

B.8. Gap analysis of priority landraces

B.8.1. Overview

What is LR gap analysis?

Gap analysis is a conservation evaluation technique that informs the prioritization of biodiversity elements for conservation action by identifying ‘gaps’ in the conservation of those elements^{174,175,176,177}. In practice, gap analysis of LR involves a comparison between the range of farmer maintained diversity (equivalent to the pattern of natural diversity in wild plant species) and that diversity already effectively represented by current on-farm conservation actions (*in situ* gap analysis) and samples of that diversity represented in gene bank collections (*ex situ* gap analysis). Note there is a difference between knowledge that a farmer maintains a landrace and the inclusion of that farmer and LR included within an on-farm project, the former is passively conserved but is subject to the range of threats facing any LR population, but the latter is actively managed to counter these threats and so will engender conservation.

Conservation gaps can be assessed at different levels: individual LR, ecogeographic, trait, and genetic variability of a specific trait. It should be highlighted that morphological analysis and traditional knowledge (farmers’ perceived diversity) can be used when data on trait/genetic characterisation are lacking.

There is now an extensive literature associated with gap analysis which essentially identifies areas in which selected elements of biodiversity are under-represented¹⁷⁸. Nevertheless, it is almost entirely restricted to identifying gaps in habitat or ecosystem conservation, not gaps within existing species or genetic diversity conservation. The use of this technique to identify gaps in networks of protected habitats for *in situ* conservation of genetic resources, namely for CWR, has already been mentioned¹⁷⁹. It is worth stressing that environmental gap analysis focuses on *in situ* conservation alone, whereas for PGRFA conservation both *in situ* and *ex situ* conservation would be considered equally as complementary conservation techniques. A systematic genetic gap analysis methodology for identifying gaps within a crop gene pool and within individual

¹⁷⁴ Noss and Cooperrider (1999)

¹⁷⁵ Eken *et al.* (2004)

¹⁷⁶ Rodrigues *et al.* (2004)

¹⁷⁷ Langhammer *et al.* (2007)

¹⁷⁸ E.g. Margules *et al.* (1988), Margules (1989), Margules and Pressey (2000), Allen *et al.* (2001), Balmford (2003), Brooks *et al.* (2004), Dietz and Czech (2005), Riemann and Ezcurra (2005)

¹⁷⁹ See Ingram and Williams (1993)

species has been developed and illustrated with the case of African *Vigna* wild relatives and LR. The study aimed at evaluating the effectiveness of current *in situ* and *ex situ* conservation actions and identifying the ‘gaps’, thus informing the development of a conservation plan for the crop gene pool¹⁸⁰. More recently, a gap analysis methodology based on GIS tools has been developed specifically for crop gene pools¹⁸¹.

Ecogeographic, taxonomic and farmers’ knowledge on LR (see B.4. National inventory of landraces), as well as threat (see B.5. Threats and threat assessment) and genetic diversity (see B.7. Genetic data analysis of priority landraces) assessments provide information that helps identify gaps in the conservation of LR. Figure 35 summarises how these types of data feed onto a gap analysis study.

Conservation gaps can be detected at different levels, both *in situ* and *ex situ* : (i) individual LR level (LR not conserved *versus* conserved), (ii) ecogeographic level (for a particular LR, areas/environmental conditions not covered by *in situ* or *ex situ* conservation activities *versus* those covered), (iii) trait level (specific LR populations that present a particular trait of interest that are not conserved *versus* populations with that same trait that are), (iv) genetic variability of a specific trait (specific LR populations that are genetically diverse for a specific trait that is not conserved *versus* those that are). The level at which gap analysis can be undertaken depends on the type of data available for the study. It should be highlighted that trait and genetic data are not always available and that the collation of information *de novo* may not be possible due to resource limitations. Therefore, in the absence of ‘real’ trait/genetic information, morphological analysis and traditional knowledge (farmers’ perceived diversity) can be used instead.

The result of an *in situ* or *ex situ* LR gap analysis is a list of LR populations that require active on-farm or *ex situ* conservation. Figure 5 illustrates both the *in situ* and *ex situ* gap analysis methodologies.

¹⁸⁰ See Maxted *et al.* (2008b)

¹⁸¹ Bioversity International *et al.* (2009) and also see R-package GapAnalysis available at: http://r-forge.r-project.org/R/?group_id=645



Home gardens with LR in Mlaky (Polana region, Slovakia) (photo: Pavol Hauptvogel).



