



The distributions and *ex situ* conservation of crop wild relatives: a global approach

Project: “Adapting agriculture to climate change: collecting, protecting and preparing crop wild relatives”

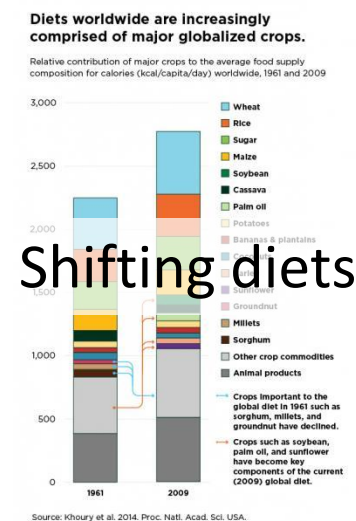
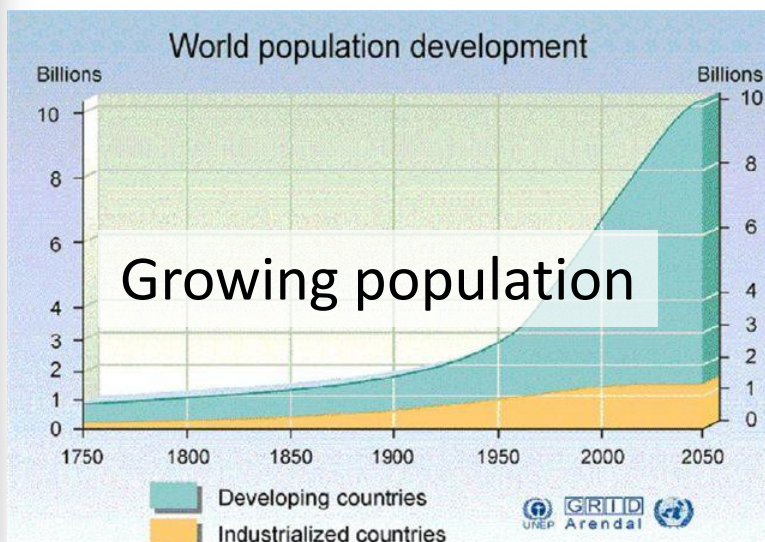
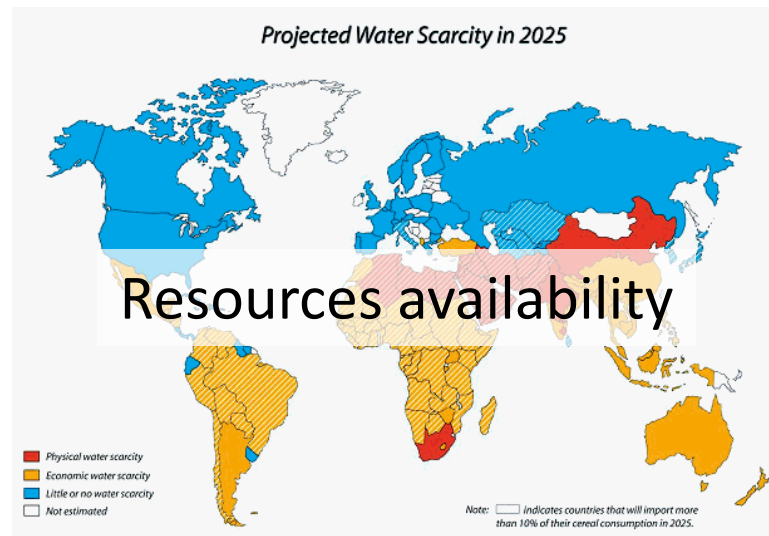
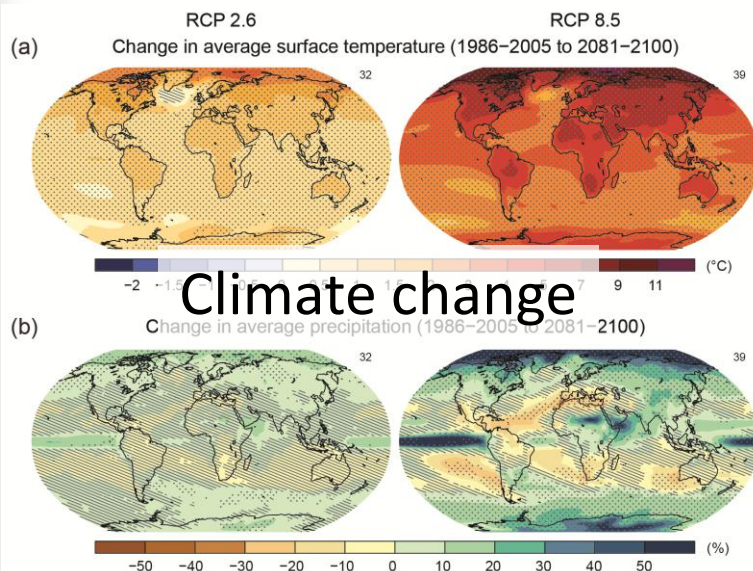
Nora P. Castañeda-Álvarez, Colin K. Khoury, Chrystian C. Sosa, Harold A. Achicanoy, Vivian Bernau, Holly Vincent, Andy Jarvis, Paul C. Struik and Nigel Maxted

PGR SECURE conference, Cambridge UK, 16-20 June 2014



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The context



The challenge

Producing more food with fewer resources available in a more **resilient** and **sustainable** manner

PGR are useful!

The **conservation** and **use** of plant genetic resources are key to cope with the challenge. Crop wild relatives are key due to **adaptive** and **novel** traits they offer for crop breeding



Methodology

- ✓ Objective: Prioritize the urgency for collection and *ex situ* conservation of the closest crop wild relatives of 81 crop gene pools
- ✓ Gap analysis methodology (adapted from Ramírez-Villegas et al., 2010)

OPEN ACCESS Freely available online

PLoS one

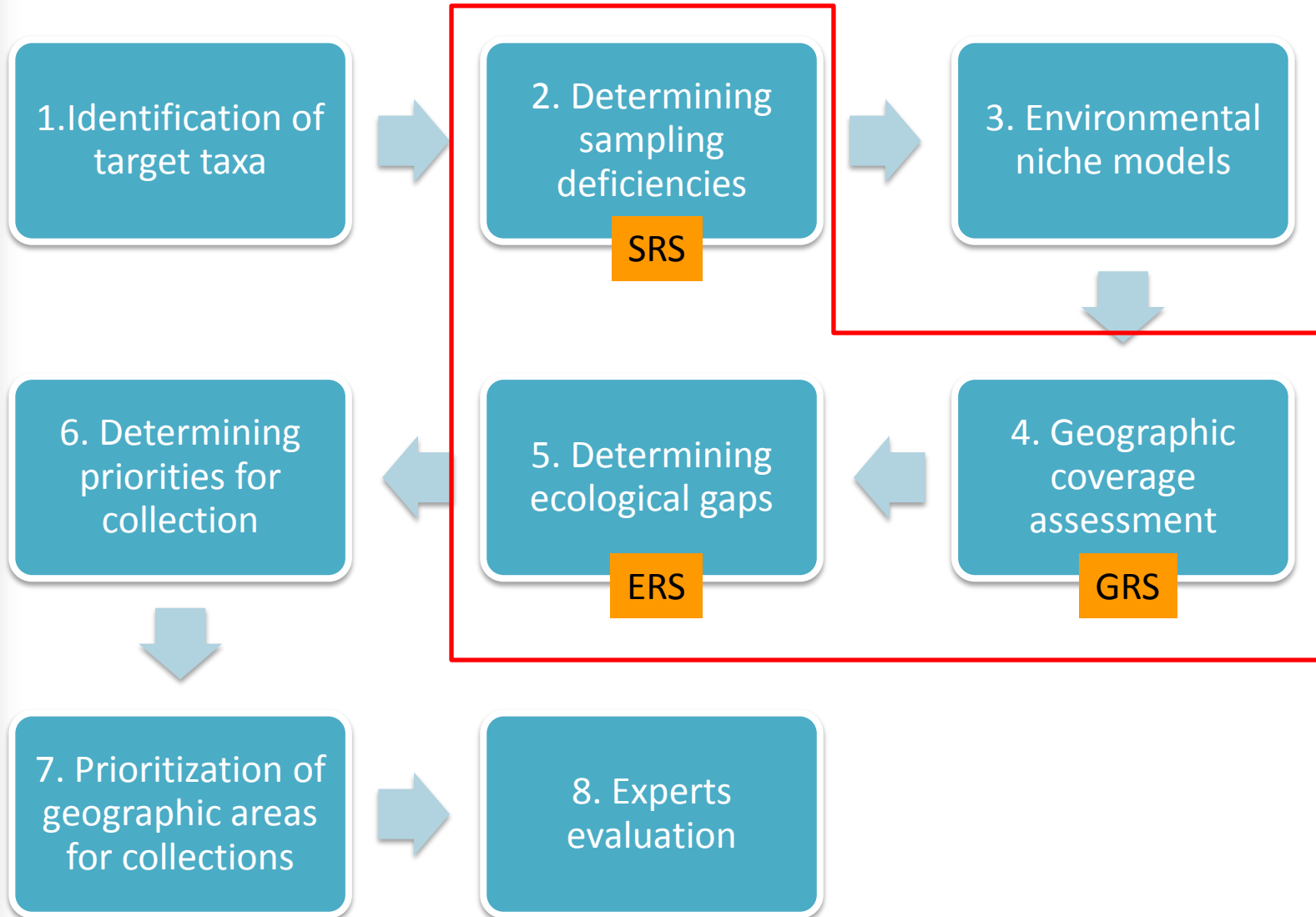
A Gap Analysis Methodology for Collecting Crop Genepools: A Case Study with *Phaseolus* Beans

