

Conservation and Sustainable Use of Plant Genetic Resources for Food and Agriculture: a Toolkit for National Strategy Development



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Nigel Maxted, Joana Magos Brehm and Shelagh Kell

On behalf of the Food and Agriculture Organization of the United Nations

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Front cover page (clockwise from top left):

Glycine soja (Chen Bin)

Coffea mauritiana (Ehsan Dulloo)

'Injir shaftaly', local variety of *Prunus persica*, Ordubad district, Nakhichevan Autonomous Republic, Azerbaijan (Mirza Musayev)

Zea mays diversity, Chiapas, Mexico (Carolina Camacho)

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SUMMARY

The Convention on Biological Diversity, the International Treaty on Plant Genetic Resources for Food and Agriculture, the Global Strategy for Plant Conservation and the recent Convention on Biological Diversity Strategic Plan each stress the need for efficient conservation of plant genetic resources for food and agriculture as a means of countering the current rate of biodiversity loss at the global and sub-global (regional, national and local) levels. Crop wild relatives (CWR) are wild plant species that are relatively closely related to crops and landraces (LR) are traditional crop varieties highly genetically diverse and locally adapted. Both possess beneficial traits that can be bred into new crop cultivars to help address changing environmental conditions and market demands.

CWR and LR are vital plant genetic resources that, if efficiently preserved and sustainably used, can increase food security, alleviate human poverty and improve ecosystem stability. However, the diversity of both CWR and LR is currently threatened by human environmental mismanagement and socio-political pressures, and is being permanently eroded or lost; yet the conservation of these resources remain largely neglected by conservation and agricultural agencies. CWR and LR diversity maybe conserved using a range of techniques applied at local, national, regional and global administrative levels; each technique and each administrative level should be applied using a coordinated approach to ensure resource conservation is maximized and available for exploitation.

At the national level, few National Strategies for CWR and LR diversity conservation have been developed and implemented, but taking such an approach together with the use of indicators to assess its efficiency will provide a step change in agrobiodiversity conservation, also making a significant complementary contribution to local and global goals. The Toolkit places particular emphasis on how National Strategies for CWR and LR conservation can be developed and implemented to help nations worldwide to systematically conserve their vital natural resources. Particular emphasis is placed on: (a) the creation of national inventories; (b) prioritizing taxa for active conservation; (c) collation of taxonomic, ecogeographic, genetic and threat data; (d) *in situ* and *ex situ* gap analysis; (e) development and implementation of complementary *in situ* and *ex situ* conservation recommendations, (f) monitoring conserved diversity; and making to critical link between conservation and use to ensure the conserved resource is sustainably exploited—each is a component stage in developing and implementing the National Strategy.

The Toolkit is divided into two parts: Part 1 addresses the policy and technical context of CWR and LR diversity conservation and is aimed at providing national PGRFA coordinators with an introduction to agrobiodiversity conservation. Part 2 addresses the practical implementation of CWR and LR diversity conservation and is aimed at providing national PGRFA scientists with detailed protocols for agrobiodiversity conservation. Part 2 is divided into two sections addressing CWR and LR conservation respectively, and within each the protocols are divided into a series of units that address specific topics in a logical sequence. Each unit contains an overview, proposed methodology, possible challenges and solutions to overcome them are discussed through applied examples, and additional materials are provided that could help the user through the preparation of their National Strategy.

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Participants at the workshop, *Conservation and sustainable use of PGRFA, a Toolkit for National Strategy development*, Lyme Regis, UK, 17–18 March 2011. From left to right: José Valls, Renzo Torricelli, Baorong Lu, Joana Magos Brehm, Valeria Negri, Ehsan Dulloo, Edwin Chiwona, Achille Ephrem Assogbadjo, Shelagh Kell, John Wiersema, Tania Carolina Camacho-Villa, Suzanne Sharrock, Nadiya Al-Saadi, Sónia Dias and Nigel Maxted.

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LIST OF ACRONYMS

COP	Conference of the Parties
CWR	Crop wild relative
CGRFA	FAO Commission on Genetic Resources for Food and Agriculture
LR	Landrace
PA	Protected area
GCDT	Global Crop Diversity Trust
GEF	Global Environmental Facility
GSPC	Global Strategy for Plant Conservation
GIS	Geographic Information Systems
IRRI	International Rice Research Institute
ITPGRFA	International Treaty on Plant Genetic Resources for Food and Agriculture
IUCN	International Union for Conservation of Nature
PGRFA	Plant Genetic Resources for Food and Agriculture
PGR	Plant Genetic Resources
SoWPGR	First report on the State of the World's Plant Genetic Resources for Food and Agriculture
SoWPGR-2	Second report on the State of the World's Plant Genetic Resources for Food and Agriculture
UNEP	United Nations Environment Programme

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PART 1. CONTEXT

1.1 Importance of agrobiodiversity for food security

A country's crop wild relatives (CWR) and landraces (LR) diversity constitute an important component of a nation's natural resources, as plant genetic resources for food and agriculture (PGRFA) they are available for utilization by national, regional and international stakeholders; and form the basis of food and livelihood security (Maxted *et al.* 2011).

CWR are species closely related to crops and are defined by their potential ability to contribute beneficial traits for crop improvement (Maxted *et al.* 2006). They have been used increasingly in plant breeding since the early 20th century and have provided vital genetic diversity for crop improvement—for example, to confer resistance to pests and diseases, improve tolerance to environmental conditions such as extreme temperatures, drought and flooding and to improve nutrition, flavour, colour, texture and handling qualities (Hajjar and Hodgkin 2007, Maxted and Kell 2009). Almost all modern varieties of crops contain some genes derived from a CWR and in monetary terms, CWR have contributed significantly to the agricultural and horticultural industries, and to the world economy (Maxted *et al.* 2008a, Maxted and Kell 2009). Furthermore, as CWR are components of natural and semi-natural ecosystems, they also play a role in ecosystem functioning and thus in broader environmental sustainability and maintenance of ecosystem services.

The particular food security value of CWR has been recognized at least since Darwin discussed their study and conservation (1868), but it was Vavilov (1926) who was the first to promote their systematic conservation in practical terms. However, CWR conservation had remained widely neglected because the responsibility for their conservation has neither been adopted by agricultural agencies (whose remit is not wild species conservation) nor environment agencies (whose focus is not on PGRFA conservation). It is only relatively recently that their systematic conservation has been addressed due to the growing interest in their use as gene donors (e.g., Maxted *et al.* 1997a, Meilleur and Hodgkin 2004, Heywood and Dulloo 2005, Stolton *et al.* 2006, Maxted *et al.* 2008a), even though their value as gene donors has been extensively documented since the 1970s (e.g., Frankel 1970, Jain 1975, Prescott-Allen and Prescott Allen 1986, Hoyt 1988). Their economic value is now understood; for example, one recent estimate is that approximately 30% of modern crop production increase is due to the use of CWR genetic diversity and that this has an annual value of approximately US \$115 billion worldwide (Pimentel *et al.* 1997).



Wild wheat CWR, *Aegilops triuncialis* growing near Meghri Armenia (photo: Nigel Maxted).



Wild cowpea CWR, *Vigna comosa* (photo: Stefano Padulosi).

LR are dynamic population(s) of traditional crop varieties that have some, if not all, of the following characteristics: historical origin, distinct identity and lacks formal crop improvement, as well as often being genetically diverse, locally adapted and associated with cultural practices and associated with traditional farming systems. The importance of LR is two-fold: they are of direct use in small-scale subsistence and commercial agriculture and constitute a potential source of novel genetic diversity for crop improvement. It can also be argued that LR diversity is more likely to be of use to plant breeders, because if a breeder cross their elite lines with a CWR then the progeny are likely to quite distinct from the elite line and the breeder will need several generations to get back to the semblance of the original elite line plus the desired CWR trait, whereas with a cross with a LR is less disruptive as the cross is with the species and obtaining the elite line plus the desired LR trait will be faster. Further, LR can be used directly by farmers, particularly in subsistence or marginal agriculture either as agricultural varieties in themselves or via crossing with locally adapted LR without suffering the potential yield loss that crossing with a CWR is likely to incur.



Cucurbit landrace 'Santorini' (photo: Nigel Maxted).



Paul Watkins with wheat landrace 'Squarehead Master' (photo: Nigel Maxted)

The increasing human population, periodic food shortages and current and expected effects of climate change have all led to raised awareness of the need for more attention to be paid to global and national food security. Globally, agriculture is being practiced in more adverse or marginal environments, whether due to human degradation of habitats, the demand for food forcing the expansion of agricultural lands or the effects of climate change. As a consequence, there is growing demand for the development of new varieties that can be adapted to these marginal environments and to the changing environmental conditions that have been rapidly evolving in recent years (Heywood *et al.* 2007), as well as those expected in the coming decades due to the effects of climate change. This has stimulated the search for genetic material that can be used to confer pest and disease resistance and tolerance to various environmental conditions—in particular, resistance to drought, flooding and heat stress—in turn enhancing productivity, for which CWR and LR are potential sources (Heywood, 2007; Negri *et al.* 2009). Additionally, inter- and intra-species crossing techniques have rapidly developed, facilitating the use of LR and CWR diversity in the improvement and creation of new varieties. Some examples include the use of: *Oryza rufipogon* to confer cold tolerance and other abiotic stress resistance in rice (*O. sativa*) in China (Song *et al.* 2005), *Thinopyrum intermedium* and *Th. ponticum* to improve wheat (*Triticum aestivum*) for barley yellow dwarf virus immunity which was released all across the World (Ayala *et al.* 2001), *Arachis batizocoi*, *A. cardenasii*, *A. duranensis*, *A. stenosperma* and *A. villosa* for rust and late leaf spot resistant

to peanut (*A. hypogaea*) in India (Singh *et al.* 2003), amongst many others (see Maxted and Kell, 2009 for reviews).

Box 1. Can current crop varieties cope with changing environments?

The increasing human population and periodic food shortages have led to raised awareness of the need for global and sub-global food security. In turn, this has stimulated the search for genetic material that can be used to enhance productivity, disease resistance, and tolerance to various environmental conditions, for which CWR and LR are potential sources (Heywood 1997, Negri *et al.* 2009). As a consequence, there is a growing demand for the development of novel varieties adapted to the new environmental conditions that have rapidly 'evolved' in recent years, as well as to meet the short-term adaptation goal of breeding new varieties that address changing consumer demands (Heywood *et al.* 2007). Additionally, inter and intra-species crossing techniques have rapidly developed facilitating the use of CWR and LR diversity in the improvement and creation of new varieties.

While climate change will directly impact CWR diversity, it will also undoubtedly alter the agro-environmental conditions under which our crops grow and thus impact agricultural production. It is likely that many current crop varieties will need replacement to enable them to better suit the new and changing agro-environments (e.g. Jones *et al.* 2003, Duveiller *et al.* 2007, Deryng *et al.* 2011, Li *et al.* 2011, Luck *et al.* 2011). Failure to meet this challenge could have a devastating impact on the global economy and social well-being. Genetic diversity offers an insurance against the harmful impacts of climate change and CWR are particularly likely to contain the breadth of genetic diversity necessary to combat these impacts because of the diversity of habitats in which they grow and wide range of conditions to which they are adapted (FAO 2008). Changes in climate are also expected to augment the risk of pest and disease spread and to affect precipitation regimes and cropping patterns in cultivated species, thus also affecting LR (Veteläinen *et al.* 2009a, Mercer and Perales 2010). Nevertheless, climatic change can lead to non-analogous climate conditions and their consequences are thus difficult to predict. Therefore, CWR and LR diversity is under threat from climate change, while at the same time they offer a critical means of mitigating the predicted impact of changes in climate.

