils
I. littoralis	2	2x = 30	2 (2)	HPS	HPS	2	Heat, high precipitation, drought, precipitation seasonality, sandy soils
I. ramosissima	3	2x = 30	34 (30)	HPS	MPS	2,1	Cold, high precipitation, clay soils
I. splendor-sylvae	3	2x = 30	16 (9)	HPS	HPS	2	Heat, high precipitation, drought, precipitation seasonality, clay soils
I. tabascana	2	4x = 60	4 (2)	LPS	HPS	2	Heat, high precipitation, clay soils
I. tenuissima	3	2x = 30	3 (1)	HPS	HPS	1	Heat, cold, temperature variation, sandy soils
I. tiliacea	3	4x = 60	61 (44)	HPS	HPS	2	Heat, high precipitation, clay soils
I. trifida	2	2x,3x,4x,6x	248 (159)	MPS	MPS	2	Heat, high precipitation, drought, precipitation seasonality
I. triloba	3	2x = 30	121 (74)	HPS	MPS	2,1	Heat, drought

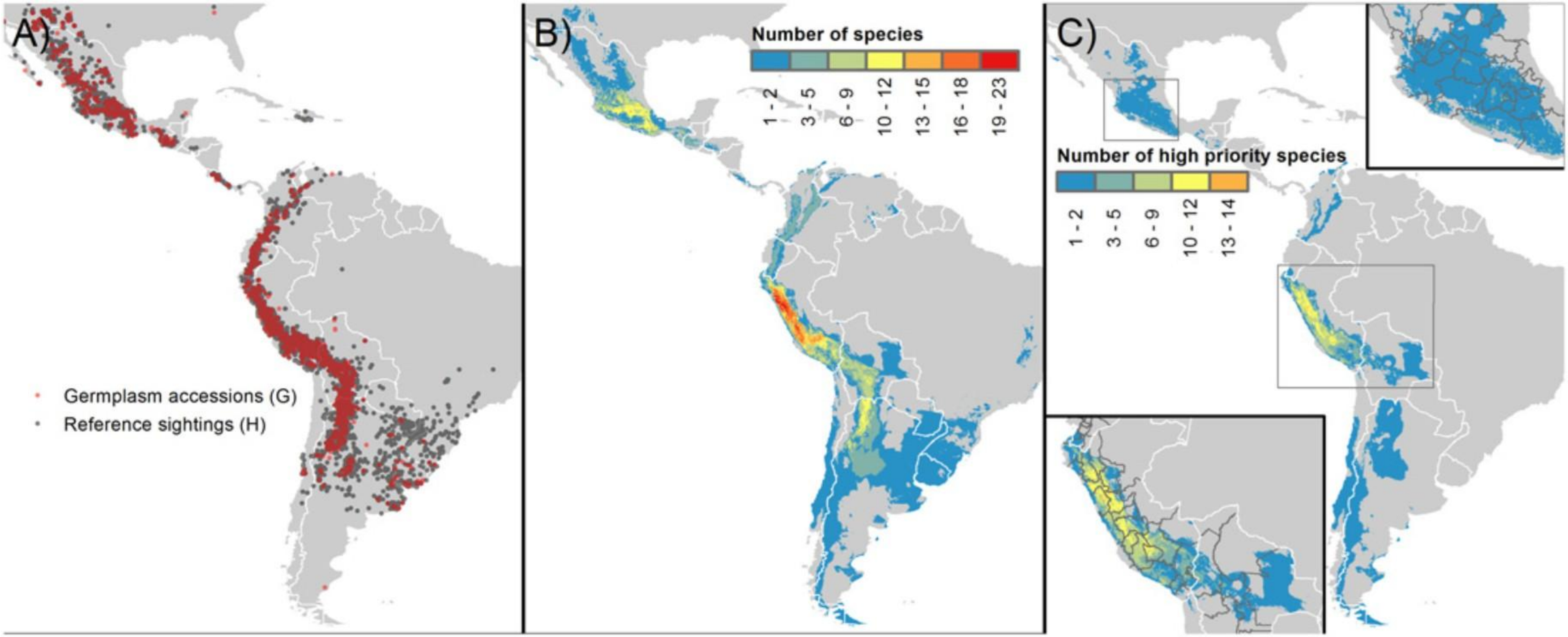
Ploidy data adapted from Nimmakayala et al. (2011). Germplasm accessions displays both the total number of accessions recorded in genebanks, as well as the number of accessions with unique geographic coordinates (i.e., unique populations) in parenthesis. HPS = high, MPS = medium, and LPS = low priority species for further collecting.