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Methodology



1. Identification of target taxa

- The Harlan and de Wet inventory (Vincent et al., 2013)



The screenshot shows the homepage of the 'Crop Wild Relatives & Climate Change' website. The header includes the 'crop wild relatives' logo and navigation links: Home, News, Why CWR, CWR Inventory (highlighted), Conservation Gaps, and Interactive Map. Below the header is the title 'The Harlan and de Wet Crop Wild Relative Inventory'. The main content area features two search options: 'Classic Search' and 'Advanced Search'. Under 'Classic Search', there is a section for 'Search by crop gene pool' with a text input field for 'Enter a genus (eg. Zea), taxon (eg. Zea mays) or crop name (eg. maize)' and a 'Search' button. Below this is a section for 'Search by crop wild relative' with a text input field for 'Enter a genus (eg. Zea) or taxon (eg. Zea diploperennis)' and a 'Search' button. At the bottom, there is a section for 'Search by native distribution'. To the right of the search forms, there is a paragraph of text explaining the importance of crop wild relatives and the Harlan and de Wet (1971) gene pool concept.

Classic Search

Advanced Search

Search by crop gene pool
Enter a genus (eg. Zea), taxon (eg. Zea mays) or crop name (eg. maize).
Enter a genus, taxon or crop name **Search**

Search by crop wild relative
Enter a genus (eg. Zea) or taxon (eg. Zea diploperennis).
Enter a genus or taxon **Search**

Search by native distribution

Crop wild relative species may be prioritised on the basis of the economic importance of the associated crop, the level of threat to CWR populations, or perhaps most importantly, the potential for CWR utilisation. Utilisation potential is determined by the ease of trait transfer between the CWR and the crop, and CWR may be assigned to different gene pools based upon these characteristics.

The Harlan and de Wet (1971) gene pool concept proposes that members of crop gene pool GP1b (primary) and 2 (secondary) are most likely to be crossable with the crop and so these become the obvious conservation priorities. However, gene pool concepts have not yet been established for

www.cwrdiversity.org/checklist

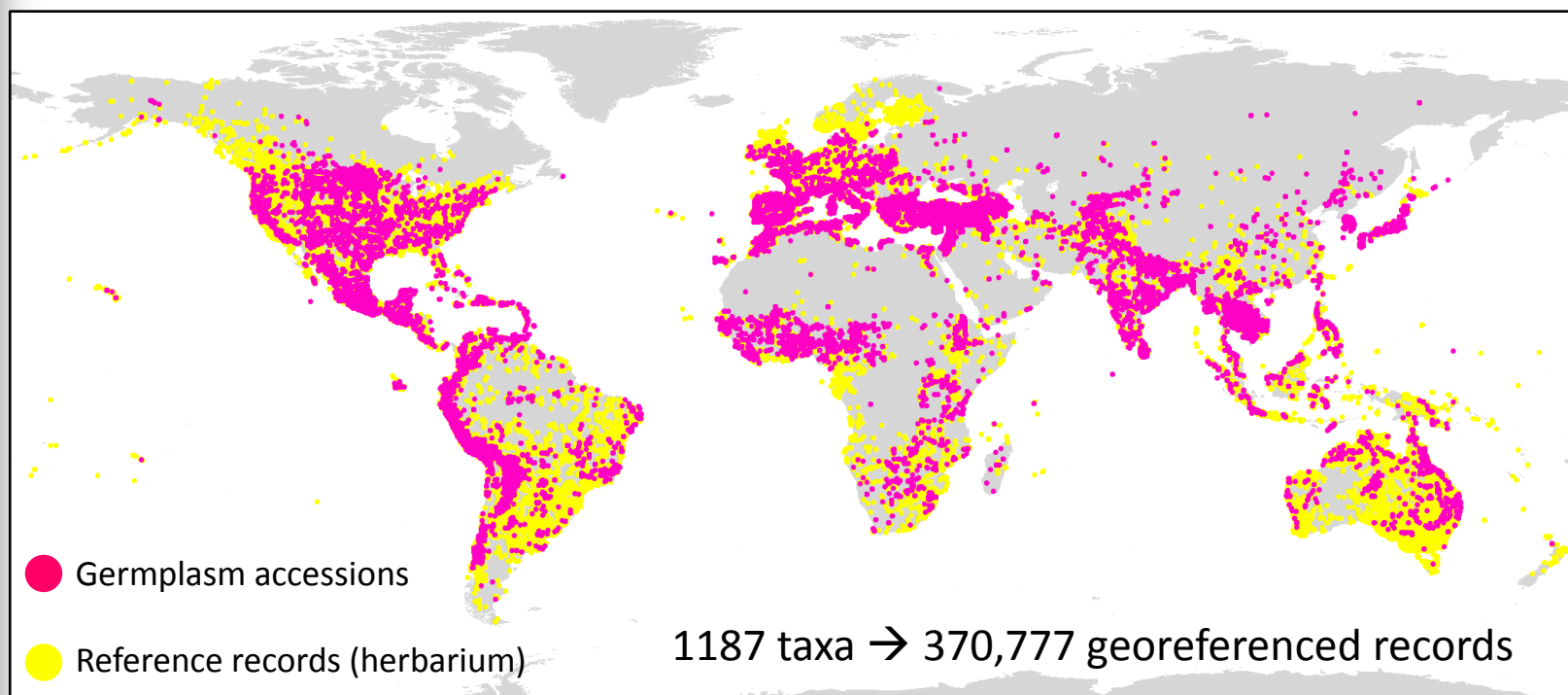
1. Identification of target taxa

- Closest CWR (GP 1 – 2, taxon groups 1-3, and confirmed/potential use) to 81 crop genepools
- 1187 CWR taxa (445 taxa – 29 priority crops)
- Records gathered from multiple sources (experts, herbaria, online databases, scientific articles, atlases, thesis)



1. Identification of target taxa

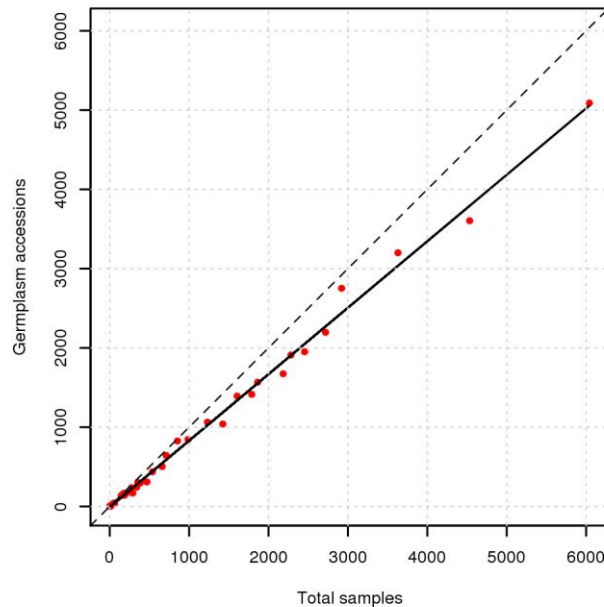
Occurrence data for all 81 crop genepools