Collecting and taking seeds for evaluation in Troyan region (Bulgaria) (photo: Tsvetelina Stoilova) (from project supported by Global Crop Diversity Trust entitled "Enrichment diversity of *Vigna* and *Phaseolus* germplasm collections - evaluation, maintenance and better utilization in correspondence with global climate change").

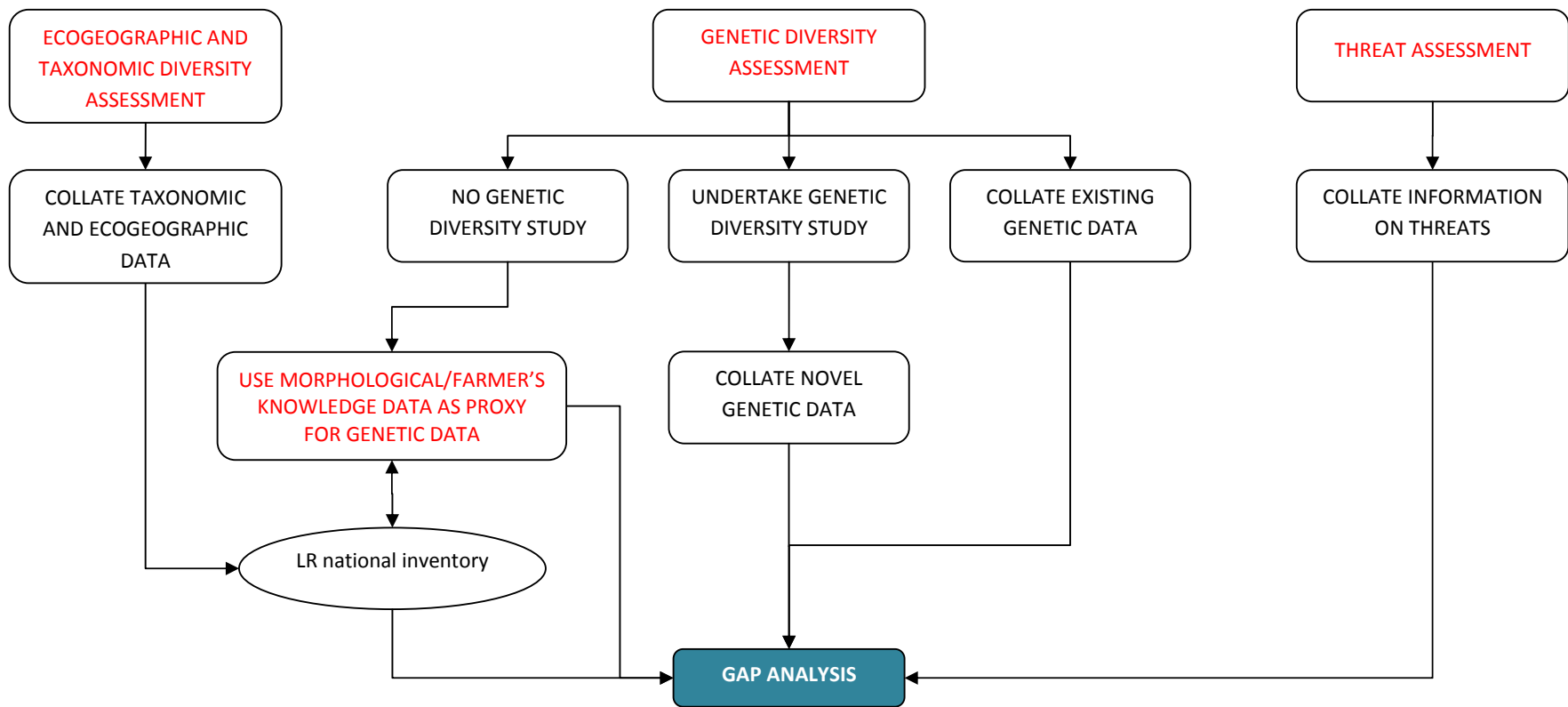


Figure 17. Data collation for LR gap analysis

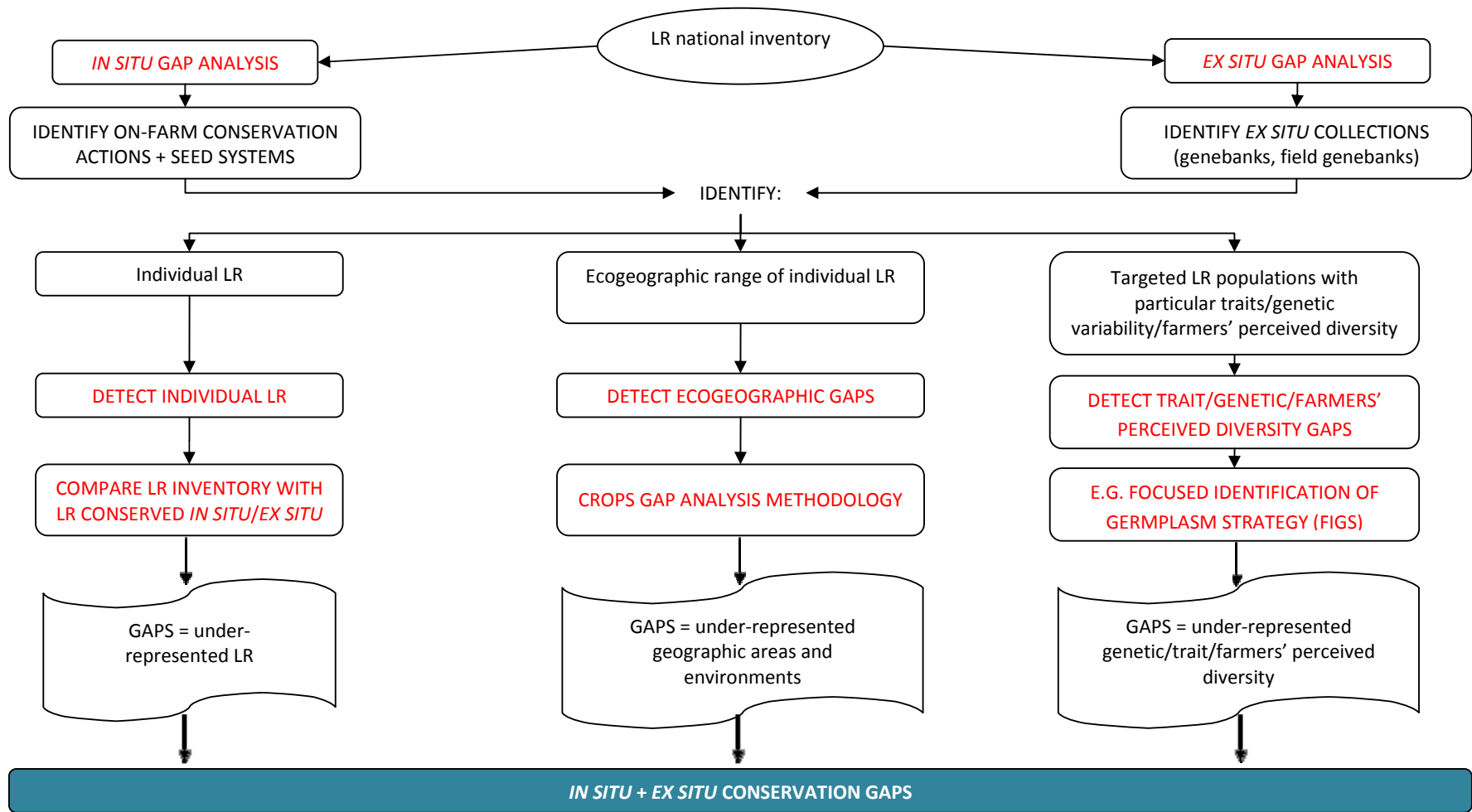


Figure 18. Landrace diversity in situ and ex situ gap analysis methodology

B.8.2. Methodology for LR gap analysis

In situ and *ex situ* gap analysis can be carried out at different levels depending on the information available.

Individual LR level: At the individual LR level, the gap analysis is undertaken to ascertain whether the target LR are actively conserved on-farm or in seed systems and whether they are adequately represented in *ex situ* collections.

- (iii) *In situ.* Review on-farm activities and seed systems that maintain LR. Compare the LR inventory with those populations known to be actively conserved *in situ* to detect priority LR not actively conserved. GAPS = LR diversity not actively conserved *in situ*.
- (iv) *Ex situ.* Review the *ex situ* accessions in gene banks and field gene banks, via direct contact with gene banks or via on-line databases (e.g. EURISCO, GENESYS, Singer). Compare the LR inventory with those populations known to be actively conserved *ex situ* to detect priority LR not actively conserved. GAPS = LR diversity not conserved *ex situ*.