Ex situ conservation priotities for *Ipomoea*– Khoury et al. 2015, Frontiers in Plant Science

Ex situ conservation priotities for potato (*Solanum* L. Section Petota)
Castaneda-Alvarez *et al*. 2015. PlosOne

Disease resistance: *S. acaule, S. bulbocastanum, S. chacoense, S. demissum* and *S. stoloniferum.*



* "Filling the gaps of wild relatives in ex situ collections: Eleusine, Ipomoea, Oryza and Solanum germplasm collection."

* Objective: Identify collection gaps in the ex situ collections of Oryza, Solanum, Ipomoea and Eleusine;

* Germplasm collecting

- **Finger millet**: *Eleusine indica; E. tristachya.*
- **Sweet potato:** *Ipomoea grandifolia, I. ramosissima, I. tiliacea, I. cynanchifolia, I. triloba;*
- **Rice :** *Oryza glumaepatula, Oryza alta, O. grandiglumis* and *O. latifolia*
- **Potato:** *Solanum chacoense* subsp. *muelleri; S. commersonii* subsp. *commersonii* and subsp. *malmeanum.*

Project Workplan

- Taxonomy
- Deposit and multiplication of accessions
- Evaluation of seed physiological quality
- Cryopreservation tests

Project Workplan

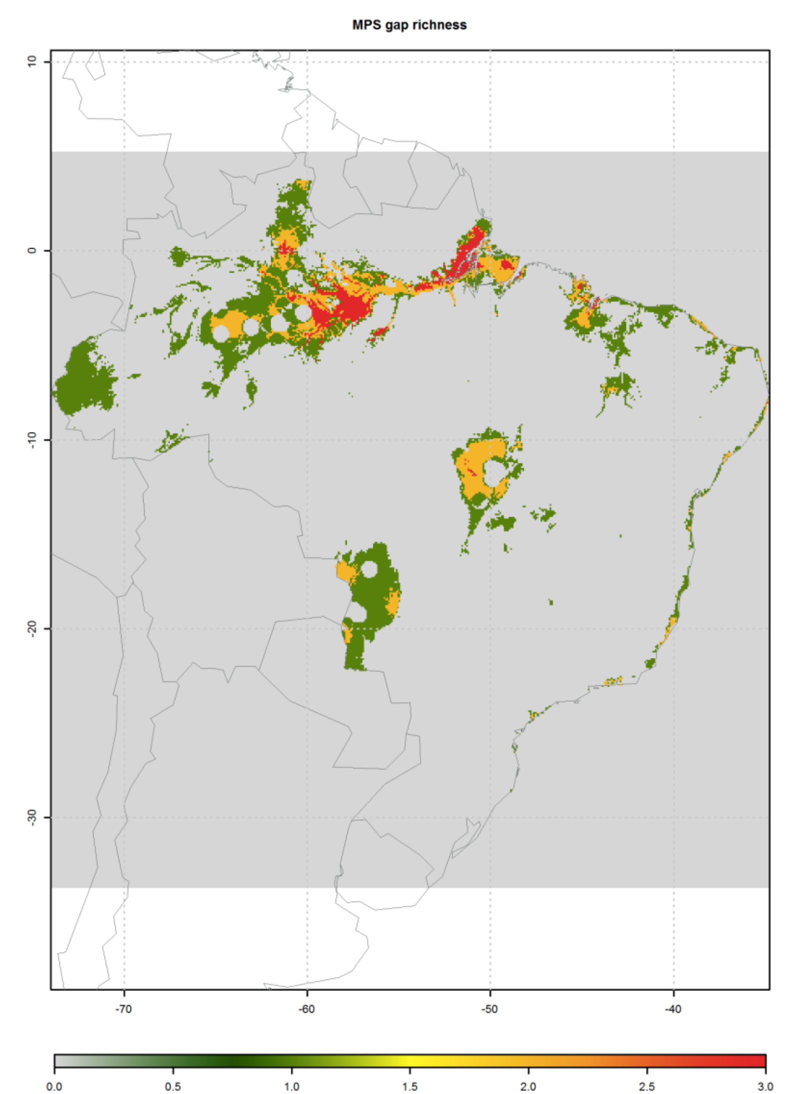
- Inventory and collection of sweet potato in indigenous areas