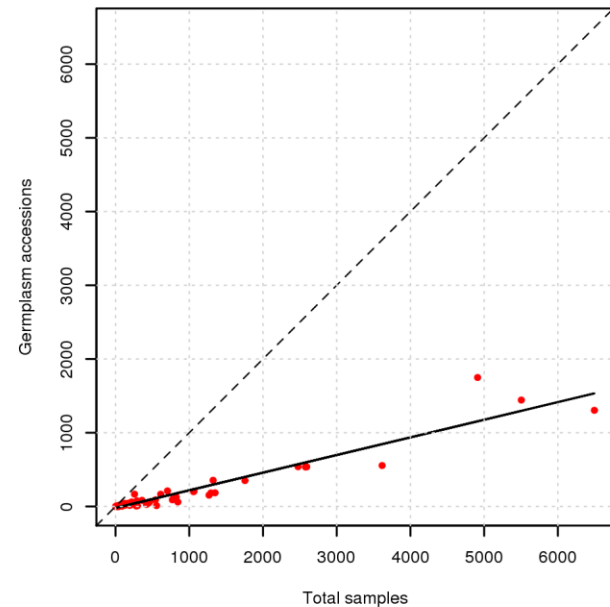
List of crops analyzed: <http://goo.gl/Y19Oum>

2. Determining sampling deficiencies

- ✓ All records are included (coords and no-coords)
- ✓ Estimation: all records vs. germplasm accessions



Wheat

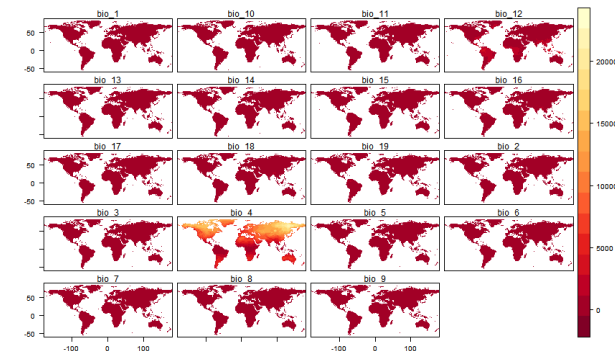


Potato

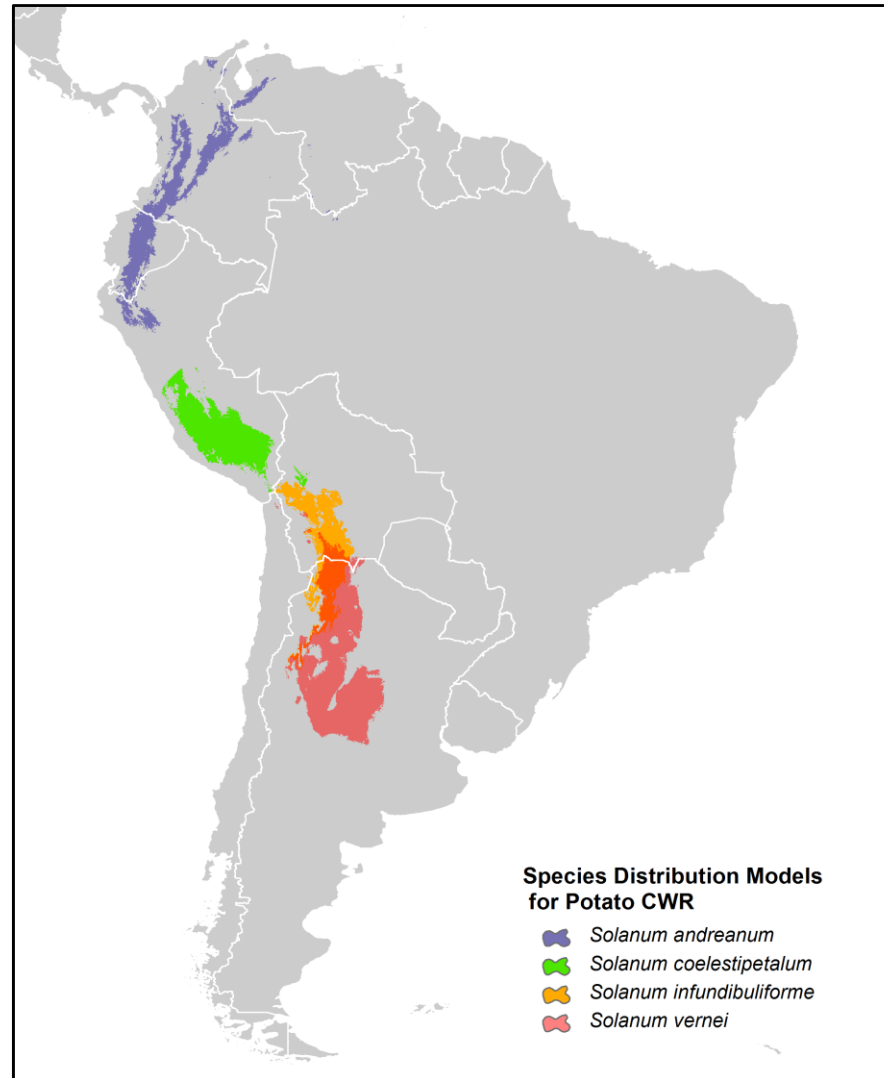


3. Environmental niche models

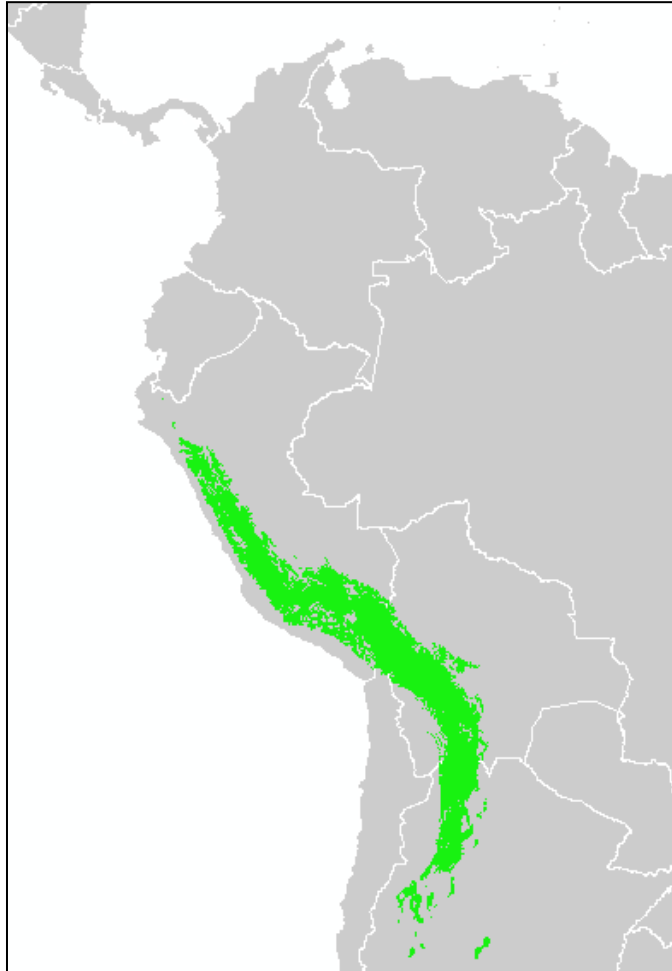
- ✓ Used in the gap analysis process for determining geographical and ecosystem representativeness deficiencies, and to suggest areas for collection
- ✓ Spatial resolution: ~4.6 km at equator (regional-country analysis)
- ✓ Modeling algorithm = MaxEnt
- ✓ 19 bioclimatic variables