New varieties may be produced by plant breeders, either independently of, or in collaboration with farmers. However, the continued cultivation of LR by farmers is also likely to continue to be of direct importance for food and livelihood security for individual families and communities; particularly the poorest people living in rural and marginal areas. LR are adapted to local environmental conditions and may be more productive, more nutritious, have a wider range of culinary uses, are less likely to suffer from pests, diseases and abiotic stresses, and have a wider cropping window. While many farmers who have replaced LR with modern cultivars have benefited, the consequences of introducing modern, highly bred, high yielding varieties into marginal lands can be disastrous because these varieties have been bred for general rather specific agro-ecosystem suitability. For example, the increase of uniformity and productivity of rapeseed agriculture led to the creation of optimal conditions for the spread of blackleg epidemic (caused by *Leptosphaeria maculans*) in Canada (Juska *et al.* 1997). Marginal lands by definition deviate from the norm and here modern cultivars grown as monocultures are not adapted to the wide range of local environmental conditions; thus, they tend to be more vulnerable to pests and diseases and the effects of extreme environmental variables, such as drought, heat stress or flooding. However, LR have been selected by farmers over millennia to provide maximum production value despite the wide range of local environmental conditions; therefore, under these marginal conditions they can still out-perform modern cultivars.

1.2 Threats and demands for agrobiodiversity

Despite the importance of CWR and LR, there is an increasing loss of this diversity due to a number of social, economic and ecological factors:

- a. CWR and LR are expected to be affected by climate change (e.g., see Parmesan and Yohe, 2003; Root *et al.* 2003; Thuiller *et al.* 2005; Jarvis *et al.* 2008; Lenoir *et al.* 2008)— changes that are expected to augment the risk of pest and disease spread and to affect precipitation regimes and cropping patterns in cultivated species (Veteläinen *et al.* 2009a; Mercer and Perales, 2010);
- b. LR are being lost due to their replacement with modern cultivars, the pressure of changing markets, as well as family needs and aspirations, which may include the abandonment of traditional practices; while CWR, like any other wild plant species are threatened by the loss, degradation and fragmentation of their natural habitats and competition from alien species;
- c. CWR are often associated with disturbed habitats such as field margins, forest edges and roadsides, and these populations are not being adequately conserved by ecosystem conservation agencies;
- d. LR are often associated with low-input traditional farming systems, many of which are being converted to more intensive high-input systems;
- e. CWR and LR diversity suffers from a lack of knowledge regarding its breadth, location and real use potential; for example, inventories are lacking for most countries and conserved CWR and LR diversity is largely uncharacterised or unevaluated (FAO 2010a). In particular, the lack of knowledge on how many traditional seed-saved varieties remain extant as well as on their traditional cultivation practices has been a severe constraint in their conservation and utilization. LR are commonly maintained by older people and diversity is being lost as their cultivation is not being undertaken by younger generations (Maxted 2006).

Further, climate change is predicted to have an even greater impact on diversity. Average temperatures are predicted to rise by 2–4°C over the next 50 years and cause considerable disturbance to regional and seasonal patterns of precipitation (IPCC 2007). Climate acts directly on growth and reproduction of plant species (e.g., Andrello *et al.* 2012) through physiological constraints and/or indirectly through ecological factors such as competition for resources (Shao and Halpin 1995), so changes in climate will inevitably affect species' survival. Several studies have already reported significant effects of climatic change over ecosystems and species (e.g. Parmesan and Yohe 2003, Root *et al.* 2003). Fischlin *et al.* (2007), for example, predict that by 2100, 10–30% of species globally are likely to go extinct as a result of climate change. Negative effects of climate change include loss, expansion, relocation and fragmentation of habitats, and changes in distribution, abundance, phenology and physiology of a wide range of species (Hughes 2000, Walther *et al.* 2002, Jarvis *et al.* 2008), as well as disruption of biotic interactions (Hughes 2000).

Thuiller *et al.* (2005) modelled the impact of different climate change scenarios on the distribution of 1350 plant species and concluded that more than half of the species are predicted to become threatened with extinction by 2080 if they are unable to disperse. On the other hand, plant taxa have the ability to respond to climatic changes, as happened during the Quaternary when there were large-scale distribution shifts (Huntley 1990), so it is expected that they still maintain the ability to do so. In fact, the Thuiller *et al.* (2005) study predicted that if taxa are able to adapt through migration, then about 22% would become Critically Endangered and 2% Extinct. Additionally, some studies have reported a shift in species distribution towards the Poles or upwards in altitude with gradual earlier seasonal migrations and breeding (e.g. Parmesan and Yohe 2003, Root *et al.* 2003, Lenoir *et al.* 2008). Specifically for CWR, a comparative study of the likely impact on three crop gene pools (Jarvis *et al.* 2008) found 16–22% of CWR species would go extinct by 2055 and the majority of species showed greater than 50% loss of distributional range and the range that remained was highly fragmented.

Yet there is increasing demand to utilise this threatened resource:

- i. If crops are to increase production levels there is a need for new trait diversity outside that which has been historically used by farmers and plant breeders—CWR and LR offer the necessary, novel genetic diversity that can enhance crop productivity or commodity improvement, promote disease and pest resistance and increase tolerance of adverse or marginal environments;
- ii. Globally, agriculture is being practiced in more adverse or marginal environments, whether due to human degradation of habitats or the demand for food forcing the expansion of agricultural lands—the desired traits to grow crops in these environments are found in LR and CWR diversity;
- iii. There is a continuous and growing demand for novel diversity by breeders to be used in the development of new varieties due to the relatively short-term commercial lifespan of modern cultivars (usually 5–10 years);
- iv. Conventional and biotechnological breeding techniques have improved dramatically in recent years enabling more precise targeting of desirable traits, relatively easy transfer to the crop and less problems with the transfer of unwanted characteristics from exotic LR and CWR material; and
- v. The conservation of CWR in existing protected areas offers an additional ecosystem service to the protected areas themselves, so for limited additional resource commitment the perceived value of the protected areas can be significantly enhanced.

While both CWR and LR diversity is threatened, at the same time it offers a critical means of mitigating its impact on food security. Despite this wide recognition, it is only very recently that efforts to systematically assess their threat status have been undertaken. There are two main reasons for this: firstly, because of the already identified gap in the remit of conservation agencies to conserve CWR, and secondly, because of the technical challenges in quantifying and locating LR diversity—a prerequisite to their threat assessment. The current status of the threat to CWR and LR diversity is outlined in Box 2.

Box 2. Threat assessment of CWR and LR diversity—current status

Significant progress has been made in assessing the loss of botanical diversity, particularly for regions where the flora is well known; for example, 21% of European vascular plant species were classified as threatened using the 1994 IUCN Red List Categories and Criteria (IUCN, 1994, and 50% of Europe's 4,700 vascular plant endemics are considered to be threatened to some degree (www.redlist.org). CWR are intrinsically no different to other wild plant species, and, like them, many are currently threatened with loss of diversity and/or extinction (Maxted *et al.* 1997b; Stolton *et al.* 2006), however, a review of Red List assessments using the more detailed current IUCN Red List Categories and Criteria (IUCN, 2001) showed that of the more than 25,000 CWR species present in Europe, less than 1% had been assessed (Kell *et al.* 2008). Further, Maxted and Kell (2009) reviewed whether the CWR within 14 global priority crop gene pools had been threat assessed and found that only one, *Solanum*, had been partially assessed using the 2001 IUCN Red List Categories and Criteria.

Even though there is currently no comprehensive global review of CWR threat assessment, if as shown by Kell *et al.* (2008) the majority of wild plant species may be considered CWR (as there is at least one crop in the majority of genera), then a Global Red List of plants would be indicative of the threat facing CWR. Therefore, when the Sampled Red List Index for Plants project (Brummitt and Bachman 2010) recently found that 20% of all plants are currently threatened with extinction it can be implied that a similar proportion of CWR are likely to also be threatened. However, more specifically for European CWR IUCN Red List assessment was recently undertaken for 591 European CWR species in 25 crop gene pools/groups (Bilz *et al.* 2011) and found that 11.5% (66) of the species are considered as threatened, with 3.3% (19) of them being Critically Endangered, 4.4% (22) Endangered and 3.8% (25) Vulnerable—a further 4.5% (26) of the species are classified as Near Threatened. While outside of Europe as part of the UNEP/GEF-supported project, 'In situ conservation of crop wild relatives through enhanced

information management and field application', Bolivian CWR were prioritized and after collating ecogeographic data for 36 CWR genera and over 310 CWR species, threat assessments were undertaken and found that 14.6% (45) of the species are considered as threatened, with 2.3% (7) of them being Critically Endangered, 7.1% (22) Endangered and 5.2% (16) Vulnerable—a further 6.5% (20) of the species are classified as Near Threatened (Mora *et al.* 2009). It is anticipated that these initiatives will act as a catalyst for more countries and regions to follow suit.

CWR resources are primarily threatened by loss, degradation and fragmentation of their natural habitats, whereas LR have been mostly affected by replacement with modern cultivars and changes in land use practices (monocultures, use of pesticides, etc.). Negri *et al.* (2009) argued that LR are the most threatened element of PGRFA because: a) they are being replaced by modern varieties promoted by agricultural advisors and breeding companies; b) the application of variety and seed certification legislation mitigates against the legal sale of LR; c) we have no idea how many traditional seed-saved varieties remain extant; d) we know widely from anecdotal evidence that LR maintainers are almost invariably elderly and their numbers are dwindling annually; e) the proportion of the total LR diversity that is currently used by farmers or breeders is not systematically conserved *ex situ* in gene banks; f) there is only a handful of working on-farm LR conservation projects that are actively maintaining LR diversity; and g) LR conservation falls outside the remit of conventional conservation agencies. Having argued that LR are so uniquely threatened compared to other biodiversity components, globally there is no agreed method of LR threat assessment and no reliable estimate of how many LR are threatened.

Unlike CWR, it is not possible to use IUCN Red List Criteria within taxa, so they cannot be applied for LR assessment. There have in recent years been several attempts to either adapt the IUCN Red List Criteria or develop a parallel set of criteria to assess the level of threat facing LR diversity (Joshi *et al.* 2004; Porfiri *et al.* (2009) Padulosi *et al.* 2012). However, there are few data available to assess LR extinction or genetic erosion—the data that are available are often not quantified rigorously, largely anecdotal or are based on variety nomenclature rather actual genetic diversity (FAO, 1999). However, there are individual papers that estimate the threat to or loss of LR diversity within a specific region; for example, Hammer *et al.* (1996) compared LR diversity extant between 1940 and 1991/93, and between 1950 and 1983/86 in Albania and southern Italy, and found that about 75% LR of all crops had been lost.

Thus it appears that the current threats to CWR and LR diversity is significant, if the potential threats posed by climate change are incorporated the threat to CWR and LR diversity is unprecedented.

At a strategic policy level the threat and use potential are recognised; the Convention on Biological Diversity (CBD) (CBD 1992 and www.biodiv.org), the International Treaty on Plant Genetic Resources for Food and Agriculture (ITPGRFA) (www.planttreaty.org/) and the Global Strategy for Plant Conservation (GSPC) (www.biodiv.org/programmes/cross-cutting/plant/) each stress the need to improve the efficiency and effectiveness of conservation actions targeting PGRFA. In decision VII/30, the Conference of the Parties (COP) of the CBD established the 2010 Biodiversity Targets (CBD 2002) that drew attention to the importance of conserving the “genetic diversity of crops, livestock, and harvested species of trees, fish and wildlife and other valuable species conserved ... restore, maintain, or reduce the decline of populations of species” and committed the parties “to achieve by 2010 a significant reduction of the current rate of biodiversity loss at the global, regional and national level as a contribution to poverty alleviation and to the benefit of all life on earth”. Specifically in relation to PGRFA, having failed to achieve previous targets, the GSPC (CBD 2010a) of the CBD calls for: “70 per cent of the genetic diversity of crops including their wild relatives and other socio-economically valuable plant species conserved, while respecting, preserving and maintaining associated indigenous and local knowledge” by 2020 in Target 9. Further, more effective CWR conservation is specifically highlighted as a priority in Target 13 of the recently established CBD Strategic Plan (CBD 2010b): “By 2020, the loss of genetic diversity of cultivated plants and domestic farm animals in agricultural ecosystems and of wild relatives is halted and strategies have been developed and implemented for safeguarding the genetic diversity of other priority socio-economically valuable species as well as selected wild species of plants and animals.” In addition, the first UN Millennium Development Goals (www.un.org/millenniumgoals/)

highlighted the need of eradicating extreme poverty and hunger.

Therefore, both CWR and LR are critical components of PGRFA that can be utilized (either directly or indirectly) for wealth creation, food security and environmental sustainability in the 21st century; as such their conservation is critical to human well-being.