- Deposit of plant specimens in Herbaria

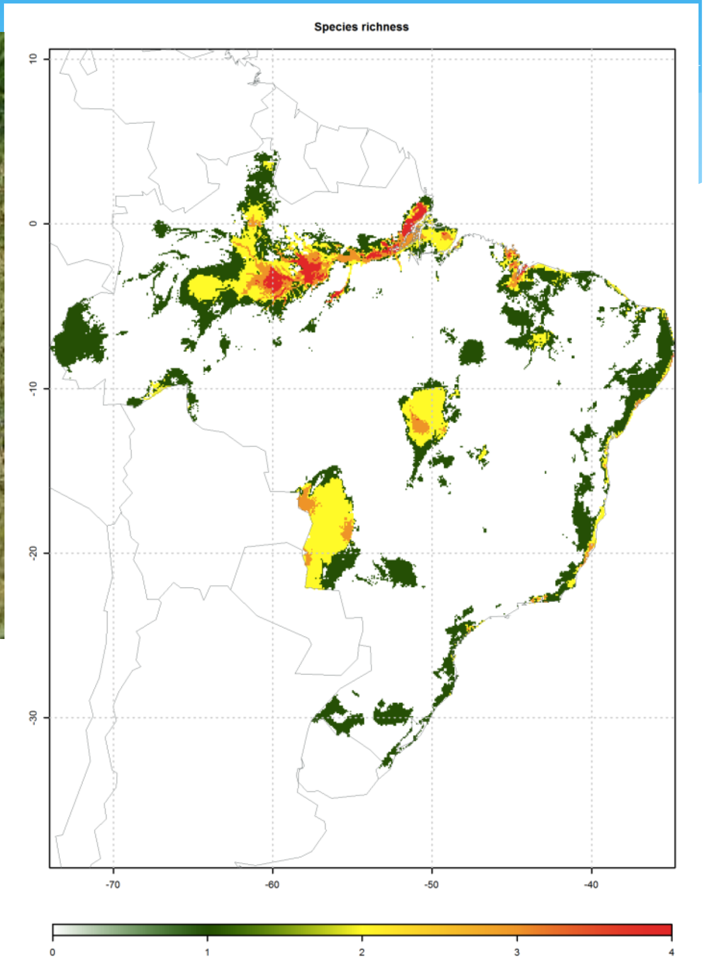
- Documentation

Gap analysis– *Oryza* spp.

TAXON	TOT	HS	GS	SRS	ATAI	STAUC	GRS	ERS	FPS	FPCAT
Oryza_alta	24	7	17	7.08	0.9	0.07	0.62	2.17	3.29	MPS
Oryza_glumaepatula	98	24	74	7.55	0.9	0.02	2.25	3.43	4.41	MPS
Oryza_grandiglumis	47	22	25	5.32	0.9	0.04	0.97	2.81	3.03	MPS
Oryza_latifolia	78	60	18	2.31	0.9	0.1	0.75	1.89	1.65	HPS