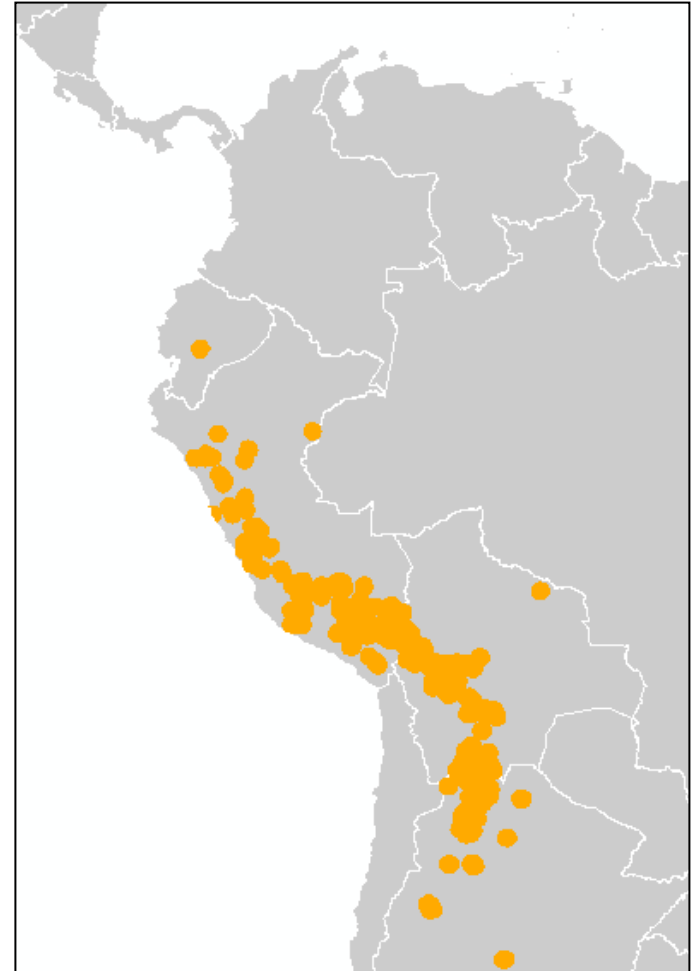
3. Environmental niche models (e.g.potato)



4. Geographic coverage assessment

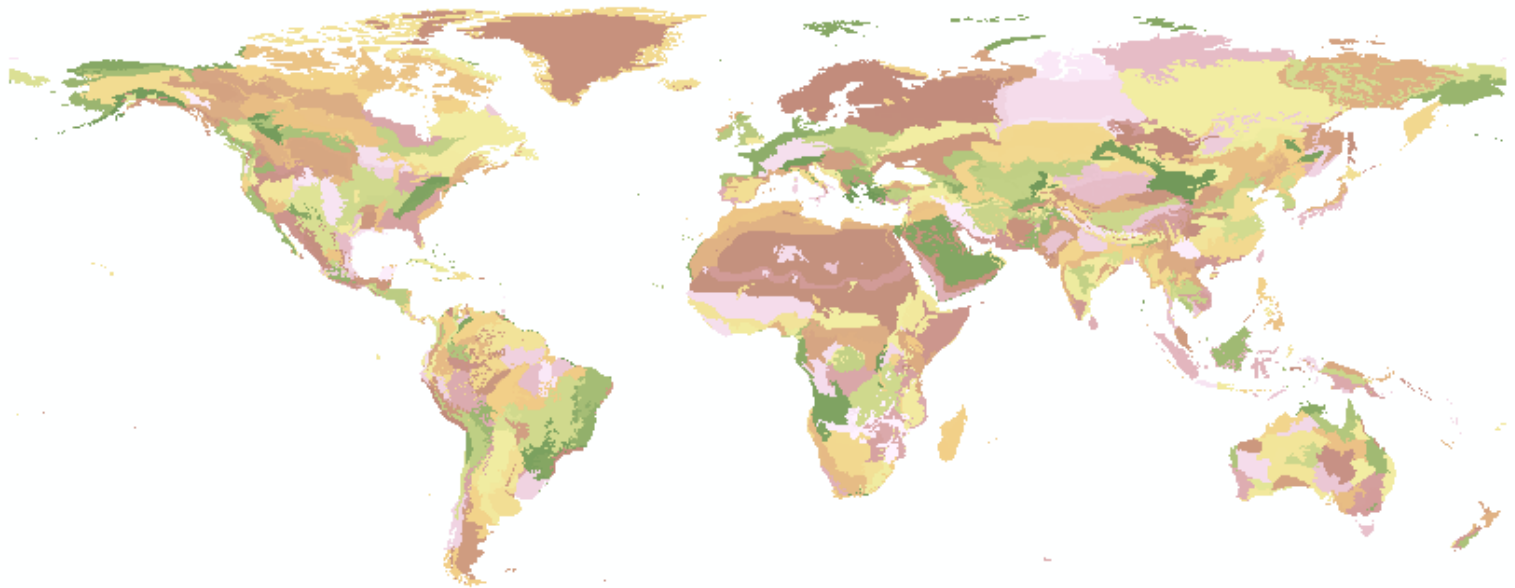


S. acaule ENM



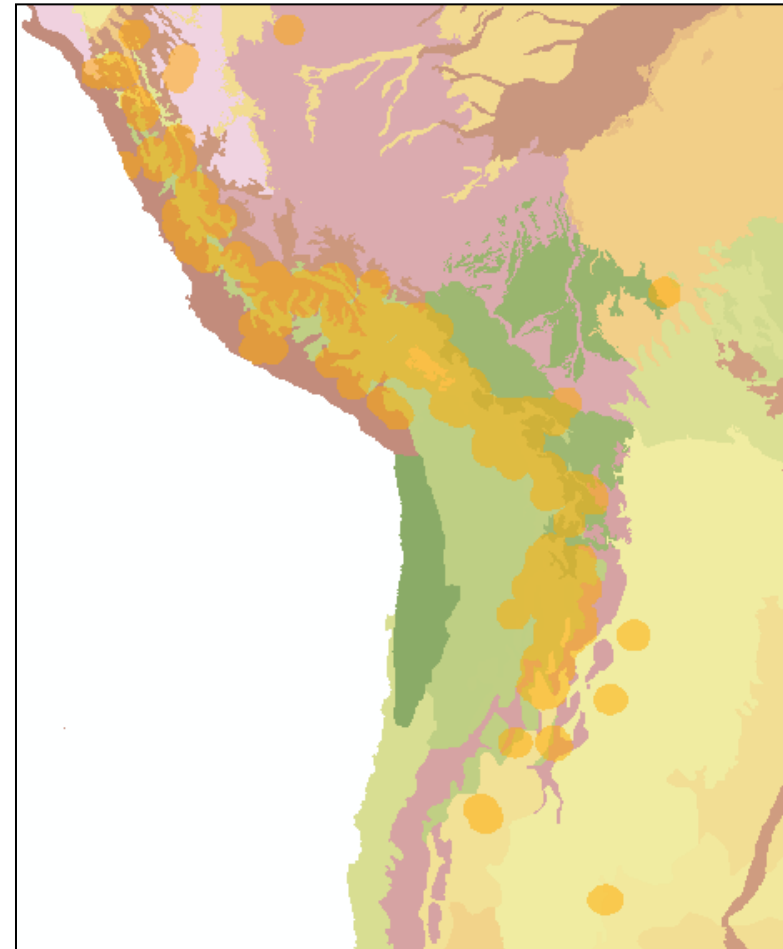
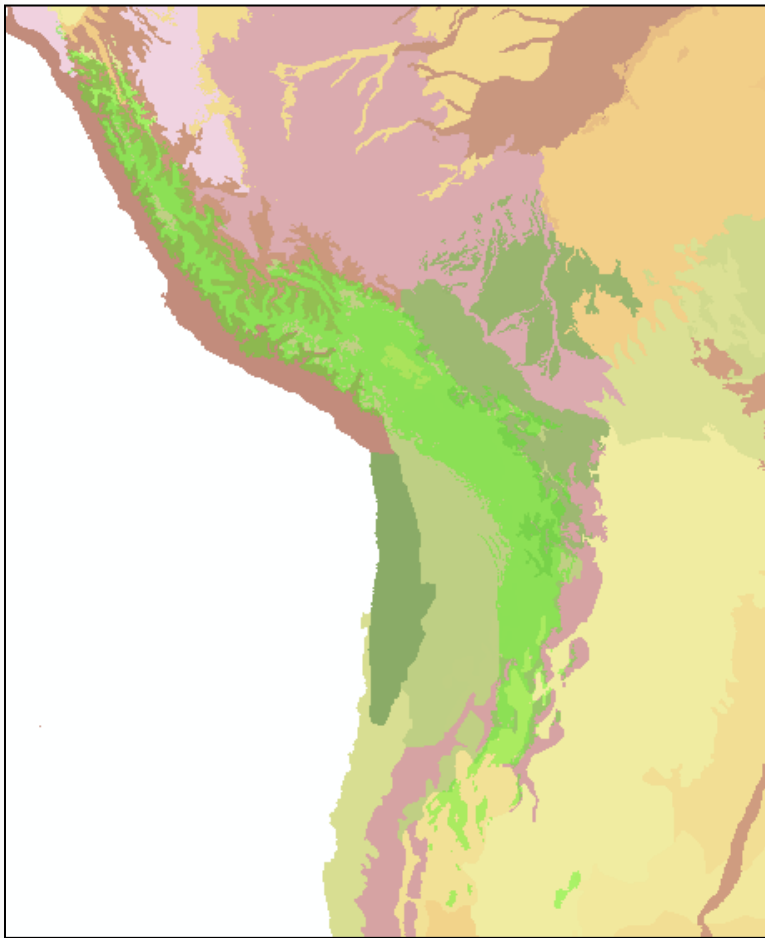
Genebank accessions (50km circular buffer)