1.3 Agrobiodiversity conservation at national and international levels

While the value of CWR and LR for food and livelihood security is widely recognized, there is a lack of knowledge about the diversity that exists and precisely how that diversity may be used for crop improvement. CWR and LR inventories are lacking for most countries—without knowledge of how many populations, crops or taxa exist and at what locations, there is no possibility to plan for their systematic conservation. Furthermore, even for some of the most important crops in terms of global or regional food security, there is a lack of knowledge of the genetic relationships between taxa in the crop gene pool. On the other hand, *ex situ* conserved diversity remains largely uncharacterized or unevaluated. In addition, the lack of knowledge of how many traditional seed-saved varieties remain extant as well as of their traditional cultivation practices has been and remains a severe constraint in their conservation and utilization (Maxted 2006, Negri *et al.* 2009).

With the degradation and extinction of CWR and LR populations, not only is unique and valuable genetic diversity being lost, but also the associated indigenous cultivation and exploitation knowledge and the socio-economic and environmental benefits associated with their continued conservation and maintenance. There is therefore an urgent need to address the continued maintenance and conservation of CWR and LR at global, regional, national and local levels in order to maximize the availability of PGRFA for crop improvement and to increase productivity and food security—particularly for the most vulnerable farmers and rural people in developing countries.

This need has been encapsulated in a number of international conventions and strategies, notably the FAO International Treaty on Plant Genetic Resources for Food and Agriculture (ITPGRFA) (www.planttreaty.org), the FAO *Global Plan of Action for the Conservation and Sustainable Utilization of PGRFA* (*Global Plan of Action*, www.globalplanofaction.org), the CBD (www.biodiv.org) and the Global Strategy for Plant Conservation (GSPC) (www.biodiv.org/programmes/cross-cutting/plant/). In 2002, the Conference of the Parties (COP) of the CBD established the 2010 Biodiversity Targets (CBD, 2002) which drew attention to the importance of conserving the “genetic diversity of crops, livestock, and harvested species of trees, fish and wildlife and other valuable species” and committed the parties “to achieve by 2010 a significant reduction of the current rate of biodiversity loss at the global, regional and national level as a contribution to poverty alleviation and to the benefit of all life on earth”. Specifically in relation to PGRFA, having failed to achieve previous targets, the GSPC (CBD 2010a) calls for: “70 per cent of the genetic diversity of crops including their wild relatives and other socio-economically valuable plant species conserved, while respecting, preserving and maintaining associated indigenous and local knowledge” by 2020 (Target 9). Further, more effective CWR conservation is specifically highlighted as a priority in Target 13 of the recently established CBD Strategic Plan (CBD 2010b): “By 2020, the loss of genetic diversity of cultivated plants and domestic farm animals in agricultural ecosystems and of wild relatives is halted and strategies have been developed and implemented for safeguarding the genetic diversity of other priority socio-economically valuable species as well as selected wild species of plants and animals.” In support of the ITPGRFA and endorsed by the COP to the CBD, the *Global Plan of Action* provides a “framework, guide and catalyst for action at community, national, regional and international levels” and “seeks to create an efficient system for the conservation and sustainable use of plant genetic resources, through better cooperation,

coordination and planning and through the strengthening of capacities” (www.globalplanofaction.org).

The SoWPGR-2 (FAO 2010a) notes that although the total number of *ex situ* holdings has increased since the First SoW Report (FAO 1998), CWR diversity is still under-represented and further effort is required to mainstream on-farm conservation of LR diversity. It also highlights the fact that relatively little progress has been made in conserving wild PGRFA outside protected areas or in developing sustainable management techniques for plants harvested from the wild. The SoWPGR-2 also notes that *ex situ* conservation gaps are recognized and that action needs to be taken to fill these gaps. Given that the *raison d’etre* for agrobiodiversity conservation is sustainable use by farmers and breeders, it is disappointing for the SoWPGR-2 to conclude that the number of plant breeders has remained relatively constant, while at the same time levels of public sector crop development have diminished and the private sector has focused on major crops alone. It can be argued that long-term security of CWR and LR conservation will pragmatically only be maintained if there is systematic use of the broad range of CWR and LR diversity conserved. There is therefore a need to strengthen plant breeding capacity and encourage greater pre-breeding initiatives that transfer adaptive traits from what many breeders regard as exotic backgrounds to more acceptable breeders’ material that avoid linkage drag of deleterious traits. One contemporary challenge for the conservation community is to work more closely with breeders to provide a more effective mechanism for access to genetic diversity of interest; an initiative of this kind has recently started in Europe (Maxted *et al.* 2012) and it is anticipated that the research will provide useful results and recommendations for other regions and countries.

CWR	LR
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Considering the socio-economic importance of CWR and LR, it is perhaps surprising that their conservation has not been more systematically addressed. The historic paradigm is that CWR and LR diversity is a resource that is and will always be readily available to breeders. Nonetheless, its erosion and extinction has reached levels where serious social and economic problems will arise unless threats are reduced and diversity secured as permanently as possible. To meet the new 2020 GSPC targets, along with other relevant international, regional and national strategies and legislation, a paradigm shift is required to systematically address the effective conservation of CWR and LR diversity, while at the same time promoting their enhanced but sustainable utilization.

The *Second Report on the State of the World’s Plant Genetic Resources for Food and Agriculture* (SoWPGR-2) (FAO 2010a) reported a substantial increase in interest and awareness of the value of CWR for crop improvement and the need to conserve these species at national level. An outline Global Strategy for CWR Conservation and Use has been drafted (Heywood *et al.* 2008), a new Specialist Group on CWR has been recently established within IUCN/SSC (Dulloo and Maxted 2008), and protocols for the *in situ* conservation of CWR have been developed since the 1990s (see Gadgil *et al.* 1996, Maxted *et al.* 1997a, Tuxill and Nabhan 1998, Zencirci *et al.* 1998, Vaughan 2001, Heywood and Dulloo 2005, Stolton *et al.* 2006,

Iriondo *et al.* 2008, Hunter and Heywood 2011, Iriondo *et al.* 2011). However, progress has been slower for systematic LR conservation which is perhaps surprising given their relative ease of utilization compared to CWR. The conservation of CWR and LR is a complex goal, involving diverse disciplines: for CWR it involves the PGRFA and nature conservation communities, and for LR it involves PGRFA, breeders and farming communities.

Breeders	Farmers communities
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Countries generally lack an adequate and reliable funding mechanism for the development and implementation of national programmes for the conservation and use of PGRFA (FAO 2010a). Nonetheless, of the 101 countries that provided information for both the *First Report on the State of the World's Plant Genetic Resources for Food and Agriculture* (SoWPGR-1) and SoWPGR-2, FAO (2010a) reported a slight increase in national PGRFA programmes from 53% in 1996 to 71% in 2009.

FAO (2010a) also reported a significant increase in the number of CWR inventories, with 28 countries reporting relevant activities compared to only 4 countries in 1996 (see Box 3). However, these surveys are generally limited to single crops or small groups of species, or to certain regions within the countries. Despite this increase, no coordinated and systematic inventorying has been undertaken for both CWR and LR and this is mainly due to: lack of financial and human resources, deficient skills and knowledge, lack of (national) coordination, unclear responsibilities, low national priority, among other factors (FAO 2010a).

Regarding the *ex situ* conservation of PGRFA, FAO (2010a) reported an increased interest in collecting CWR, LR and neglected and under-utilized species. However, the majority of *ex situ* accessions are from major food staples, such as wheat and rice. On the other hand, many countries have reported an increase in the number of *in situ* and on-farm conservation activities, though these are not always well coordinated. The *in situ* conservation of PGRFA (in particular CWR) in wild ecosystems still occurs mainly passively without active management in protected areas (PA). On-farm management of genetic diversity has increasingly become part of national programmes, and the number of on-farm management projects carried out with the participation of local stakeholders has increased somewhat (FAO 2010a). However, most countries still do not have national programmes for *in situ* conservation of PGRFA. In fact, FAO (2010a) highlighted that *in situ* and *ex situ* conservation is still very incipient and further efforts are needed.

Box 3. Examples of inventories/surveys of CWR or crops as reported in some countries

AFRICA

Benin: inventories and surveys of Egusi, yam, banana, Bambara groundnut, nutsedge, local green leafy vegetables, CWR of fonio.

Mali: 16 inventories and surveys of 12 major crops (e.g. sorghum, millet, cowpea, rice, peanut, garlic, shallot, etc.) in different parts of the country; however, there is no comprehensive coverage of wild relatives of millet, sorghum and African rice.

Senegal: inventories of agricultural species of fonio, millet, maize, cowpea and some traditional leafy vegetables.

AMERICAS

Bolivia: CWR inventories of potato (*Solanum*), cassava (*Manihot*), sweet potato (*Ipomea*), quinoa and “cañahua” (*Chenopodium*), peanut (*Arachis*), beans (*Phaseolus*), peppers (*Capsicum*), tree tomato (*Cyphomandra*), papaya (*Vaconcella*), cherimoya (*Annona*), pineapple (*Ananas*), blackberry (*Rubus*), cocoa (*Theobroma*), cashew (*Anacardium*), palm (*Bactris*) and Acai (*Euterpe*); can be found at <http://www.cwrbolivia.gob.bo/inicio.php>.

Brazil: CWR and crop inventories of cucurbits, cotton, peanuts, rice, cassava, maize and “pupunha”.

ASIA AND THE PACIFIC

Japan: survey to determine what LR were cultivated (1984-2000).

Lao People’s Democratic Republic: survey of CWR and/or LR with the purpose of *ex situ* conservation of rice, and other annual or perennial crops (e.g. maize, cassava, sweet potato, sugarcane).

Sri Lanka: CWR inventories of rice, *Piper*, green gram/black gram (*Vigna*), banana, *Cinnamomum* and can be found at http://www.agridept.gov.lk/other_pages.php?heading=CWR.

NEAR EAST

Jordan: sixteen target crops gene pools of global or regional significance and their wild relatives were studied and strategies for their conservation (2002-2005).

Pakistan: CWR of particular crops have been identified (e.g. wheat, barley, rice, Sorghum, millet, cotton, mustard, kenaf, chickpea, pome fruits, tree nuts, etc.).

Uzbekistan: CWR of *Allium*, *Malus*, *Juglans*, *Pistacia*, *Amygdalus*, *Hordeum*.

Sources: FAO Country Reports (2010b), Hunter and Heywood (2011)

1.4 Use of agrobiodiversity for crop improvement

There are numerous ways in which LR/CWR diversity use in breeding can be promoted, but traditionally this has focused on identifying traits of interest through phenotypic characterization and evaluation. This has in many cases proved prohibitively expensive. The First SoW Report (FAO 1998) highlights the fact that two thirds of globally conserved *ex situ* germplasm lack basic passport data, 80% lack characterization data and 95% lack evaluation data, making the use of such germplasm, including CWR germplasm, much more difficult than it need be. The SoWPGR-2 (FAO 2010a) details several new international initiatives since 1998 that support the increased characterization and evaluation of germplasm, including the fairly widespread adoption of core collections that are adequately characterized and evaluated. However, it still concludes that “the country reports were virtually unanimous in suggesting that one of the most significant obstacles to a greater use of PGRFA is the lack of adequate characterization and evaluation data and the capacity to generate and manage such data”.

Box 4. Use of PGRFA diversity for crop improvement

LR and CWR present a tangible resource of actual or potential economic benefit for humankind at national, regional and global levels. Exploitation of their diversity has existed for millennia, with farmers using variation within and between species to improve their crops from the beginnings of agriculture. For example, subsistence farmers in Mexico would annually grow cultivated corn near its wild relatives to facilitate introgression between the CWR and the crop as a means of crop enhancement (Hoyt, 1988). These species and this process are as important to humankind today as they were to the earliest farmers. Developments in the biotechnology industries are now allowing more precise transfer of genes, even in the case of CWR from more distantly related species, further enhancing the value of LR and CWR.