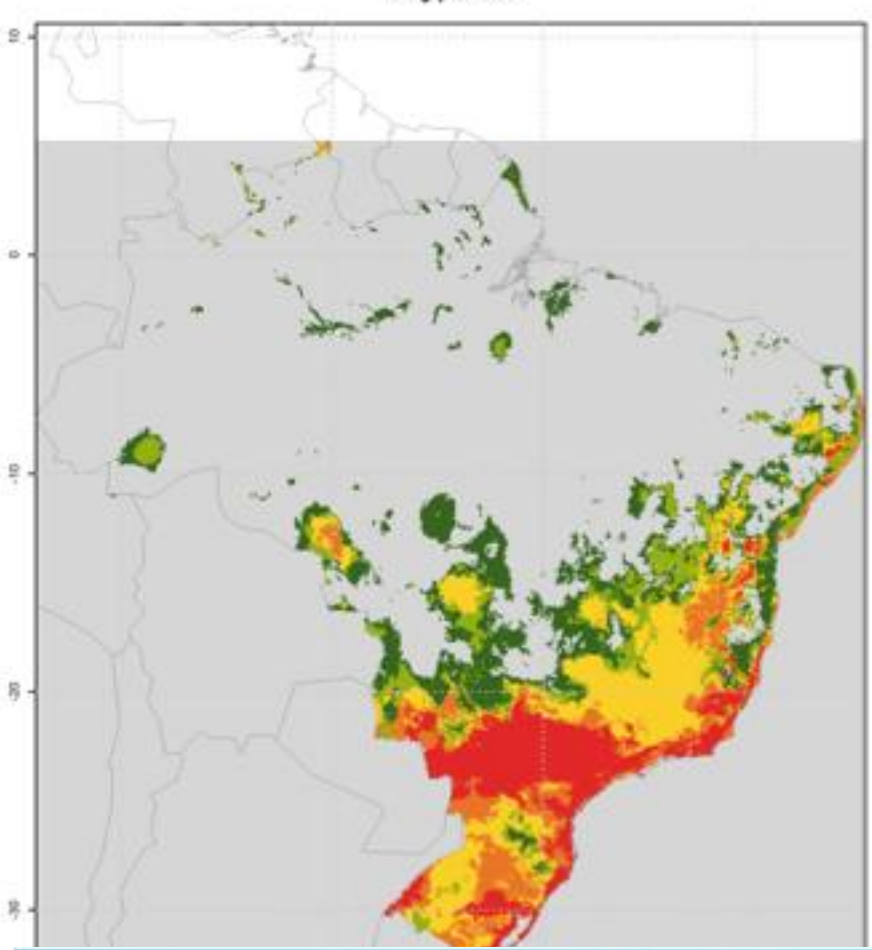


Collecting *Oryza* spp.



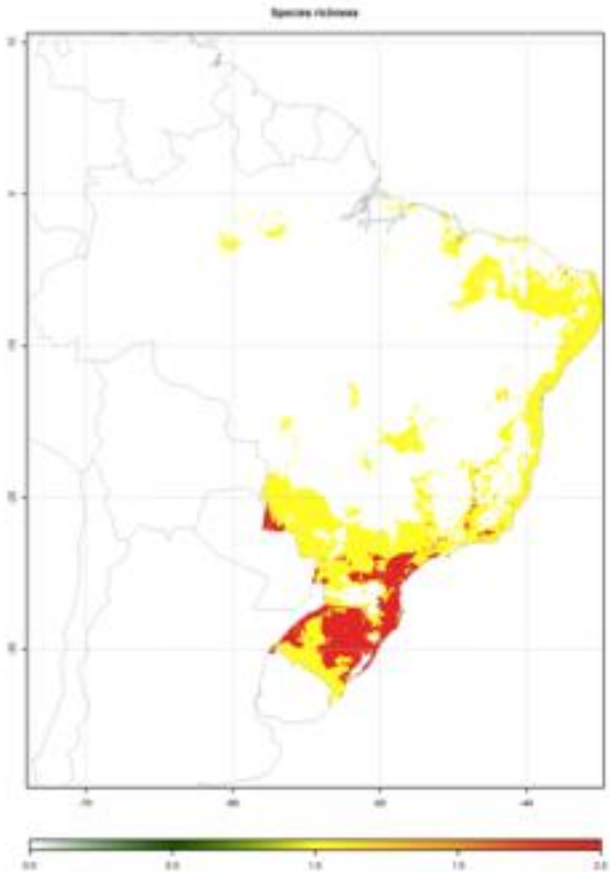
Gap analysis– *Ipomoea* spp.

TAXON	TOTAL	HS	GS	SRS	ATAUC	STAUC	GRS	ERS	FPS	FPCAT
Ipomoea_cynanchifolia	48	48	0	0	0.76	0.14	0	0	0	HPS
Ipomoea_grandifolia	230	230	0	0	0.9	0.01	0	0	0	HPS
Ipomoea_ramosissima	187	187	0	0	0.8	0.05	0	0	0	HPS
Ipomoea_tiliacea	190	190	0	0	0.89	0.07	0	0	0	HPS
Ipomoea_triloba	154	154	0	0	0.83	0.03	0	0	0	HPS



Gap analysis– *Eleusine* spp.