5. Identification of ecological representativeness gaps



WWF, terrestrial ecoregions

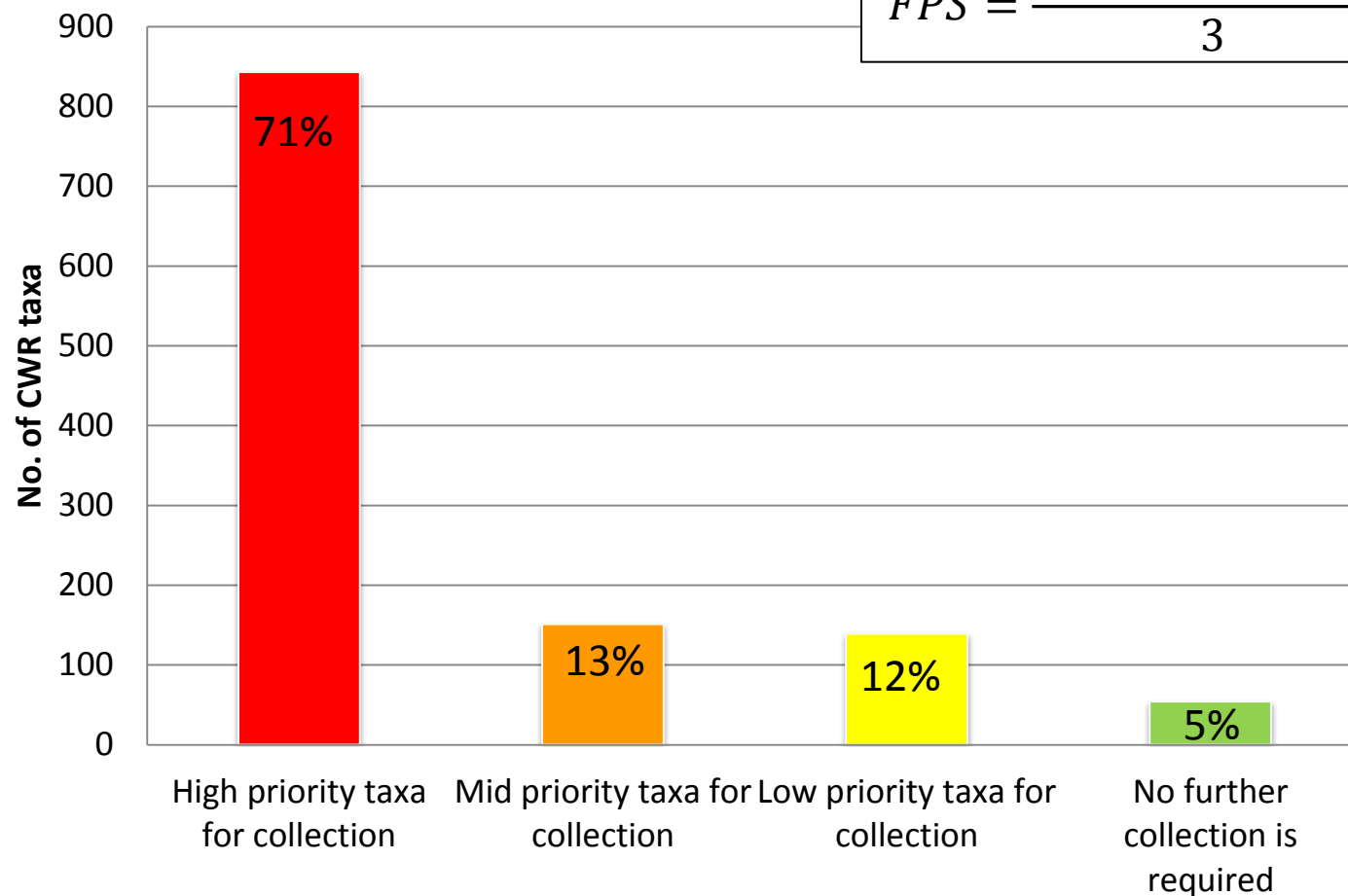
5. Identification of ecological representativeness gaps