Tanksely and McCouch (1997) and Hajjar and Hodgkin (2007) argued that breeders were not fully exploiting the potential of CWR. Historically, breeders relied on searching for specific beneficial traits

associated with particular CWR taxa rather than searching more generally for beneficial genes, and they avoided transfer into polyploid crops where transfer was more difficult (e.g., rice, sorghum and sweet potato). The likely use of LR diversity is thought to be extensive but precise quantification is limited because of the potential commercial sensitivity of the information to competing breeding companies. The use of CWR diversity in crop improvement programmes for 29 major crops has recently been reviewed by Maxted and Kell (2009), who reported that for these crops, there are 234 references that report the identification of useful traits in 183 CWR taxa (Figure 1). The review showed that the degree to which breeders use CWR species varies between crops, with CWR use being particularly prominent in barley, cassava, potato, rice, tomato and wheat improvement, rice and wheat being the two crops for which CWR have been most widely used, both in terms of number of CWR taxa used and successful attempts to introgress traits from the CWR to the crop. The number of publications for the papers detailing the use of CWR in breeding has increased gradually over time-presumably as a result of technological developments for trait transfer-with 2% of citations recorded prior to 1970, 13% in the 1970s, 15% in the 1980s, 32% in the 1990s and 38% after 1999. The most widespread CWR use has been and remains in the development of disease and pest resistance, with the references citing disease resistance objectives accounting for 39%, pest and disease resistance 17%, abiotic stress 13%, yield increase 10%, cytoplasmic male sterility and fertility restorers 4%, quality improvers 11% and husbandry improvement 6% of the reported inter-specific trait transfers. It can also be seen from this review that since the year 2000 the number of attempts to improve quality, husbandry and end-product commodities has increased substantially. However, the exploitation of the potential diversity contained in CWR species appears to be hit and miss as the approach by breeders to CWR use has not been systematic or comprehensive; therefore, the vast majority of CWR diversity remains untapped for utilization.

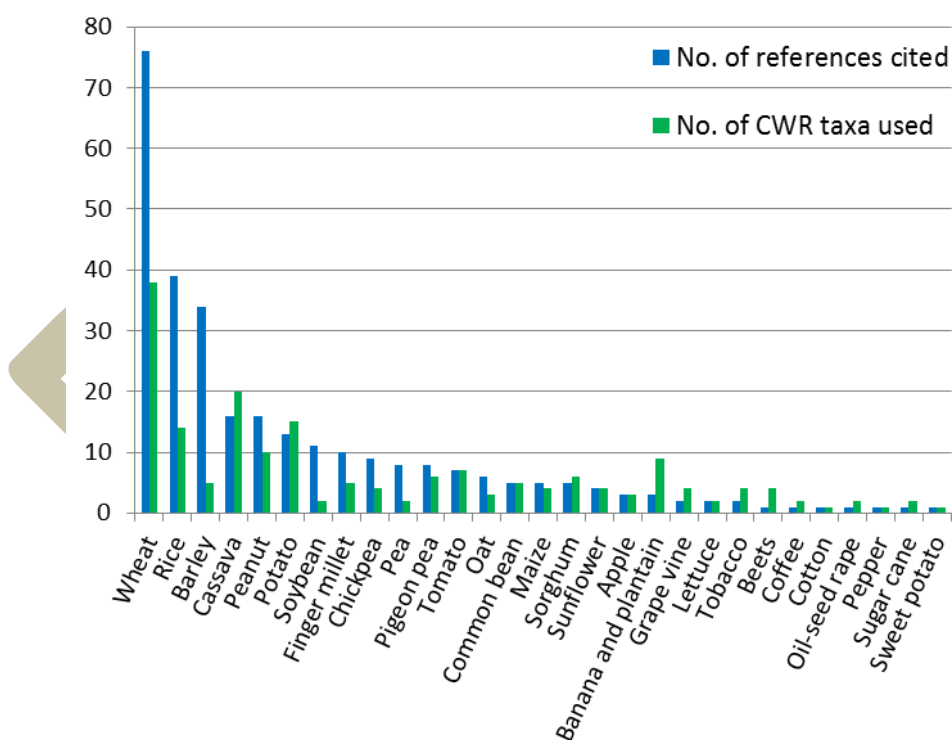


Figure 1. References to use of CWR

The bottleneck over systematic characterization and evaluation has been acknowledged almost since the need for their conservation was recognized in the late 1960s and early 1970s (Frankel and Bennett, 1970). It could be argued that simply increasing the amount of 'traditional' characterization and evaluation is unlikely to result in the required step change in the exploitation of LR/CWR diversity. However, such novel techniques as using 'next

generation technologies' to screen thousands of samples of germplasm for those interesting gene variants that are adaptively important (Nordborg and Weigel, 2008) or 'predictive characterization' which uses spatial analysis of germplasm passport data to predict which germplasm might have desired traits (see Bhullar *et al.* 2009), offer an alternative to conventional characterization and evaluation. Ultimately, unless the professionals involved with LR/CWR conservation can ensure that conserved germplasm is held in a form better suited for breeders and other user groups and that there is less of a barrier between conservation and utilization, then the use of conserved PGRFA diversity is not likely to improve.

1.5 Strategies for agrobiodiversity conservation

There are a number of potential approaches to achieve systematic global or sub-global (regional, national and local) CWR and LR conservation. Regardless of the approach, the systematic conservation of CWR and LR diversity involves the complementary application of *in situ* and *ex situ* strategies. The fundamental difference between these two strategies is: *ex situ* involves the location, sampling, transfer and storage of populations to conserve a particular species away from the original location, whereas *in situ* conservation involves the location, designation, management and monitoring of populations to conserve a particular species within its natural habitat or where it has developed its distinctive characteristics (Maxted *et al.* 1997c). *In situ* conservation strategies have two distinct techniques: genetic reserve and on-farm conservation. Genetic reserves are designated for wild species (such as CWR) and are defined as "the location, management and monitoring of genetic diversity in natural wild populations within defined areas designated for active, long-term conservation" (Maxted *et al.* 1997b). On-farm targets LR conservation and is defined as "the sustainable management of genetic diversity of locally developed crop varieties (landraces), with associated wild and weedy species or forms, by farmers within traditional agricultural, horticultural or agri-silvicultural systems" (Maxted *et al.* 1997b). The precise combination of *in situ* and *ex situ* techniques will vary according to the species being conserved, resources available for conservation and the potential value and use of the species.

Historically, PGRFA have primarily been conserved using *ex situ* methods (e.g., see Frankel and Bennet 1970, Frankel 1973, Frankel and Hawkes 1975, Brown *et al.* 1989, Frankel *et al.* 1995, Guarino *et al.* 1995, Hawkes *et al.* 2000, Smith *et al.* 2003) (Box 5). However, recent research has questioned whether LR diversity can be effectively conserved *ex situ* due to the genetic bottleneck associated with sampling and multiplication/regeneration in gene banks and the constantly and relatively rapidly changing genetic diversity within populations (Negri and Teranti, 2010), and has highlighted the fact that CWR are very poorly represented in *ex situ* collections worldwide (Maxted and Kell, 2009), most attention having been paid to maintaining obsolete cultivars, breeding lines, genetic stocks and LR. It is also widely agreed since the inception of the CBD that *in situ* conservation should be the primary conservation strategy, with *ex situ* employed as a backup, because in contrast to *ex situ* conservation, *in situ* conservation promotes natural gene exchange and continued evolution of LR and CWR populations (CBD 1992, FAO 1996, 2001, Brush 1999, Maxted *et al.* 1997a, Heywood and Dulloo 2005, Stolton *et al.* 2006, Negri *et al.* 2009).

Box 5. PGRFA conservation techniques

There are two fundamental strategies used for PGRFA conservation and within each there are a range of techniques (FAO 1996):

In situ techniques

In situ conservation is the conservation of ecosystems and natural habitats and the maintenance and recovery of viable populations of species in their natural surroundings and, in the case of domesticates

or cultivated species, in the surroundings where they have developed their distinctive properties (CBD, 1992). *In situ* conservation involves the location, designation, management and monitoring of target taxa in the location where they are found (Maxted *et al.* 1997c). There are relatively few practical examples of *in situ* conservation for CWR species, but examples include *Zea perennis* in the Sierra de Manantlan, Mexico (UNESCO 2007); *Aegilops* species in Ceylanpinar, Turkey (Ertug Firat and Tan 1997); and *Solanum* species in Pisac Cusco, Peru (IUCN 2003). *In situ* conservation of LR is also deficient but few examples do exist: sorghum, chickpea, field peas, and maize in Ethiopia (Worede 1997), and threatened crop LR that showed a potential market and/or a good adaptation to local soil and climatic conditions (wheat, flax, lentil, grass pea, chickpea, cowpea and faba beans) in Georgia (Jorjadze and Berishvili, 2009).

- Genetic reserve¹ conservation involves the conservation of CWR in their native habitats. It may be defined as “the location, management and monitoring of genetic diversity in natural wild populations within defined areas designated for active, long-term conservation” (Maxted *et al.* 1997c). Practically, this involves the location, designation, management and monitoring of genetic diversity at a particular location. The site is actively managed, even if that active management only involves regular monitoring of the target taxa, and conservation is long term, because significant resources will have been invested to establish the genetic reserve (Maxted *et al.* 2008d). This technique is the most appropriate for the bulk of CWR species, whether they possess orthodox or non-orthodox seeds.

- On-farm conservation involves conserving LR within traditional farming systems and has been practised by farmers for millennia. Each season the farmers keep a proportion of harvested seed for re-sowing in the following year. Thus, the LR is highly adapted to the local environment and is likely to contain locally adapted alleles or gene complexes. On-farm conservation may be defined as: “the sustainable management of genetic diversity of locally developed landraces with associated wild and weedy species or forms by farmers within traditional agriculture, horticulture or agri-silviculture systems” (Maxted *et al.* 1997c).

- Home garden conservation – crops are grown as small populations and the produce is used primarily for home consumption. Home garden conservation is a variation on on-farm conservation and may be defined as: “the sustainable management of genetic diversity of locally developed traditional crop varieties by individuals in their back-yard” (Maxted *et al.* 1997c). Its focus is usually on vegetables, medicinal plants and spices (e.g., tomatoes, peppers, coumarin, mint, thyme, parsley, etc.). Orchard gardens, which are often expanded versions of kitchen gardens, can be valuable reserves of genetic diversity of fruit and timber trees, shrubs, pseudo-shrubs, such as banana and pawpaw, climbers and root and tuber crops as well as the herbs.

Ex situ techniques

Ex situ conservation is the conservation of components of biological diversity outside their natural habitats (CBD, 1992). The application of this strategy involves the location, sampling, transfer and storage of samples of the target taxa away from their native habitat (Maxted *et al.* 1997c). LR and CWR seeds can be stored in gene banks or in field gene banks as living collections. Examples of major *ex situ* collections include the International Maize and Wheat Improvement Centre (CIMMYT) gene bank with more than 160,000 accessions (i.e., samples collected at a specific location and time), the International Rice Research Institute (IRRI) with the largest collection of rice genetic resources, and the Millennium Seed Bank at the Royal Botanic Gardens, Kew with the largest collection of seed of 24,000 wild species. Important national/regional collections include: coffee in Côte d’Ivoire, Ethiopia, Cameroon, Kenya, Madagascar and Tanzania; sesame in Kenya; cassava in Malawi, Zambia and Tanzania, and sweet potato in Mauritius, Zambia, Swaziland and Tanzania (FAO 2010a).

Furthermore, integral to *in situ* management of PGRFA are a number of potential positive socio-economic and environmental outcomes; these may include improved diet and nutrition, increased self-sufficiency and livelihood security for farmers and rural communities, maintenance of indigenous knowledge and local cultural practices, low-input sustainable land management practices, and the maintenance of ecosystem services—all factors that add weight to the need for promoting, supporting and sustaining *in situ* management of PGRFA.