Ecogeographic level: At the ecogeographic level, the gap analysis is undertaken to ascertain whether the whole ecogeographic range of individual LR are represented *in situ/ex situ*. Environmental data can be used as a proxy for abiotic traits such as extreme temperatures, drought, etc.

- (iii) *In situ:* a comparison between ecogeographic range of individual LR and that element of the range that is conserved formally on-farm will help target new *in situ* activities. GAPS = ecogeographic areas not covered by on-farm activities.
- (iv) *Ex situ:* a comparison between individual LR ecogeographic diversity and where that diversity has been previously sampled and conserved *ex situ* will help target further collections and active *ex situ* conservation. GAPS = ecogeographic areas where previous sampling and *ex situ* conservation has not occurred or where further germplasm collection is required to supplement existing collections, especially if the collection was made over 10 LR generations previously.

See figure 38 for the methodology developed for gap analysis of crops⁷².

Trait level: At the trait level, the gap analysis is undertaken to ascertain whether specific LR populations with a particular trait of interest (e.g. gluten content) are conserved *in situ/ex situ*.

- (iii) *In situ.* A comparison between LR distribution among farmers together with trait/genetic/farmers' perceived diversity data and where it is actively conserved will help target new *in situ* activities. GAPS = specific populations

with the trait of interest/genetic characteristic (or high diversity, etc.) not actively conserved *in situ*.

- (iv) *Ex situ*. A comparison between LR distribution among farmers together with trait/genetic/farmers' perceived diversity information and where it has previously been collected will help target further collections and active *ex situ* conservation. GAPS = specific populations with the trait/genetic diversity/farmers' perceived diversity of interest not conserved *ex situ*.

GIS-based predictive characterization can be used to identify those populations that are likely to contain desirable traits (e.g. insect pest resistance). Focused Identification of Germplasm Strategy (FIGS) is a predictive characterisation technique and can be used in this context. The basic steps of a FIGS analysis for LR are:

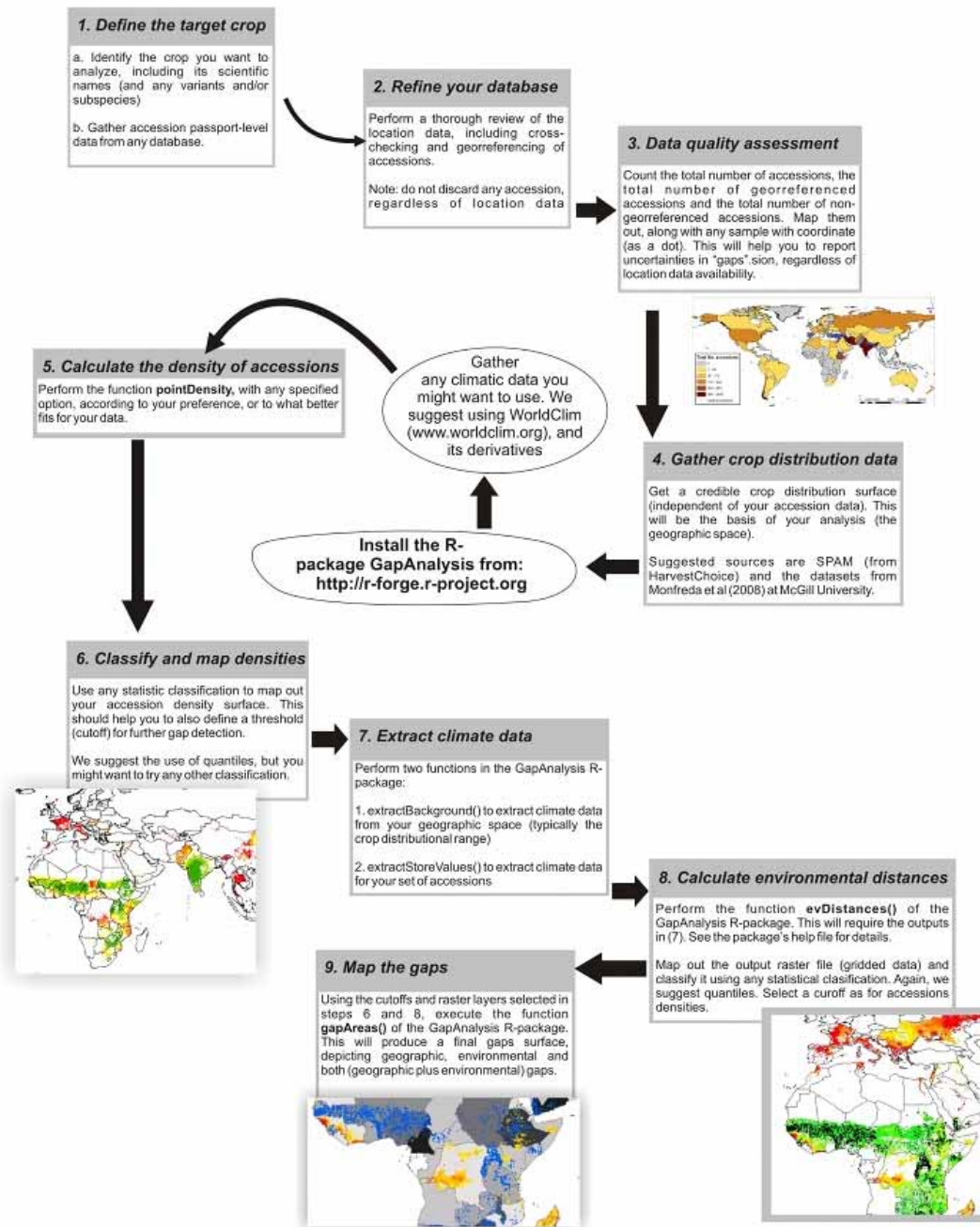


Figure 19. Crops gap analysis methodology at ecogeographic level ¹⁸²

- Compile the geographic distribution of the LR;
- Gather characterisation and evaluation data regarding the trait of interest from *ex situ* collections databases and georeference the samples that contain the trait of interest;

¹⁸² Ramírez-Villegas *et al.* (2010)

- Gather environmental information (e.g. climate, soil, elevation, topography) (see ‘Additional materials and resources’ for sources of data) and extract environmental data for each LR accession/population using a GIS software (e.g. DIVA-GIS);
- Utilise the existing characterization and evaluation data to identify sites where the required variation exists;
- Produce profiles of the sites identified above in terms of environmental, ecological and any other relevant data;
- Look for similar environmental profiles amongst other sites and develop a sampling strategy using clustering, principal component analysis etc.;
- Identify whether *ex situ* accessions are available or active on-farm conservation is carried out and whether it is necessary to collect *de novo* from the identified sites in order to complete the *ex situ* collection or to target populations for *in situ* conservation.

Box 86. GIS-based predictive characterisation

Predictive characterisation is a means of identifying *in situ* populations/*ex situ* accessions likely to contain desirable traits (e.g. insect pest resistance) and has been successfully applied in research on crop wild relatives. Focused Identification of Germplasm Strategy (FIGS) is a technique of predictive characterisation that can be used for that purpose but can also be used for landraces. It is an innovative approach that brings together information available on PGR and the environments in which they evolved through GIS technology. It combines climatic and ecogeographic information, species distribution data, and distribution of a particular trait (e.g. pest or disease resistance), in order to create environmental profiles of the habitats in which a given population (genotype) containing the desirable trait evolved. FIGS finally identifies the populations or accessions most likely to contain the desirable adaptive traits. FIGS has been used to successfully identify seven new resistance alleles to powdery mildew (genePm3) from an initial number of 16,089 wheat accessions (see Bhullar *et al.* 2009). The utilization of FIGS methodology can thus aid breeders’ selection in identifying *in situ* populations or *ex situ* accessions most likely to contain the traits of interest.

Source: MacKay *et al.* (2004), Bhullar *et al.* (2009)

Genetic variability of a specific trait level: At the genetic variability of a specific trait level, the gap analysis is undertaken to ascertain whether, for each LR, adequate genetic (trait expression) variability within a trait is represented *in*

situ/ex situ. Alternatively, farmer's perceived (morphological) diversity can be used as a proxy for genetic diversity.

- (i) *In situ*: a comparison between LR distribution among farmers together considered together with genetic diversity information (or morphological/farmer's perceived diversity) and where that trait expression variability is actively conserved, will help target new *in situ* activities. GAPS = genetic diversity/farmers' perceived diversity not currently conserved *in situ* on-farm.
- (ii) *Ex situ*: a comparison between LR distribution among farmers together with genetic diversity information (or morphological/farmer's perceived diversity) and where it has been previously collected, will help target further collections and active *ex situ* conservation. GAPS = genetic diversity/farmers' perceived diversity not conserved *ex situ*.