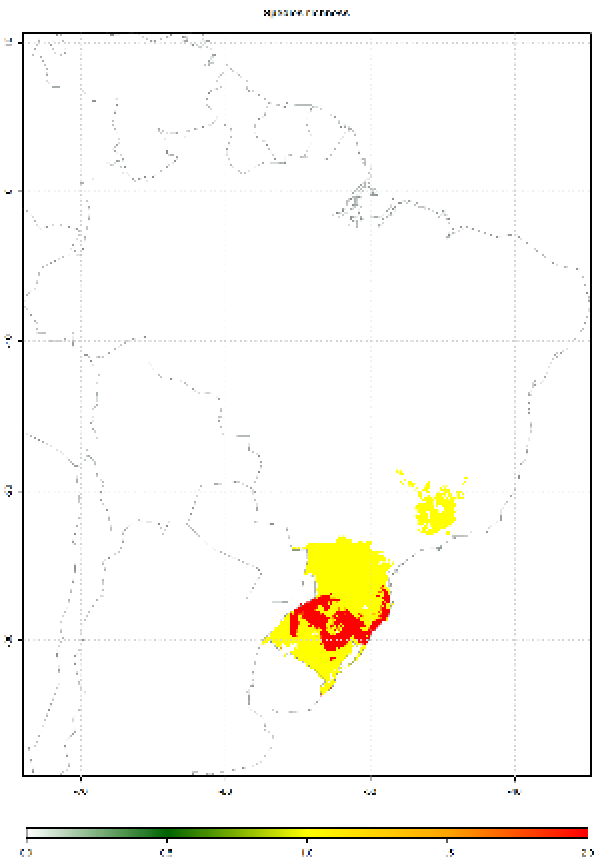
TAXON	TOTAL	HS	GS	SRS	ATAUC	STAUC	ASD15	GRS	ERS	FPS	FPCAT
Eleusine_indica	836	835	1	0.01	0.825	0.017	1.8857	0.06	0.63	0.231	HPS
Eleusine_tristachya	201	175	26	1.29	0.967	0.01	1.6298	2.43	5	2.909	MPS

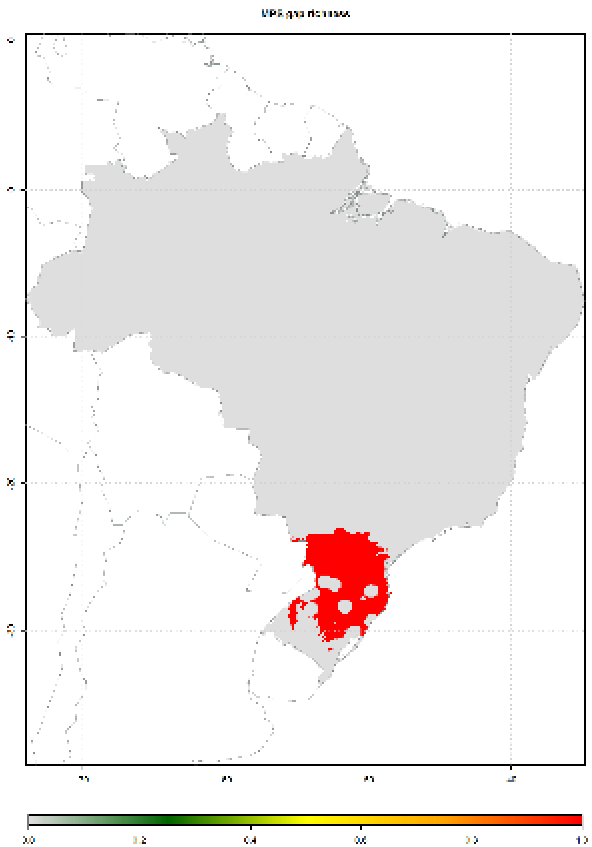


Collecting - *Eleusine* spp.

Gap analysis– *Solanum* spp.