Of the two conservation strategies (*in situ* and *ex situ*), the highest proportion of LR and CWR diversity is actively conserved *ex situ*; although the coverage is far from systematic. It is

difficult to quantify the amount of LR diversity held *ex situ* because whether the material is LR is often not recorded. For LR there is also the problem over whether nomenclatural or genetic distinction is used to identify them; just because two farmers say they are growing different LR and give them different names, are they really genetically different? We have better knowledge of the *ex situ* conservation status of CWR, but most of this knowledge is based on studies of European gene bank collections. The First SoW Report (FAO, 1998) estimated that 4% of governmental, 14% of CGIAR and 6% of private gene bank holdings were of wild species; however, these included both CWR and non-CWR wild species. Dias and Gaiji (2005) estimated that approximately 4% of *ex situ* holdings in European gene banks are of CWR (37,528 accessions of 2629 species in 613 genera out of a total of 925,000 accessions of 7950 species in 1280 genera). The ratio of the number of accessions of cultivated species to wild species is striking, with an average of 167 for each cultivated species and 14 for each wild species, giving a ratio of 12:1, which is particularly surprising given that most diversity is located in wild species (Maxted *et al.* 2008a). Later, Dias *et al.* (2012) calculated that a total of around 9% of gene bank accessions held by European gene banks are of wild origin and that these represent 7,279 species. This increase is most likely due to improved information management in gene banks and an increase in the number of gene banks providing data to the central European repository, EURISCO (<http://eurisco.ecpgr.org>), rather than a significant increase in the number of CWR samples being collected and stored.

There are few examples of on-farm conservation projects that have proven sustainable in the longer term, but methodologies for the design, establishment, management and monitoring of CWR in genetic reserves are available (see Gadgil *et al.* 1996, Maxted *et al.* 1997b, Heywood and Dulloo 2005, Stolton *et al.* 2006, Iriondo *et al.* 2008); however, full practical implementation remains limited. As noted by Meilleur and Hodgkin (2004), there are: “weak links between the ‘site-selection and/or management-recommendations’ process and the ‘official-protected-site and/or management-change-designation’ process”. In other words, moving from the stage of identifying genetic reserve sites and making management recommendations, to official site designation and practical management remains a significant challenge. The lack of notable examples of the ‘CWR site selection to reserve establishment’ process may possibly be explained by the inherent requirement to bring together the agricultural conservation community who identify the priority CWR taxa and sites and the ecological conservation community who actively manage the protected areas in which the CWR genetic reserves would be established. However, there are some notable examples of activities that have made a significant contribution to the process of conserving CWR *in situ*; these include the conservation of:

- Wild emmer wheat (*Triticum turgidum* var. *dicoccoides*) in the Ammiad reserve in the eastern Galilee, Israel (Anikster *et al.* 1997; Safriel *et al.* 1997);
- A close, perennial wild relative of maize (*Zea diploperennis*) in the MAB Sierra de Manantlán Biosphere Reserve endemic to Southwest Mexico (UNESCO, 2007);
- Various crop and forest CWR in reserves established in Kaz Dağ, Aegean Region, Ceylanpinar of Southeast Turkey, and Amanos, Mersin in Turkey (Firat and Tan, 1997; Tan, 1998; Tan and Tan, 2002);
- Forage *Vicia* and *Lathyrus* in Turkey (Maxted and Kell, 1998; Maxted *et al.* 2003);
- *Lathyrus grimesii* in Nevada, USA (Hannan and Hellier, in Pavek *et al.* 1999);
- Various cereal, forage and fruit trees in CWR reserves established in Lebanon, Syria, Palestinian Territories and Jordan (Amri *et al.* 2008a, b);
- Grain CWR within the Erebuni Reserve near Yerevan, Armenia (Avagyan, 2008);
- Wild bean populations (*Phaseolus* spp.) in Costa Rica (Zoro Bi *et al.* 2003; Baudoin *et al.* 2008);

- *Phaseolus*, *Gossypium*, *Cucurbita*, *Zea* and *Lycopersicon* in Latin America (Debouck, 2001);
- *Solanum jamesii*, *S. fendleri* and other species in Pisac Cusco, Peru (Bamberg in Pavek *et al.* 1999);
- Wild *Coffea* species in the Mascarene Islands (Dulloo *et al.* 1999);
- *Allium columbianum*, *A. geyeri* and *A. fibrillum* in Washington State, USA (Hannan and Hellier, Pavek *et al.* 1999; Hellier, 2000);
- *Carya floridana* and *C. myristiciformis* in the southern States of the USA (Grauke, Pavek *et al.* 1999);
- *Capsicum annuum* var. *aviculare* in Mexico (Tewskbury *et al.* 1999);
- *Beta vulgaris*, *Brassica insularis*, *B. oleracea* and *Olea europaea* in France (Mitteau and Soupizet, 2000);
- *Vitis rupestris*, *V. shuttleworthii*, *V. monticola* in central–Southeast USA (Pavek *et al.* 2003).

Although these can be cited as positive examples of *in situ* CWR conservation, in many cases the sites identified may not be managed in the most appropriate manner to conserve the genetic diversity of the populations as described by Iriondo *et al.* (2008; 2012) and they therefore do not in themselves constitute the desired global network of genetic reserves that is needed to systematically conserve CWR genetic diversity.

<i>In situ</i> conservation	<i>Ex situ</i> conservation

The conservation of CWR and LR usually results from a combination of conservation actions at the macro- and micro-levels. Macro-conservation deals with the political, economic and strategic planning issues on habitat, species or genetic diversity conservation and can be implemented at global, regional, national and local levels. In other words, macro-conservation deals with the development of strategies targeting the conservation of specific elements of biodiversity, in this case of CWR and LR, but not its practical implementation. Micro-conservation comprises the distinct, practical, conservation actions (which make use of specific *in situ* and *ex situ* techniques) focused on individual habitats, species or intra-specific genetic diversity in order to implement the strategies developed at the macro-conservation level (Figure 2). As such the development and application of National Strategies for CWR and LR Conservation can be thought of as involving macro- and micro-conservation decision making and practically involving a combination of *in situ* and *ex situ* techniques.

or institutions, and should not be seen as alternative but rather as a holistic matrix to maximize overall CWR or LR diversity conservation.

Box 6. Examples of the monographic approach to CWR conservation

At global level: Conservation strategy for Aegilops species

Taxonomic, ecological, geographic and conservation information for 22 *Aegilops* species were collated from ICARDA, EURISCO, GRIN and SINGER datasets, and subsequently used to identify gaps in current conservation and to develop a systematic conservation strategy for the genus. A total of 9866 unique geo-referenced records were collected between 1932 and 2004. Predicted distribution maps were obtained for the *Aegilops* taxa and compared in conservation gap analysis using GIS tools. The *ex situ* conservation status of each taxon was assessed and used to provide a priority ranking and nine out of the 22 taxa were identified as priorities for *ex situ* conservation. Future *ex situ* collections were recommended in several countries across the World. In addition, five complementary regions for *in situ* conservation of *Aegilops* diversity were identified in various countries. Within these five regions, 16 protected areas were identified as potential sites to establish genetic reserves. In addition, the most important *Aegilops* hotspot (on the Syrian/Lebanese border) was found to be outside a protected area and so recommendations for a novel protected area was made.

Source: Maxted *et al.* (2008b)

At regional level: Collection of wild rice in East and Southern Africa

A collecting programme targeting wild rice in East and Southern Africa took place. The collecting strategy was developed from an initial ecogeographic study based on several African and international herbaria and available literature on occurrence and distribution of the target species within in the region, as well as on information provided by the national programme staff. A total of 17 collecting missions were undertaken in Kenya, Malawi, Mozambique, Namibia, Tanzania, Uganda, Zambia and Zimbabwe between April 1997 and April 1998. Passport data and herbarium specimens were collected for each accession during the collecting missions. Threats to the wild rice species were assessed as genetic erosion indicators. Seed fertility, maturity and production were also registered.

Source: Kiambi *et al.* (2005)

<i>Aegilops</i> sp.	Wild rice from East or Southern Africa
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Box 7. Examples of the monographic approach to LR conservation

At regional level: Safeguarding and preservation of the biodiversity of the rice gene pool

A project coordinated by the International Rice Research Institute (IRRI) and financed by the Swiss Agency for Development and Cooperation (SDC) was carried out from 1994 to 2000 in 22 countries in Asia, sub-Saharan Africa, and Costa Rica. The project comprised three main components:

- Collection and *ex situ* conservation of cultivated and wild rice taxa;
- On-farm management of rice LR;
- Strengthening germplasm conservation by National Agricultural Research Systems (NARS), Non-Governmental Organizations (NGOs) and farmer organizations.

Regarding *ex situ* conservation of rice diversity, 165 collecting missions were carried out in 22 countries from 1995–2000. A total of 24,718 samples of *Oryza sativa* were collected, as well as 2,416 samples of 16 *Oryza* taxa, weedy types and mutative hybrids, and four species from three related genera (*Hygroryza*, *Leersia* and *Prospychochloa*). The samples were then sent to the International Rice Gene bank (IRG) at IRRI for long-term *ex situ* conservation.

The two objectives of the on-farm conservation management component of the project were: (i) to increase knowledge on farmers' management of rice diversity, including the factors that contribute to it and its genetic implications, and (ii) to identify strategies to involve farmers' managed systems in the overall conservation of rice resources. Three study countries and sites (in India, Vietnam and the Philippines), that represented a broad cross section of rain-fed lowland and upland farming systems with different agricultural, policy and economic conditions, were selected. Biological and social sciences experts, as well as NARS and local people were involved in this component of the project. Socio-economic surveys, questionnaires on farmers' management of diversity, anthropological methods (including semi-structured and unstructured interviews), field seed collections, surveys for biotic constraints, and molecular marker analyses and field trials were used during the project in order to understand and optimise the on-farm management of rice LR diversity.

The third component of the project focused on the upgrading of gene bank facilities and facilitating germplasm collection of NARS, as well as on the training of national personnel and scientists participating in the on-farm conservation research on the skills needed to collect and conserve rice germplasm. Between 1995 and 1999, IRRI staff trained more than 670 people in 48 training courses in 14 countries and at IRRI headquarters in the Philippines. The training encompassed field collection and conservation, characterization, wild rice species, data management and documentation, gene bank management, seed health, analysis of socioeconomic data, and isozyme and molecular analysis of germplasm.

Source: IRRI (2000)

At national level: Races of maize in Mexico

The authors studied 32 races of maize in Mexico using morphological, cytological, genetic and agronomic characteristics and geographical distribution.

Source: Wellausen *et al.* (1952)

At whichever level of application, the monographic and floristic approaches target priority crops or crop gene pools and aim to systematically conserve them via a network of on-farm locations or genetic reserves, with backup in *ex situ* collections. Both the monographic and floristic approaches can be implemented at different scales: global, national, and local. A fourth macro-conservation scale of implementation might be added where there is a distinct continental or regional level of conservation activities between the global and national, as is the case of the Southern African Development Community, Sub-Saharan Africa, North Africa, Europe or West Asia.

Box 8. Examples of the floristic approach to CWR conservation

Floristic approach at regional level: CWR Catalogue for Europe and the Mediterranean

The CWR Catalogue for Europe and the Mediterranean (Kell *et al.* 2005) was created by generating a list of crop genera, matching these genera with those that occur in Europe and the Mediterranean, and then extracting the taxa within the matching genera.

The crop genus list was generated from four information sources: Mansfeld's World Database of Agricultural and Horticultural Crops (Hanelt and IPK Gatersleben, 2001; IPK Gatersleben, 2003), the 'Enumeration of cultivated forest plant species' (Schultze-Motel 1966) (for forestry species), the Community Plant Variety Office list of plant varieties (www.cpvo.eu.int) (for ornamental plants) and the Medicinal and Aromatic Plant Resources of the World (MAPROW) (U. Schippmann, pers. comm. Bonn 2004). This was matched with floristic data in Euro+Med PlantBase (version 2006), which is a database of the Euro-Mediterranean flora, including data on the status of occurrence of taxa in countries and/or

sub-national units. The CWR Catalogue was generated by extracting the taxa within the genera in Euro+Med PlantBase matching the crop genus names.