It should be re-stressed that different local named LR can be the same LR and LR with the same local name can include two distinct genetic entities. In which case trait expression variability assessment should be accompanied by a molecular study to provide clarification.

B.8.3. Examples and applied use of LR gap analysis

Box 87. *Ex situ* gap analysis at geographic and trait levels in the pearl millet germplasm

A review of the *ex situ* accessions of pearl millet LR from Asia conserved at the International Crops Research Institute for the Semi-Arid Tropics (ICRISAT) gene bank was undertaken. Based on passport and characterization data and using GIS tools, geographical gaps (areas that were not represented *ex situ*) as well as diversity in one or more traits gaps were identified. Geographical gaps included 134 distinct districts of 14 provinces in India and 12 districts of Punjab province in Pakistan. Gaps in diversity for one or more traits comprised a total of 208 distinct districts in 12 provinces. Among all districts, gaps in the diversity for all traits were found in India; gaps in the diversity of panicle length and width were found in Pakistan, gaps in the diversity for one or more traits and at the same time common to geographical gaps were identified in India.

Source: Upadhyaya *et al.* (2010)

Box 88. Predictive association between traits and ecogeographic data

Given that gene bank collections often lack characterisation and evaluation (trait) data, Focused Identification of Germplasm (FIGS) was used to predict missing trait information for LR. Ecogeographic data for 14 Nordic LR of barley (*Hordeum vulgare* L.) were used to correlate with morphological traits using a modern multi-linear data modelling method (multi-linear partial least squares [N-PLS]). This method proved to be efficient in targeting germplasm for future collecting and complement or replace the current core collection selection method when trait information is missing.

Source: Endresen (2010)

Box 89. Global *ex situ* gap analysis for sweet potato

More than 5000 records of sweet potato LR were obtained from the Germplasm Resources Information Network (GRIN), the EURISCO Catalogue and The CGIAR System-wide Information Network for Genetic Resources (SINGER). The gap analysis was undertaken using three main steps:

1. *Geographic distances and collection densities.* Both the distribution and geographical frequency of accessions were evaluated: the number of accessions in a 3000 Km radius circular neighbourhood within a limited geographic space was calculated thus defining the “known distribution” of the crop. High density areas were detected in Paraguay and the Caribbean; the Philippines, Indonesia and Papua New Guinea were well sampled, whereas the areas in the Malay Archipelago were under-represented in *ex situ* collections. Some areas in China appeared poorly sampled, but this may have been due to inadequate access to national data sets. In Portugal, data were found to have poor quality. Significant gaps were also detected in western Africa, Tanzania, Kenya, Angola, Democratic Republic of Congo, Ethiopia, Madagascar and northern India indicating further collecting is required.

2. *Environmental distances.* The environmental representativeness of each accession in relation to the entire geographic area in which the crop is grown was assessed. All different environments should be represented *ex situ*, even the rarer ones. Accession collection sites were characterized using the Worldclim set as environmental layers (Hijmans *et al.* 2005, available at: <http://www.worldclim.org/>) to derive 19 bioclimatic indices (Busby 1991). These variables were used to calculate the Mahalanobis distance (Mahalanobis 1936) between each of the points where the crop is known to be grown (defined by a mask layer). P5 (maximum temperature of warmest month) was discarded due to the high considerable collinearities between the variables in the data set of Bioclim. The analysis of the environmental representativeness of the sweet potato collection showed that previously identified geographic gaps were in fact already environmentally represented by other accessions: in western Africa, southern Madagascar, Tanzania, Angola, southern China, Brazil, part of the Malay archipelago and Bangladesh. Ecogeographic gaps were detected in northern China, northern India, northern Nigeria, part of Chad and southern Brazil, thus indicating the need of further collecting.

3. *Selection of sampling areas and areas with gaps.* Two thresholds (determining the areas not represented enough by the set of accessions) were selected based on statistics (one for the sampling density layer, and the other one for environmental distances) and used to cut off both previously calculated surfaces.

In summary, significant geographic gaps in the collection were detected in coastal West Africa (Sierra Leone, Guinea and Liberia), northern Nigeria, part of Chad, regions in Ethiopia, eastern Madagascar, northern India and some isolated areas in the Malay Archipelago. China appears to be a well sampled country, but with very limited data accessibility thus inducing a gap in the collections. Environmental gaps were also identified and further collecting efforts should focus in these gaps. Issues of data availability and quality should be the focus in areas such as North America.