TAXON	TOTAL	HS	GS	SRS	ATAUC	STAUC	ASD15	GRS	ERS	FPS	FPCAT
Solanum_calvescens	10	9	1	1	0.996	0.003	4.4304	1.01343	5	2.338	HPS
Solanum_commersonii	546	468	78	1.429	0.976	0.002	0.3883	8.73641	10	6.722	LPS
Solanum_chacoense	99	90	9	0.909	0.982	0.006	0.385	1.4983	7.1429	3.183	MPS





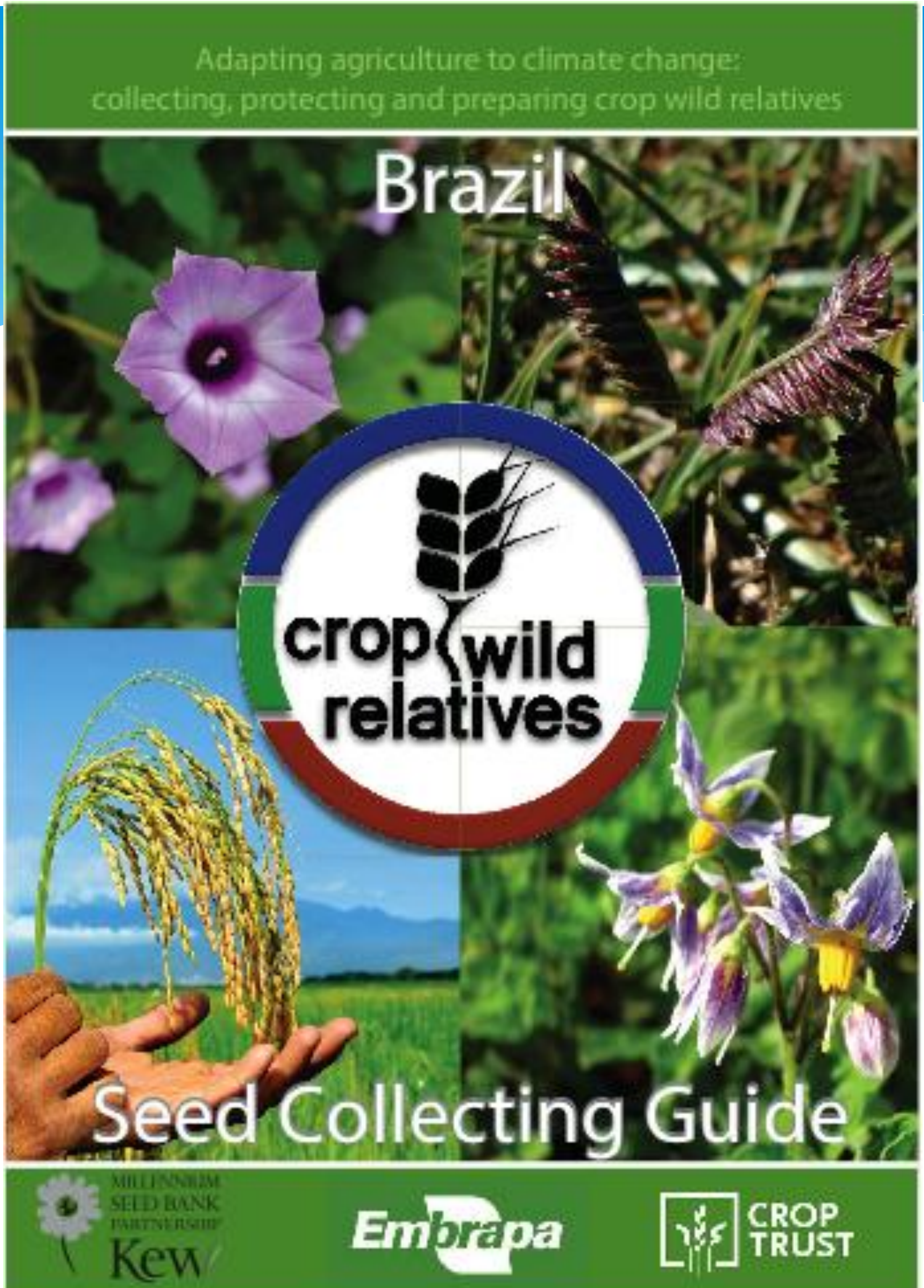
Collecting – *Solanum* spp.

S. chacoense

Collecting and multiplication – Germplasm genebank

S. commersonii

Inventory, collection and conservation of sweet potato varieties in the Krahô Indigenous Land



Thanks!

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