Source: Kell *et al.* (2008)

Floristic approach at national level: Inventory of Portuguese CWR

The Portuguese CWR inventory was developed from a geographically filtered list from the CWR Catalogue for Europe and the Mediterranean (Kell *et al.* 2005). To ensure that all important crop genera as well as nationally grown crops were considered, several documents were used for validation [the complete list of agricultural, vegetables, fruits and ornamental species produced by the Portuguese National Catalogue of Varieties (DGPC 2003), the Temperate and Boreal Forest Resources Assessment 2000 (TBFRA-2000) (UNECE/FAO 2000) for the forestry crops; a priority list of ornamental genera representing the recommendations from the Herbaceous Ornamental Crop Germplasm Committee (HOCGC) (OPGC 2002), the report by Pimenta (2004) on an updated list of ornamental plant species grown in Portugal]. Twenty-two priority species for conservation were identified based on eight criteria (native status, economic value, threatened status, *in situ* and *ex situ* conservation status, global and national distribution, and legislation) and combining different prioritization schemes (Magos Brehm *et al.* 2010). An ecogeographic survey, gap analysis, and species distribution modelling with current and future climate data were undertaken for target species. Additionally, a genetic diversity analysis for a subset of priority species was carried out. The results obtained with these different methodologies were combined in order to provide *in situ* and *ex situ* conservation recommendations for these wild plant resources.

Source: Magos Brehm (2008), Magos Brehm *et al.* (2008a, 2010)

Priority Portuguese CWR	Priority Portuguese CWR
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Box 9. Examples of the floristic approach to LR conservation

At regional level: Traditionally cultivated crops in Mexico

An ethnobotanical study of the cultivated crops at the “milpas”, a traditional poli-crop farming system, at the NW of Yucatán, was carried out. “Milpas” are important traditional farming systems with many LR of different crops. They are characterised particularly by maize (*Zea mays*), beans (*Phaseolus* spp.) and pumpkins (*Cucurbita* spp.), together with many other crops (e.g. chillies and tomatoes) that vary from one region to another. It is a more resilient system than if the crops were cultivated as monocultures and these crops have an adaptive potential to different climates (from semi-deserts to temperate and tropical) and to all altitudes. “Milpas” are the main farming systems for the rural communities of this area because they produce the main food crops. The diversity of this system allows the cultivation of many species and many LR which possess distinct characteristics. The authors focused on the more historically and culturally important crops produced at the “milpas”.

Source: Terán *et al.* (1998)

At regional level: Landraces in Central Italy

Since 1981, exploration and collecting missions allowed the identification of more than 400 LR from different plant species (forages, cereals, pulses, garden crops and fruit trees) found on-farm in Central Italy. The author studied current LR management and use by farmers and discussed the reasons why they have been maintained on-farm. Three case-studies (cowpea ‘fagiolina’ in the Trasimeno lake area, Perugia; emmer ‘farro’ at Monteleone di Spoleto, Valnerina, Terni; the ‘fagiolo a pisello’ - *Phaseolus*

vulgaris L. - at Colle di Tora, Rieti) of efficient on-farm conservation were presented and threats identified.

Source: Negri (2003)

At national level: Vegetable landraces in England and Wales

An initial exercise for UK crop LR (Scholten *et al.* 2004) found a significant wealth of LR diversity that was often highly geographically localized and critically threatened with extinction. Previous studies indicated that maximum LR diversity was maintained in vegetables. A vegetable inventory was needed to provide the baseline data to a) identify conservation needs, b) enact systematic *in situ* and *ex situ* conservation, c) monitor change (including the assessment of genetic erosion), and d) enhance their use in meeting changing market demands and in promoting UK food security. LR data were collated from UK seed banks, via media releases and advertisements and by using an online questionnaire, internet searches, email correspondence, telephone calls and face to face meetings with a broad range of interest groups, companies and individuals. The results indicated that (i) seed banks do not contain the full range of English and Welsh vegetable LR diversity available, (ii) nationally registered 'B' List LR varieties are under threat as they are often maintained *in situ* by small commercial companies with limited resources, (iii) other vegetable LR are maintained *in situ* by commercial seed companies, NGOs, individual farmers, allotment-holders and home gardeners, but no direct governmental support is provided, and (iv) there has been a significant loss of vegetable LR diversity in England and Wales and much of the remaining diversity is threatened. The need to put in place strategies to capture this diversity and nurture the culture that is responsible for creating and maintaining it was identified. Recommendations for the initiation of a LR protection scheme in England and Wales, enhancement of *ex situ* LR collections, education and public awareness of local LR diversity, and revision of opportunities for supporting LR cultivation through policy and legislative instruments were made.

Source: Kell *et al.* (2009)

LR in Italy	Vegetable LR in the UK
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1.6 Global agrobiodiversity conservation

A global approach aims at the systematic conservation of CWR and LR diversity as a means of maintaining global food security and meeting consumer choice. At global level, the monographic approach (targeting specific crops and crop gene pools) has to be used since there is no global Flora or list of CWR taxa, or checklist of global LR diversity. The requirement for a global approach is especially important because CWR and LR diversity, like plant diversity in general, is not evenly spread across the globe, but is concentrated into botanical (Mittermeier *et al.* 1999, Myers *et al.* 2000) and crop diversity hotspots (Vavilov 1926, Hawkes 1983), and maintaining food security requires a global overview if it is to be successful. Conservation in these highly diverse hotspots is thus necessarily independent of national political borders and needs to be coordinated if it is to be effective.

In response to this challenge, the FAO Commission on Genetic Resources for Food and Agriculture (CGRFA) has called for the development of a network of *in situ* conservation areas to conserve CWR diversity (Activity 4 of the *Global Plan of Action for the Conservation and Sustainable Utilization of Plant Genetic Resources for Food and Agriculture* – FAO 1996). Within this context, the CGRFA commissioned a thematic background study on ‘the establishment of a global network for the *in situ* conservation of crop wild relatives: status and needs’ (Maxted and Kell 2009) to support the preparation of the SoWPGR-2 and as a basis for updating the *Global Plan of Action*. The objective of this study was to provide sufficient baseline information for planning the future work of the Commission in the establishment and monitoring of a network of *in situ* conservation areas for CWR using the gap analysis methodology developed by Maxted *et al.* (2008c). Specifically, the study aimed to:

- Identify which important areas for CWR are already part of existing protected areas, in particular in the centres of origin or diversification;
- Pinpoint existing conservation gaps in order to assess which important areas for CWR are yet to be protected within and outside existing protected areas;
- Provide the foundations for a long-term and cost-effective strategy for CWR conservation.

The crops included in this background study were, firstly, those that have been identified as being of major importance for food security in one or more sub-regions of the world (FAO 1998) and that are listed in Annex I of the ITPGRFA (FAO 2001), which is a list of PGRFA established according to criteria of food security and country interdependence. These are: finger millet (*Eleusine coracana*), barley (*Hordeum vulgare*), sweet potato (*Ipomoea batatas*), cassava (*Manihot esculenta*), banana/plantain (*Musa acuminata*), rice (*Oryza sativa*), pearl millet (*Pennisetum glaucum*), potato (*Solanum tuberosum*), sorghum (*Sorghum bicolor*), wheat (*Triticum aestivum*) and maize (*Zea mays*). Each of these crops supplies more than 5% of the plant-derived energy intake in one or more sub-regions of the world (FAO 1998). Secondly, three further crops that are listed in Annex I of the ITPGRFA were also considered to be priority crops, because they are regionally important, and data were readily available—cowpea (*Vigna unguiculata*), faba bean (*Vicia faba*) and garden pea (*Pisum sativum*). These priority crops represented different crop groups (cereals, food legumes, roots and tubers), with different breeding systems (cross-pollinating, self-pollinating, clonally propagated), as well as crops of temperate and tropical origin (Maxted and Kell 2009).

The authors made preliminary recommendations for the establishment of a global network of *in situ* conservation areas for the highest priority CWR species¹ from the 12 crop gene pools for which distribution data were available for the study. Although the locations of priority species were selected for only 12 crop gene pools they were located across the globe, primarily in the

¹ Primary and secondary wild relatives and/or CWR which are known to be threatened or have limited distributions.

centres of crop diversity identified by Vavilov (1926), which remain the hotspots of crop and CWR diversity today (see Figure 3- Note the eight Vavilov Centres of origin / diversity, indicated by blue enclosed lines, are likely to contain further priority site for other crop gene pools). The approach undertaken by the authors, a monographic approach at global level, included:

- A review of the uses of each crop and its socio-economic importance;
- Discussion of taxonomic issues, listing of the taxa in the crop gene pool and their degree of genetic and/or taxonomic relatedness;
- Notes on the distribution of the crop and its wild relatives, locating centre(s) of diversity;
- A review of crop breeding efforts that have utilized wild relatives;
- Identification of the highest priority taxa for immediate inclusion in the CWR genetic reserve network, with supporting justification;
- Identification of the highest priority sites for immediate inclusion in the CWR genetic reserve network, with supporting justification;
- Recommended conservation actions and requirements for further research.

The systematic *in situ* conservation of LR is far from being initiated either at the global or national level, and global or national networks of on-farm sites for LR conservation are yet to be implemented. In fact, Veteläinen *et al.* (2009b) highlighted the difficulty of systematically conserving all LR diversity on-farm due to the high numbers of existing LR but stressed that a coherent global network of on-farm conservation should be established in order to actively conserve the highest priority LR globally. A similar point could equally be made nationally for each individual country's priority crops.

The point should be stressed that although there is a strong logic for an intergovernmental institution on biodiversity for food security, in cooperation with international partners from environment and agriculture leading the required research and the establishment of global CWR and LR networks, national agencies do have a role. There is an onus on each country to conserve its CWR and LR diversity *in situ* and this will require the establishment of national networks of genetic reserves and on-farm sites. Where there is coincidence between global and national priorities, the national sites may also contribute to the global network.

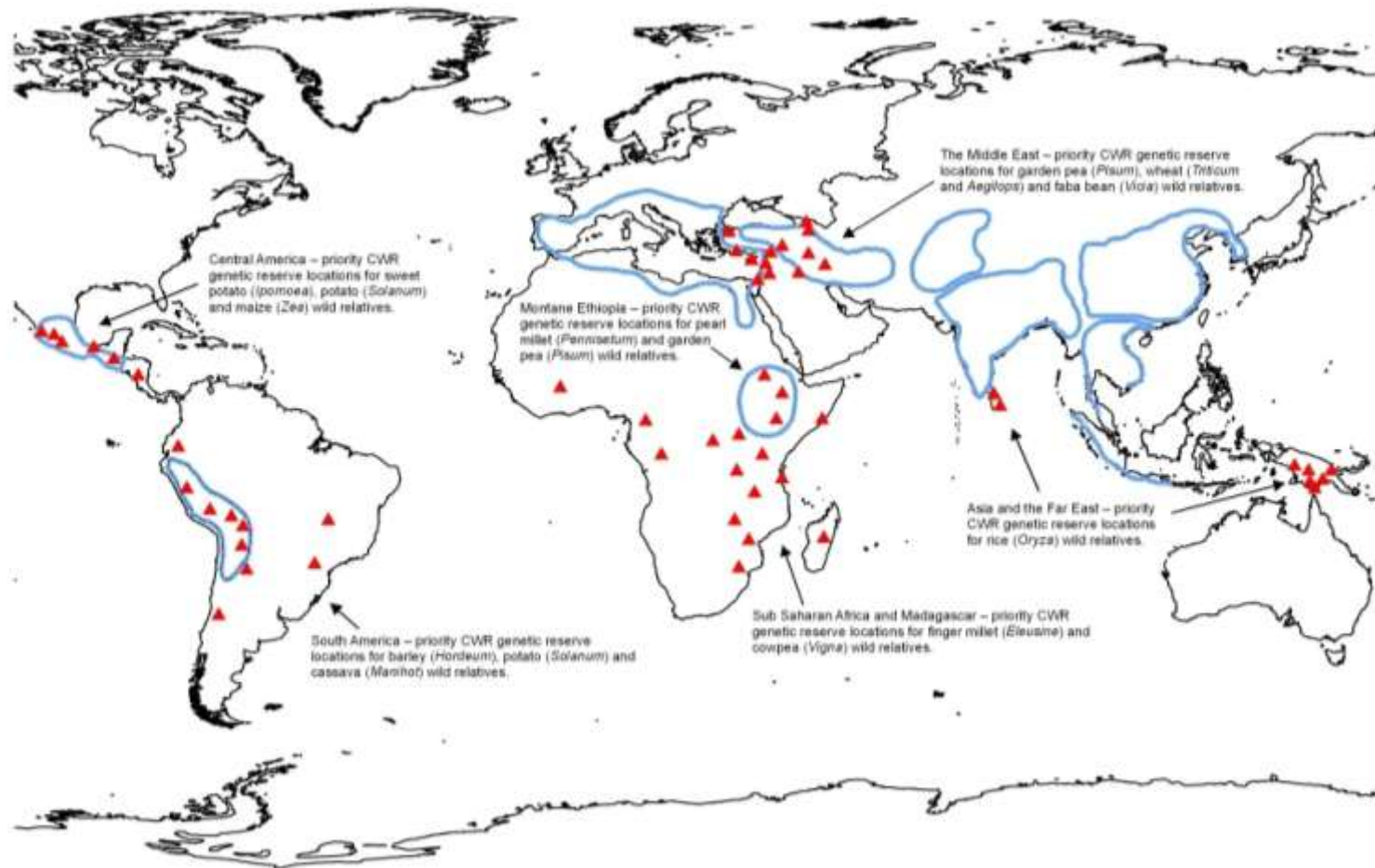


Figure 3. Global priority genetic reserve locations for CWR of 12 food crops²

² Maxted and Kell (2009)