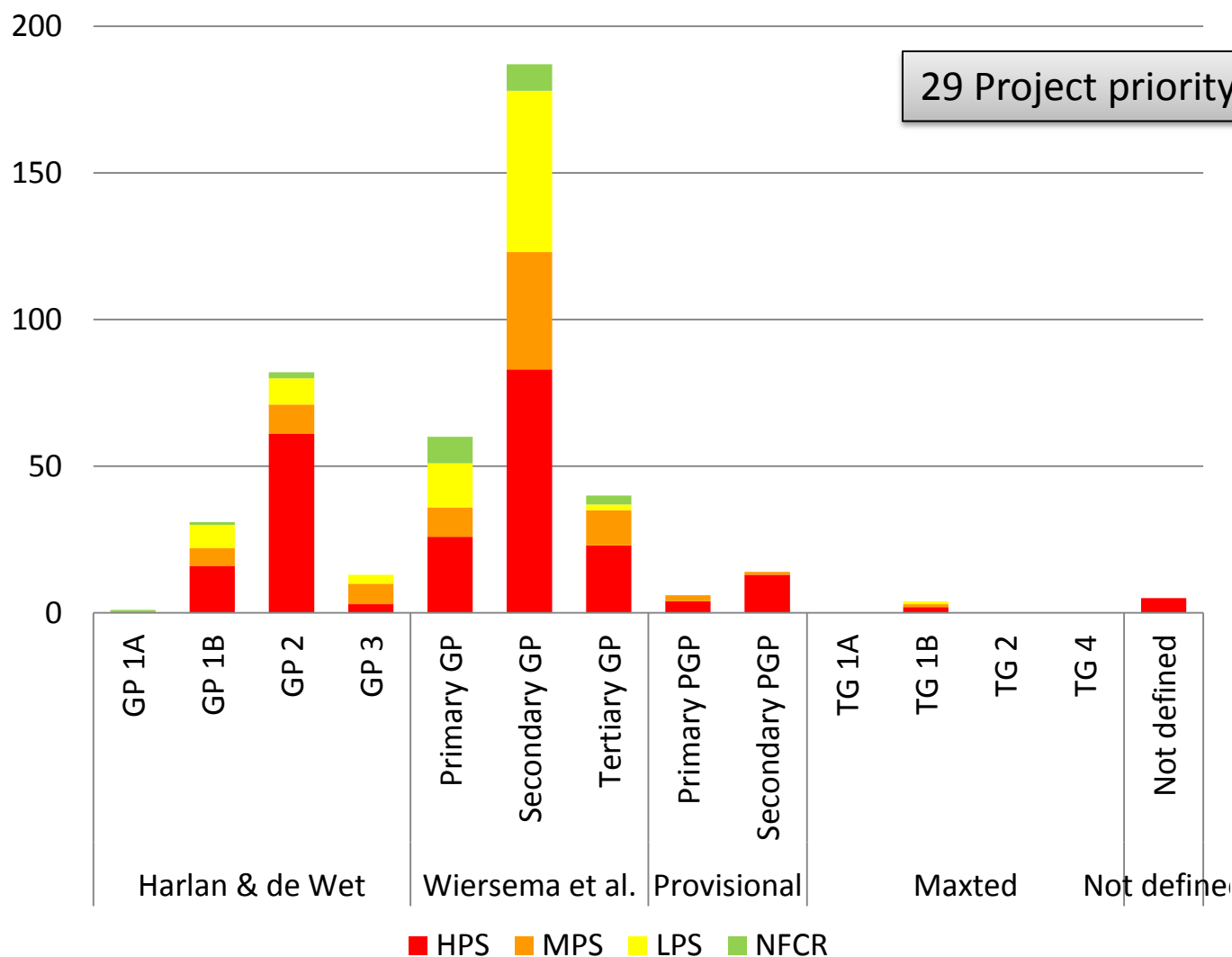


Establishing priorities for field collections

$$FPS = \frac{SRS + ERS + GRS}{3}$$

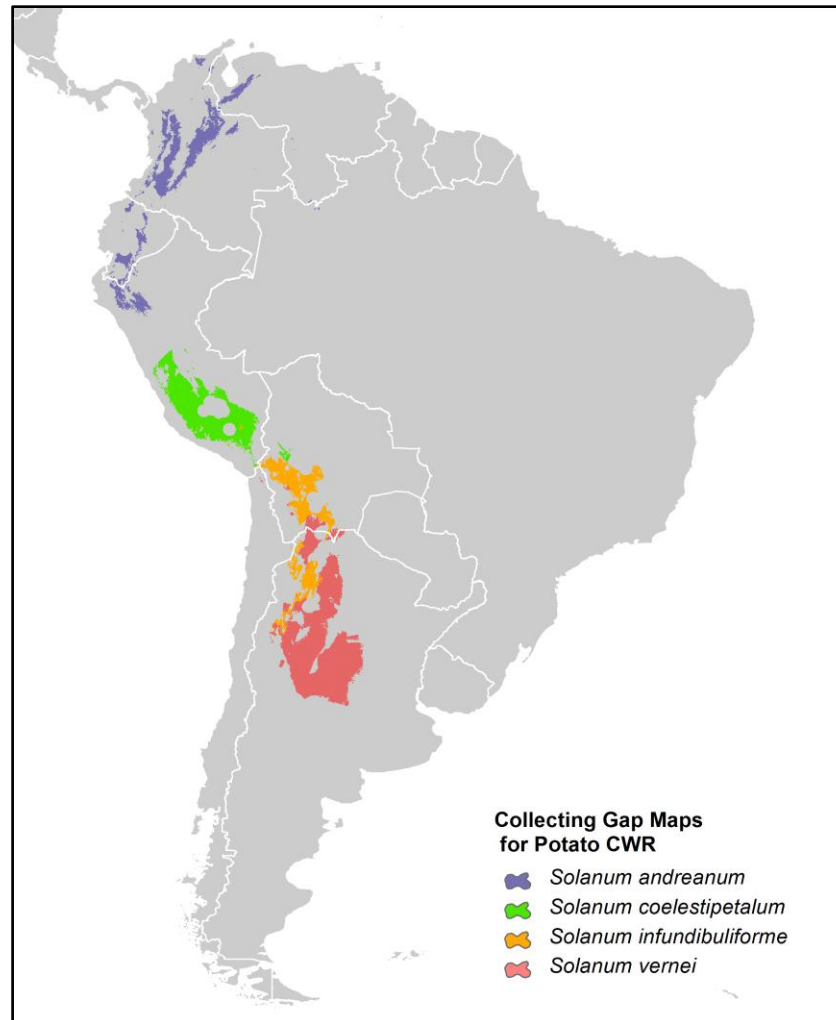


6. Establishing priorities for collection



7. Geographic areas suggested for collections

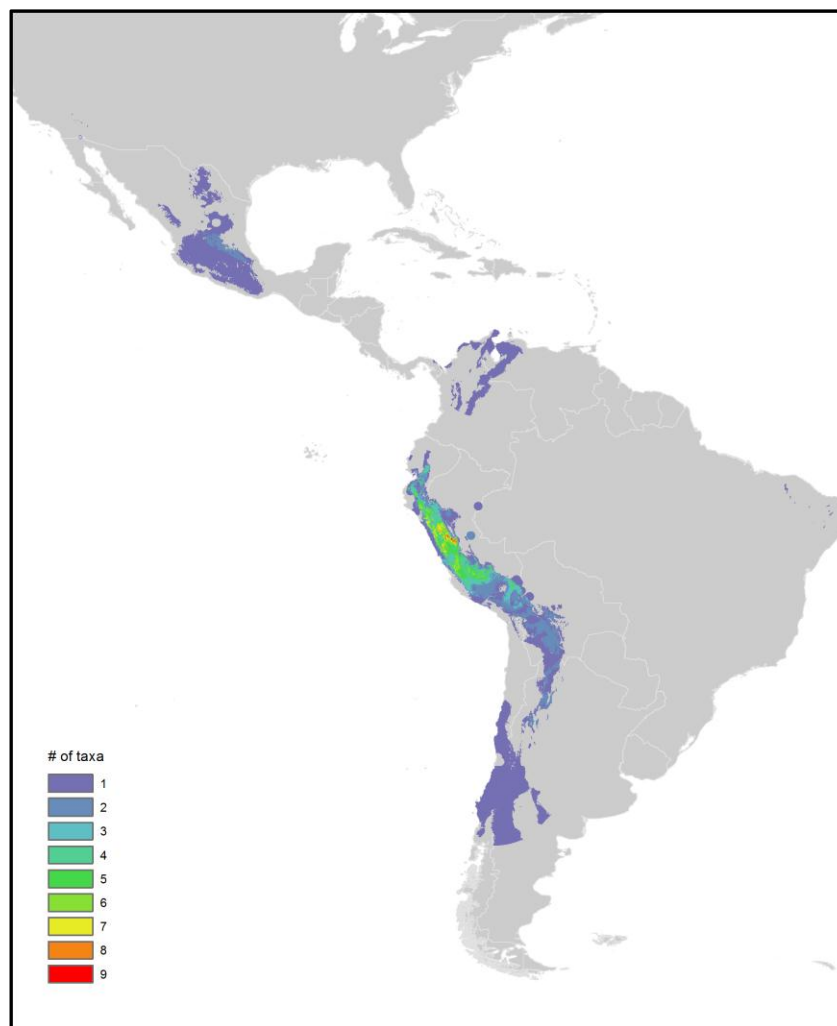
Species collecting gaps (e.g. potato)





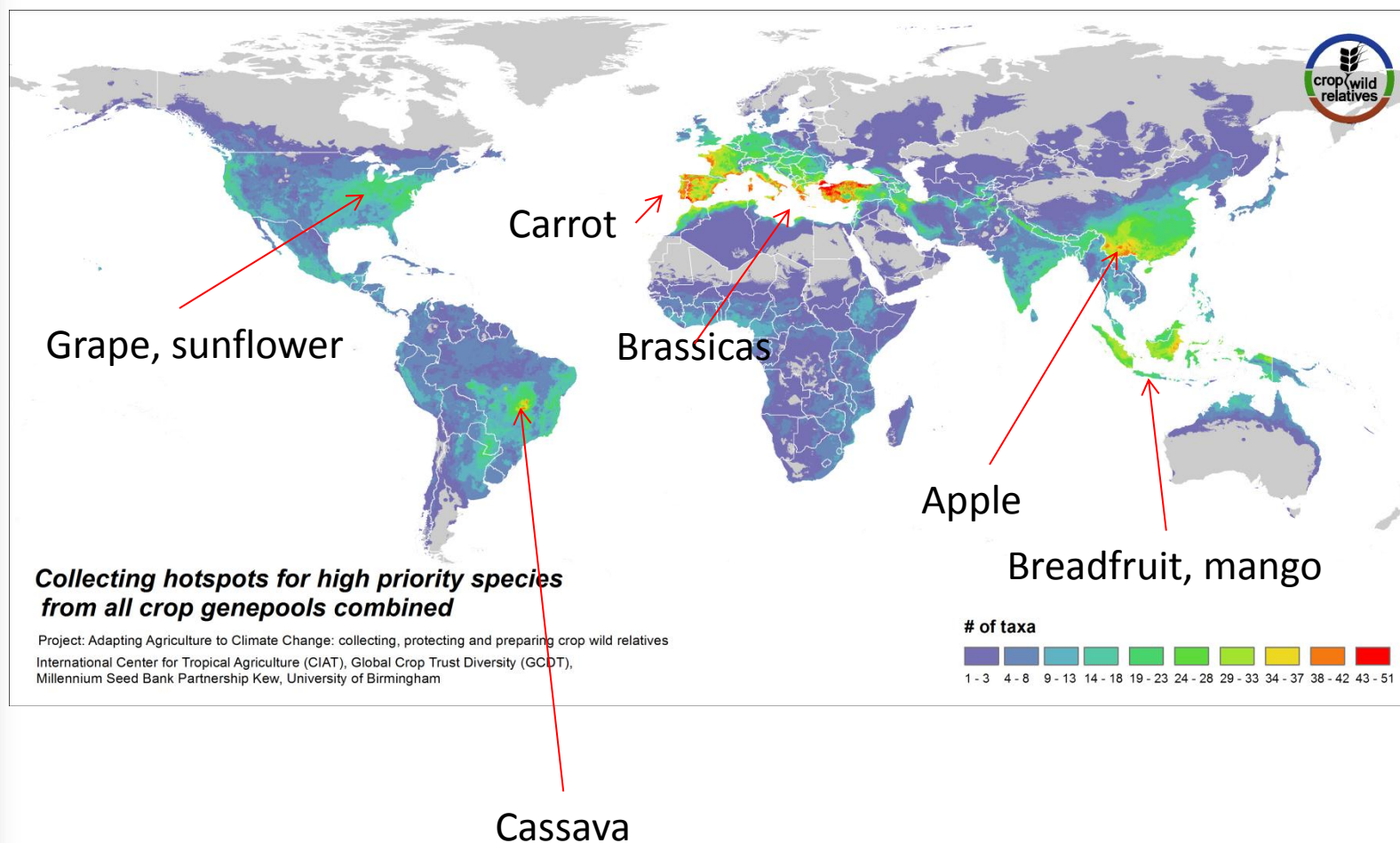
7. Geographic areas suggested for collections