Source: Bioversity International *et al.* (2009)

B.8.4. List of references used to compile the text

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B.8.5. Additional materials and resources

Methodological references:

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WW
W


The Gap Analysis site : <http://gisweb.ciat.cgiar.org/GapAnalysis/>


Examples of crop gap analysis:


WW
W Examples of LR gap analyses (barley, cassava, chickpea, common wheat, durum wheat, groundnut, lentil, maize, pigeon pea, potato, rice, sorghum, soybean, sweet potato): <http://gisweb.ciat.cgiar.org/GapAnalysis/?cat=8>


Focused Identification of Germplasm Strategy (FIGS):


 Bari A, Street K, Mackay M, Endresen DTF, De Pauw E and Amri A (2012) Focused identification of germplasm strategy (FIGS) detects wheat stem rust resistance linked to environmental variables. Genetic Resources and Crop Evolution. [doi:10.1007/s10722-011-9775-5](https://doi.org/10.1007/s10722-011-9775-5)


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WW
W Trait mining website: <http://code.google.com/p/trait-mining/>

 R-package GapAnalysis: http://r-forge.r-project.org/R/?group_id=645

Biodiversity occurrence data (*ex situ* sources):

 Dias S, Arnaud E and Dulloo E (2010) Info for food – EURISCO and promoting agrobiodiversity use. Symposium “Towards the establishment of genetic reserve for crop wild relatives and landraces in Europe”. 13-16 September, Funchal, Madeira.

WW EURISCO (on-line gene bank databases):
W http://eurisco.ecpgr.org/home_page/home.php

WW CGIAR System-wide Information Network for Genetic Resources
W (SINGER): <http://singer.cgiar.org/>

WW Germplasm Resources Information Network (GRIN): <http://www.ars-grin.gov/>
W

WW Genesys – Gateway to Genetic Resources: <http://www.genesys-pgr.org/>
W

WW The International Crops Research Institute for the Semi-Arid Tropics
W (ICRISAT): <http://www.icrisat.org/>

WW ECPGR Central Crop Databases (*Allium, Avena, Arachis, Beta, Brassica, Capsicum, Cannabis sativa, Cicer, Cichorium, Cucurbits, Cyphomandra, Dactylis, Festuca, Glycine, Hordeum, Lactuca, Lathyrus, Lens, Linum usitatissimum, Lolium, Lupinus, Malus, Medicago, Phaseolus, Phleum, Physalis, Pisum, Poa, Prunus, Pyrus, Ribes, Rubus, Solanum spp., Solanum lycopersicum, Solanum melongena, Solanum muricatum, Solanum tuberosum, Umbellifer, Vicia faba, Vigna, Vitis, Zea mays, Secale, Spinacia oleracea, Trifolium, Triticale, Triticum*, minor forage grasses, minor forage legumes, minor fruit trees, minor leafy vegetables):
W http://www.ecpgr.cgiar.org/germplasm_databases/central_crop_databases.html.

Biodiversity occurrence data:

WW Global Biodiversity Information Facility: <http://www.gbif.org/>
W

WW Inter-American Biodiversity Information Network (IABIN):
W <http://www.oas.org/en/sedi/dsd/iabin/>

Crop data:

Crop distributions surfaces and other agricultural data available at the
WW Land Use and Global Environmental Change website of the Department of
W Geography at McGill University:
<http://www.geog.mcgill.ca/~nramankutty/Datasets/Datasets.html>.

Environmental data:


WW Bioclimatic variables: WorldClim - Global Climate Data:
W <http://www.worldclim.org/>


WW Soil: World Soil Information: <http://www.isric.org/data/data-policy>
W

WW Topography: The CGIAR Consortium for Spatial Information (CGIAR-
W SCI) srtm.csi.cgiar.org

WW Other: GeoNetwork - <http://www.fao.org/geonetwork/srv/en/main.home>
W

Gazetteers and other ways of searching places names:

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W

WW Getty Thesaurus of Geographic Names:
W http://www.getty.edu/research/conducting_research/vocabularies/tgn/

WW Global Gazetteer Version 2.2: <http://www.fallingrain.com/world/>
W

 Google Earth: <http://www.google.com/earth/index.html>