1.7 National agrobiodiversity conservation

Several decisions have to be made before starting to develop National Strategies for CWR and LR Conservation (see Boxes 10 and Box 11), and these made be affected by the availability of existing data and resources. The first step is the creation of a CWR or LR inventory from existing botanical or crop data. Once the relevant taxa have been identified and collated, it is likely that a prioritization step will be undertaken because the number of taxa usually exceeds those that can be realistically actively conserved using the available resources. Next, the available baseline taxonomic, ecogeographic, genetic and threat data are collated for the priority taxa. Specifically regarding LR, maintainers' knowledge about the LR they grow is also relevant and should be gathered. Subsequently, a threat assessment and gap analysis study is carried out, culminating in the formulation of a National Strategy with clear conservation goals and recommendations for *in situ* and *ex situ* actions. As a result, a network of national conservation areas (genetic reserves for CWR and on-farm locations for LR) will be established, as well as *ex situ* conservation actions to ensure a safety backup of the genetic diversity. How to produce National Strategies for CWR and LR Conservation is discussed in detail in Part 2 of the Toolkit. The National Strategies for CWR and LR Conservation developed for any individual country aims at the macro-conservation level to maximise conserved taxonomic, ecogeographic and genetic diversity of the country's CWR or LR, while at the same time promoting its use. While at the micro-conservation level, effective conservation will be implemented at the individual conservation areas, gene bank managers and farmer communities.

Box 10. Options for *in situ* and on-farm conservation of PGRFA

Option 1 – Floristic or monographic approach

Taking the floristic or monographic approach refers to the breadth of coverage of the conservation strategy. A floristic approach means that a conservation strategy is developed for CWR and/or LR diversity that occurs in a defined geographical area, which may be a sub-national area such as an administrative unit or protected area, a whole country, a supra-national region, or even the whole world. A monographic approach on the other hand is restricted to certain crop gene pools, but like the floristic approach may be carried out at any geographical scale. Although both approaches may be carried out at any geographic scale, the floristic approach is most likely to be national in scope, while the monographic approach is more likely to be global in scope because it involves the development of a conservation strategy for a crop gene pool and therefore would ideally encompass all the areas of the world in which the target taxa are native (in the case of CWR) or where they are being cultivated (in the case of LR).

Both approaches will ultimately conclude with the systematic conservation of priority CWR and LR diversity via a network of *in situ* conservation and on-farm conservation sites, with backup in *ex situ* collections. Whether a floristic or monographic approach is taken is likely to depend on: a) the quantity and quality of existing data, b) the resources available to prepare the conservation strategy, and c) the scope of the parent organization undertaking the conservation; for example, an international cereal research institute is likely to focus monographically on cereal crops, while a national biodiversity institute is likely to adopt a more floristic approach. It is worth noting that if the goal is to maximize CWR and LR diversity it is likely that both approaches need to be combined (National Strategies and crop gene pool strategies for the highest priority crops).

Option 2 – Local, national, regional or global geographic scales

CWR and LR conservation strategies should ideally be complementary, depending on the geographical units included, even though the individual geographic scale is likely to be dictated by the remit of the parent organization undertaking the conservation. There is a need to develop interacting CWR/LR conservation strategies, such that one geographic level strategy is not seen in isolation, but contributes to the other levels. For example, a country's national CWR and LR conservation strategy should link with local, regional and ultimately the global strategy such that nationally designated on-farm and genetic

reserve sites become part of a combined network of sites overseen at national level but managed at local level (individual genetic reserves), as well as part of a regional and global network overseen by the appropriate regional and global agencies. Therefore, it is not a choice between geographic scales, but the real choice is whether or not to ensure complementarity in approach between interacting CWR/LR conservation strategies to ensure they form a series of local, national, regional and global *in situ* CWR/LR conservation sites. In practice, however, it should be acknowledged that in implementing such a complementary geographic approach is feasible for systematic CWR conservation now but is likely to be a longer term option for LR conservation if for no other reason than the extent of knowledge available on LR diversity.

Option 3 – Centralized or participatory conservation

It is difficult to precisely categorize the contribution of local communities and farmers *versus* conservationists to address global food security. While an overview is required to identify CWR and LR diversity hotspots and implement genetic reserve or on-farm conservation in a network that maximizes the conserved CWR and LR diversity for the benefit of all humanity, it is equally important to recognize that on-farm or genetic reserve conservation is impossible without local community or farmer approval and action. It is perhaps inevitable that targeted global conservation involves a top-down approach but local communities have been managing, manipulating and exploiting CWR and LR diversity for millennia and so maintaining a complementary bottom-up approach is equally important. Therefore, just as CWR/LR conservation at local, national, regional and global scales interact to ensure effective complementary conservation, both centralized and participatory approaches to conservation also ensure effective complementary conservation.

Option 4 – On-farm conservation or conservation of traditional farming systems

The growing literature associated with LR conservation highlights a distinction in focus between at least two distinct, but associated, conservation activities. The distinction between the two is based on whether the focus is the conservation of genetic diversity within a particular farming system or the conservation of the traditional farming system itself, irrespective of what happens to the genetic diversity of LR material within that system (Maxted *et al.* 2002). These two variants of LR conservation are obviously interrelated, may often be complementary and may in certain cases be seen as one, but in other instances this may not be the case. For example, the introduction of a certain percentage of modern cultivars to a traditional farming system may sustain the system at that location, but could lead to gene replacement or displacement and therefore genetic erosion of the original localized LR material. The choice between the two is dependent on whether the parent organization undertaking the conservation wishes to conserve specific but dynamic LR or the system itself that maintains the agro-environment in which the native LR can continue to evolve.

Option 5 – Farmer or conservationist based in situ conservation

At first it might be thought that although farmers are key players in on-farm conservation of LR, they play a minimal role in CWR conservation. However, experience from the limited number of projects that have established genetic reserves (e.g., Firat and Tan 1997, Hunter and Heywood 2011) has shown that even where genetic reserves are established in association with existing protected areas, farmers are commonly involved. The reason being many CWR are found in pre-climax vegetation so population conservation requires controlled grazing or cutting. Therefore, even when undertaking genetic reserve CWR conservation, it commonly involves conservationists working with farmers.

It is more obvious that farmers and conservationists will need to work together to conserve LR diversity; however, it should be recognized that occasionally the LR conservation may be in conflict with the development aspirations of the local community, partially freezing the dynamic nature of LR diversity. Although the conservationist should never try to restrict or deny these aspirations, the conservationist may be able to promote LR diversity maintenance within the on-farm system by facilitating some form of Participatory Plant Breeding or Participatory Varietal Selection, which may vary from simply aiding farmer selection to full-blown crossing of lines and LR to generate segregating diversity for selection and production of improved breeders' lines (e.g., see Friis-Hansen and Sthapit 2000). Experience from past projects that have promoted on-farm conservation of LR has also shown that the conservationist can have a key role in helping farmers develop alternative niche markets for the LR, raising the value of the

resource and so sustain LR maintenance (Heinonen and Veteläinen 2009, Nikolaou and Maxted 2009, Martin *et al.* 2009, Veteläinen *et al.* 2009b).

Option 6 – Status quo or legislative protection

To promote sustainable *in situ* CWR/LR conservation there is a need to encourage and facilitate stronger legislative protection of sites (i.e. genetic reserve or on-farm) designated for conservation. Experience from ecosystem and wild species conservation has repeatedly shown that the establishment of protected areas requires significant investment of resources and once established legislative protection is required to ensure the long-term sustainability of the conservation investment. This protection is equally applicable for sites designated as genetic reserves or on-farm sites where the *status quo* without specific protection is unviable. This is particularly important for CWR hotspots/sites designated in Vavilov Centres of Origin, all of which are located in developing countries, which are likely to contain the highest proportion of unique CWR and LR diversity that we know is threatened and must be conserved if we are to seriously address global food security.

Option 7 – In situ or ex situ conservation

In situ and *ex situ* conservation should not be viewed as alternatives or in opposition to one another but rather should be practised as complementary approaches. The adoption of this holistic approach requires the conservationist to look at the characteristics and needs of the CWR or LR being conserved and then assess which combination of techniques offers the most appropriate option to maintain genetic diversity. Hawkes *et al.* (2000) suggested that to formulate the conservation strategy, the conservationist may also need to address not only genetic questions but also the practical and political ones:

- What are the species' storage characteristics?
- What do we know about the species' breeding system?
- Do we want to store the germplasm in the short, medium or long term?
- Where the germplasm is located and how accessible is it/does it need to be?
- Are there legal issues relating to access?
- How good is the infrastructure of the gene bank?
- What back-up is necessary/desirable?
- How might the resource be best exploited?

Given answers to these questions, the appropriate combination of techniques to conserve the CWR or LR can then be applied in a pragmatic and balanced manner.

Option 8 – Conservation or conservation linked to use

Historically, there have been two camps of thought in biodiversity conservation—those who see conservation as an end in its self (e.g., see McNeely and Guruswamy 1998) and those who believe there should be a direct and intimate link between conservation and use (humans conserve diversity because they wish to exploit it) (Maxted *et al.* 1997c). This utilitarian concept is fundamental to PGRFA conservation where the goal is to ensure that the maximum possible genetic diversity of CWR or LR diversity is maintained and available for potential utilization.

Source: Maxted *et al.* (2012)

1.8 Local agrobiodiversity conservation

National Strategies for CWR and LR Conservation result in the systematic representation of a nation's CWR or LR diversity in a network of *in situ* conservation or on-farm sites and, as a back-up measure, *ex situ* storage of genetically representative population samples in national and/or local gene banks. The implementation of the National Strategies at local level means that specific decisions regarding *in situ* and *ex situ* conservation actions and techniques need to be implemented locally and these will involve individual protected area/farmer or gene bank manager actively promoting CWR/LR conservation within areas or gene banks that they manage. A systematic, clear and constant dialogue and coordination between the developers of the National Strategies, national agencies and local organizations (NGOs, farmers organizations, nature reserve managers, etc.), is thus fundamental. Although ideal locations for CWR genetic reserves or LR on-farm sites may have been identified at national level, there is an obvious need to confirm on-site that not only the desired CWR/LR diversity is actually present at the site, but also that there are enough economic and social conditions to maintain and actively conserve them or that those conditions can be created.

Local organization	Local organization
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The location and establishment of specific CWR *in situ* genetic reserves within the existing national network of PAs is an ideal way forward given possible financial constraints and the significant additional costs associated with the creation of new PAs for CWR conservation. However the latter should not be excluded from consideration, especially in countries with a limited existing PA network. Determination of the actual number of specific genetic reserves will be directed by science but will ultimately be pragmatic as it will be dictated by the financial resources available for *in situ* conservation as well as governmental and regional will. The practical implementation of the *in situ* genetic reserves within or outside existing PAs should be addressed at policy level and a strong commitment should be made. The National Strategies for CWR and LR Conservation should thus be integrated and linked to the GSPC (through the GSPC national focal point), the ITPGRFA, the National Biodiversity Strategies and Action Plans (NBSAPs)—the principal instruments for implementing the CBD at national level (<http://www.cbd.int/nbsap/>)—and to the National Plant Conservation Strategies, when existing. Whether CWR are conserved *in situ* within PAs or outside of them, it is advisable that the sites have some form of legal protection to help prevent sudden threats to conserved populations. On the other hand, local communities living within the target sites where genetic reserves are to be implemented should be actively involved so a holistic and thus efficient approach to conservation of CWR is implemented. Awareness of National Strategies for CWR and LR Conservation should therefore be raised among the different stakeholders. These can take the form of local community conservation (training) workshops. Agreements with private owners (e.g. tax incentives) could be made, not only to ensure CWR are properly managed but also to recognise the local communities' role in conserving such a valuable resource.