Genepool collecting gaps (e.g.potato)



7. Geographic areas suggested for collections

Global collecting hotspots for High Priority Taxa, for 76 crop gene pools

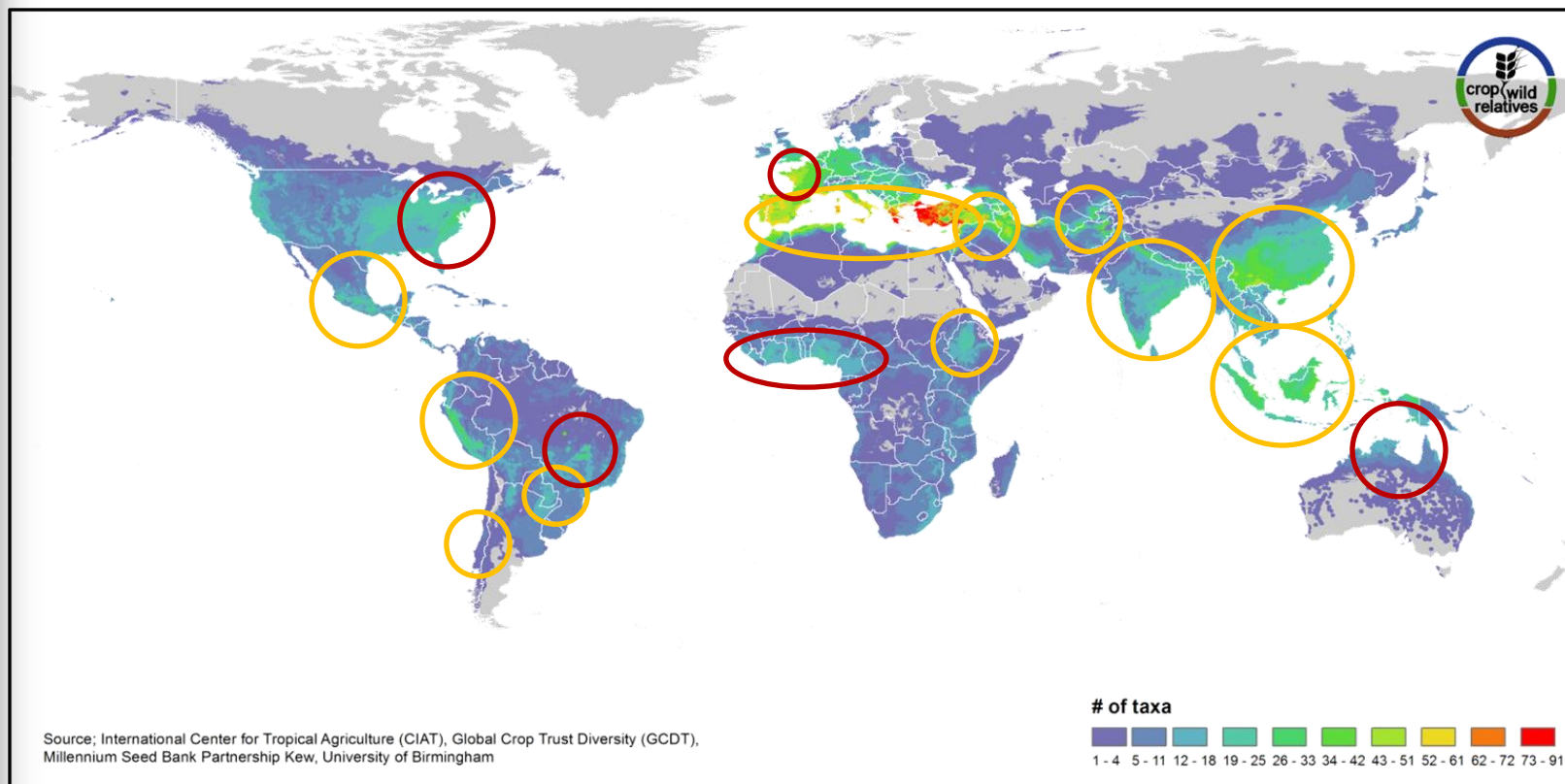




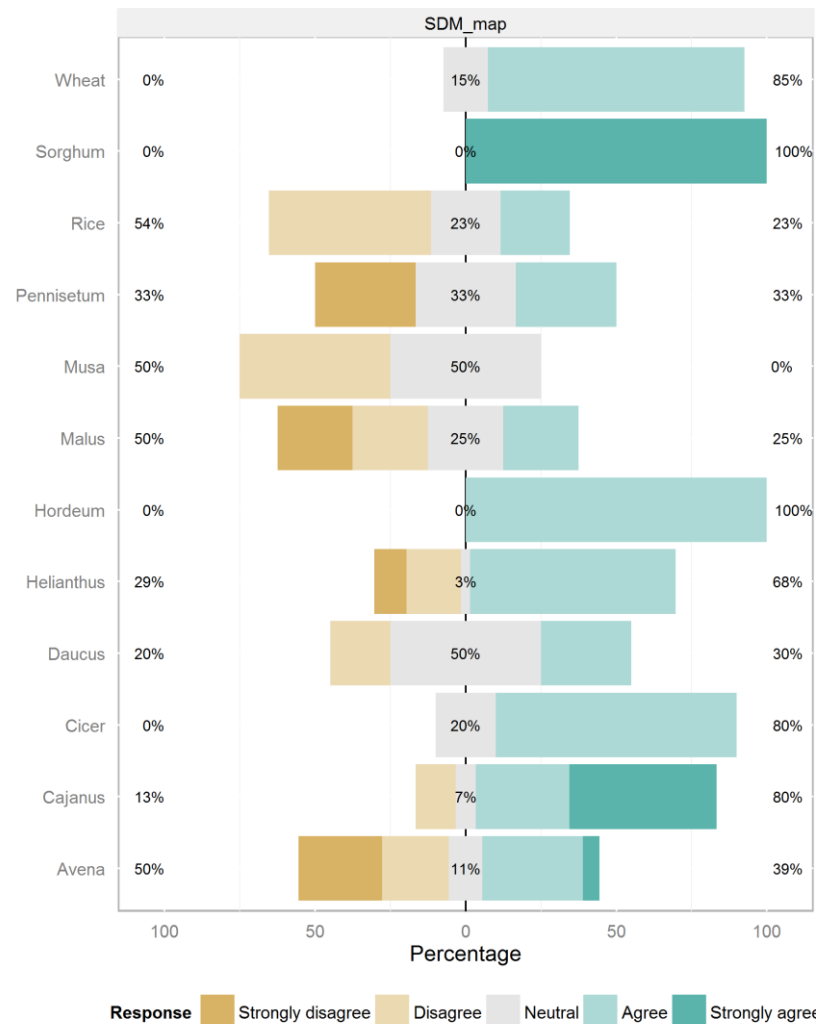
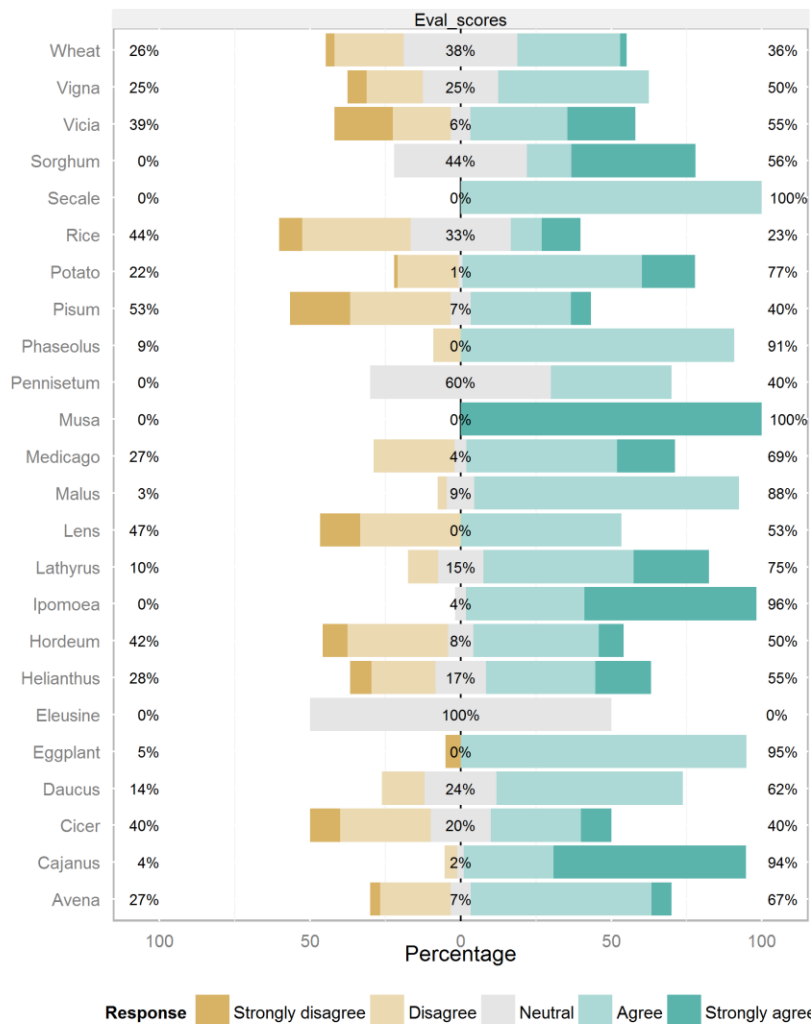
Species richness (81 gene pools)



Global distribution of the CWR of 81 crop gene pools



8. Experts Evaluation



2 cm

A



A global initiative on crop wild relatives

- Identify, collect, conserve, document use of key CWR for climate change adaptation (in developing countries)
- 10 years funding pledged by Norwegian government, starting 2011
- Target crops:

<i>Avena sativa</i>	Oat	<i>Malus domestica</i>	Apple	<i>Secale cereale</i>	Rye
<i>Cajanus cajan</i>	Pigeonpea	<i>Medicago sativa</i>	Alfalfa/Lucerne	<i>Solanum melongena</i>	Eggplant/Aubergine
<i>Cicer arietinum</i>	Chickpea	<i>Musa acuminata</i>	Cavendish banana	<i>Solanum tuberosum</i>	Potato
<i>Daucus carota</i>	Wild carrot	<i>Musa balbisiana</i>	Guangdong plantain	<i>Sorghum bicolor</i>	Sorghum
<i>Eleusine coracana</i>	Finger millet	<i>Oryza glaberrima</i>	African rice	<i>Triticum aestivum</i>	Bread wheat
<i>Helianthus annuus</i>	Sunflower	<i>Oryza sativa</i>	Rice	<i>Vicia faba</i>	Faba bean
<i>Hordeum vulgare</i>	Barley	<i>Pennisetum glaucum</i>	Pearl millet	<i>Vicia sativa</i>	Common vetch
<i>Ipomoea batatas</i>	Sweet potato	<i>Phaseolus lunatus</i>	Lima bean	<i>Vigna subterranea</i>	Bambara groundnut
<i>Lathyrus sativus</i>	Grass pea/Common chickling	<i>Phaseolus vulgaris</i>	Garden bean	<i>Vigna unguiculata</i>	Cowpea
<i>Lens culinaris</i>	Lentil	<i>Pisum sativum</i>	Garden pea		



Adapting Agriculture to Climate Change:
Collecting, Protecting and Preparing
Wild Relatives

CWR Project Gap Analysis Results S

International Center for Tropical Agriculture
30 April 2013

The screenshot displays a Google Sheet titled "Country and Taxa Prioritization Scores". The sheet contains a table with the following columns: Taxon_shortname, Taxon_fullname, Priority, Genepool/Taxon Group, Threat, Relevance to Food Security in Developing Countries, Current Breeding Demand, and Total Score. The table lists various taxa, including Oryza barthii, Oryza brachyantha, Oryza eichingeri, Oryza glaberrima, Oryza glumipatula, Oryza grandiglumis, Oryza latifolia, Oryza longistaminata, Oryza malampuzhaensis, Oryza meridionalis, Oryza minuta, Oryza nivara, Oryza officinalis, Oryza perennis cubensis, Oryza punctata, Oryza rhizomatis, Oryza ridleyi, and Oryza rufipogon. An inset image shows hands holding green peas and yellow grains, with text about adapting agriculture to climate change in Mozambique.

	Taxon_shortname	Taxon_fullname	Crop_code	Priority	Genepool/ Taxon Group	Threat	Relevance to Food Security in Developing Countries	Current Breeding Demand	Total Score
213	Oryza_barthii	Oryza_barthii							
214	Oryza_brachyantha	Oryza_brachyantha	rice						
215	Oryza_eichingeri	Oryza_eichingeri	rice	1	3	1	3	0	2
216	Oryza_glaberrima	Oryza_glaberrima	rice	1	2	1	3	2	2
217	Oryza_glumipatula	Oryza_glumipatula	rice	2	2	1	3	0	2
218	Oryza_grandiglumis	Oryza_grandiglumis	rice	0	3	1	3	2	2
219	Oryza_latifolia	Oryza_latifolia		2	3	1	3	2	2
220	Oryza_longistaminata	Oryza_longistaminata		3	2	1	3	2	3
221	Oryza_malampuzhaensis	Oryza_malampuzhaensis					3	0	30
222	Oryza_meridionalis	Oryza_meridionalis					3	0	30
223	Oryza_minuta	Oryza_minuta					3	0	32
224	Oryza_nivara	Oryza_nivara					3	0	32
225	Oryza_officinalis	Oryza_officinalis					3	2	30
226	Oryza_perennis_cubensis	Oryza_perennis_cubensis					3	2	28
227	Oryza_punctata	Oryza_punctata					3	0	30
228	Oryza_rhizomatis	Oryza_rhizomatis					3	2	30
229	Oryza_ridleyi	Oryza_ridleyi					3	0	30
230	Oryza_rufipogon	Oryza_rufipogon					3	0	26

Adapting agriculture to climate change:
collecting, protecting and preparing crop wild relatives

Mozambique

LEGUMINOSEAE
Genepool 2 of Bambara groundnut



A global initiative on crop wild relatives

- ✓ Project is supporting partners to carry out the collecting work.
- ✓ A duplicate of the collected material will remain in country.
- ✓ Collections underway in Italy, Cyprus and Portugal.
- ✓ Selected pre-breeding projects will be undertaken (GCDT)
- ✓ Germination protocols available from the Seed Information Database (SID, kew website)
- ✓ Material will go into Svalbard through the CG network backup system, it is likely much of that material will be breeding lines
- ✓ Seed material will be available under the SMTA from the MSB and partners – seed lists online





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<https://twitter.com/CropWildRelativ>



<https://www.facebook.com/cropwild.relative>

www.cwrdiversity.org

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