Community training workshop

Regarding LR diversity, the implementation of on-farm conservation priorities may be quite challenging. The following steps will need to be taken: (i) Find out whether the target farmers have socio-economic conditions to maintain LR, (ii) Reformulate the *in situ* conservation goals (if needed), (iii) Integrate on-farm priorities with national/international agri-environmental schemes, (iv) Convince farmers to use and maintain LR, (v) Find out whether the priority target on-farm sites occur within formal PAs, (vi) Ensure local crop diversity exists in sufficient quantities within the production systems, (vii) Ensure local crop diversity is accessible to farmers, (viii) Ensure local crop diversity is valued among farmers, and (ix) Ensure farmers benefit from the use of local crop diversity (Jarvis *et al.* 2011).

In parallel to the establishment of the *in situ* priorities, there is also a need to locate, sample, transfer and store *ex situ* samples of priority CWR and LR. *Ex situ* conservation should not only provide a back-up or complementary mode of conservation, but also provide a practical means of access for the germplasm user community; therefore, even if populations are adequately conserved *in situ* they should be duplicated *ex situ* for the benefit of the germplasm user community. Practically, the numbers of examples of local communities actually using CWR and/or LR diversity in their crop maintenance systems may be limited but as with *in situ* conservation, the local communities living within the target sites where collections are to be made should be actively involved and where these communities do use this diversity, the germplasm should also be maintained in local community gene banks. It is vital to establish community seed banks so local CWR/LR diversity is promoted and efficiently utilised. Community seed banks aim at identifying important traditional varieties and orienting the agricultural community towards conserving and cultivating them. These community seed banks have a vital role in ensuring food security especially in arid or semi-arid lands where food is short after extended periods of drought. Therefore, in a global change scenario where climatic changes are already happening, community seed banks are of utmost importance.

Fromal gene bank

Community seed bank

1.9 Policy drivers of agrobiodiversity conservation and use

There are numerous drivers of policy change with regard to the conservation and use of agrobiodiversity:

- The intrinsic value of CWR and LR to safeguard food security, especially in a climate change scenario.
- The direct use of LR, especially to subsistence or marginal agriculture and poor communities, and indirect use as a potential source of novel genetic diversity for breeding.
- The indirect use of CWR for the improvement of crop varieties better adapted to changing environments (e.g., pest and disease resistance, temperature resistance, higher and more stable yield) and to meet consumer demands. In fact, Pimentel *et al.* (1997) estimated that the contribution of agrobiodiversity to yield increase is about 30% of production and that a significant amount of this is due to wide crosses with wild accessions. As an example, in the 1970s the US maize crop was severely threatened by corn blight which destroyed almost US\$ 1,000 million worth of maize and reduced yields by as much as 50% in 1978 (FAO 2005). Blight resistant genes from Mexican maize CWR were used to solve this problem (Prance 1997).
- Improving food quality and for medicinal purposes. CWR have been utilised to donate genes coding for higher nutritional value (e.g., the introduction of genes for higher protein content in wheat—Khan *et al.* 2000) and for increased medicinal qualities (e.g., high levels of anti-cancer compounds in broccoli have been produced with genes from wild *Brassica oleracea* L.—Hodgkin and Hajjar 2007).
- The national economic benefits and wealth creation that arise from: (i) the creation of new niche markets based on the use of LR and traditional products manufactured with LR, (ii) the industry development based on the large scale (and possibly international) commercialization of new improved varieties, (iii) the eco-tourism development based on the conservation and sustainable utilization of PGRFA.
- The reduced probability of economic losses with crops that fail to adapt to changing environments, potentially reducing production and insurance costs, and ultimately increasing the GDP or reducing foreign dependency.
- The environmental sustainability and social development that results from the active conservation and sustainable utilization of PGRFA.
- The public opinion which forces governments to take action.
- The international recognition of a “Green economy” approach.
- The international obligations towards reaching the GSPC targets for 2020 (namely target 9, CBD 2010a), the Aichi targets of the CBD Strategic Plan (namely target 13, CBD 2010b) and the UN Millennium Development Goals (www.un.org/millenniumgoals/) in eradicating extreme poverty and hunger.

1.10 Aim of the PGRFA Toolkit

In this Toolkit we address the issue of how such a systematic approach to CWR and LR conservation can be realized by nations, with an emphasis on integration with local and global levels of implementation. The Toolkit is intended to help countries develop national CWR and LR conservation strategies by following several basic steps:

- Creation of inventories;
- Prioritization for conservation action;
- Genetic data analysis;
- Ecogeographic surveying;
- Gap analysis;
- Establishment and implementation of *in situ* and *ex situ* conservation goals;
- Monitoring of diversity conserved;
- Promoting the use of diversity;
- Data management.

It is important to stress there is no single method for developing National Strategies for CWR and LR Conservation because of issues concerning resource and baseline biodiversity data availability, the local community where the National Strategy is to be implemented, as well as the focal area and remit of the agencies which are responsible for formulating and implementing the strategy. Nevertheless, the process of developing National Strategies for CWR and LR Conservation can be viewed as a series of decisions and actions that follow the same basic pattern in all countries. The Toolkit should thus be viewed as a framework and guide for developing National Strategies for CWR and LR Conservation within which the suggested steps do not necessarily have to be followed in the same predefined order, but in order to develop an effective and efficient long-term National Strategy, have to be implemented within the confines of the available data and resources.

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PART 2. THE TOOLKIT

2.1 What is a Toolkit?

The term “toolkit” may be used to describe many forms of information and content. People typically think of a “toolkit” as a container with a range of tools suitable for working in construction. But a toolkit can be more a set of nails, screws, saws, hammers and chisels; they may also be used in other contexts. In essence “toolkits” for constructing or other types of task are no different. A quick search of the web will find hundreds of “toolkits” available for addressing a broad range of tasks, possibly composed of a library of targeted advice, information and networking for special communities, a series of guidelines and checklists that describe the structure, functions, policies of an organization or task, a series of publications, each designed to help accomplish specific tasks and bring about particular outcomes, an attempt to put into one place all the information required to achieve a task, learning modules, case studies, action plans, policies, resources, forums and contacts—all designed to help implement a task. Each toolkit will by definition be unique as it is designed to achieve a task but it is likely to include but not be limited to:

- Information grouped into categories in order to provide targeted direction for the specific audience;
- Information specifically organized within categories to provide direction on when to read, in what order to read and how to apply the information (similar to pathfinders);
- Information grouped by specific parts of the overall audiences by categories such as levels of involvement in the programme, level of competencies and/or outcomes expectations;
- Content that includes a mission/purpose, outcomes or performance expectations;
- Interactive content;
- Content that can be printed or captured so that it can be personalized by audiences/groups.

In general, a toolkit aims to provide information specifically related to direction on how to accomplish the specific task. Therefore, for any worker faced with a task, a toolkit offers complementary tools to help achieve that task. Although the worker will be guided through its application, he or she decides exactly which tools to employ in which order according to his or her circumstances. It is important to stress that the toolkit should be an aid but not a prescription.

2.2 Users of the Toolkit

This Toolkit is designed primarily for use by developing countries with limited resources and knowledge on their CWR and LR diversity and how to conserve it. Three different groups of users may access and use this Toolkit: (i) FAO national focal points, (ii) agencies responsible for planning and implementing national strategies, such as the national agricultural or environmental agencies (iii) NGOs (e.g. farmers’ organizations), local institutions (e.g. gene banks, universities, research institutes), and individual scientists. The mechanisms of delivering the Toolkit to its users and how it can fit in the wider context of PGRFA conservation is illustrated in Figure 4.

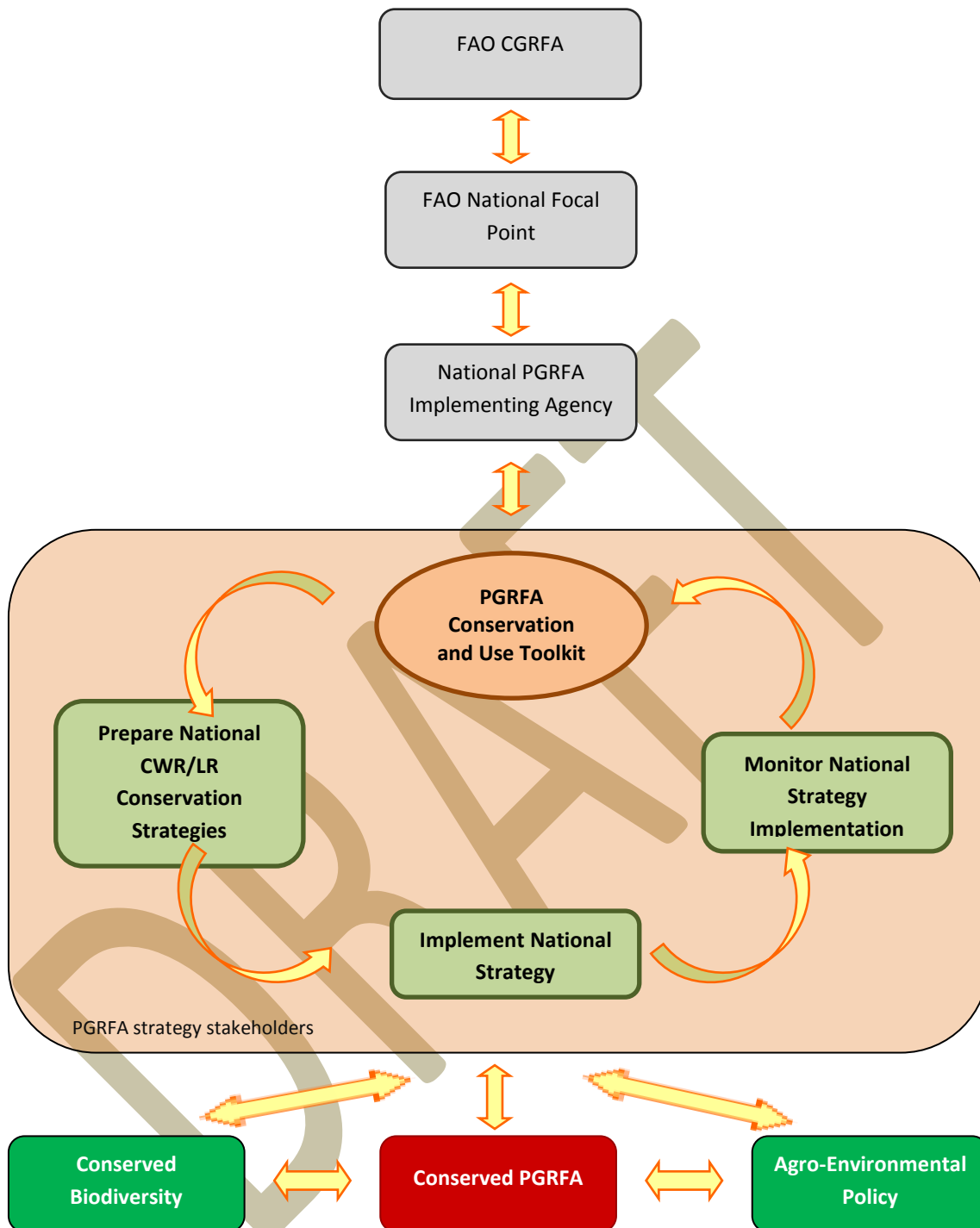


Figure 4. Schematic diagram of Toolkit relationship to PGRFA conservation

2.3 How to use the Toolkit

The Toolkit is designed for the user as a sequential but flexible process that culminates in the production of a National CWR or LR Conservation Strategy. Nevertheless, it is possible to enter through several entry points. Figure 5 is a schematic view of how this Toolkit can be used.

HOW TO USE THE AGROBIODIVERSITY TOOLKIT

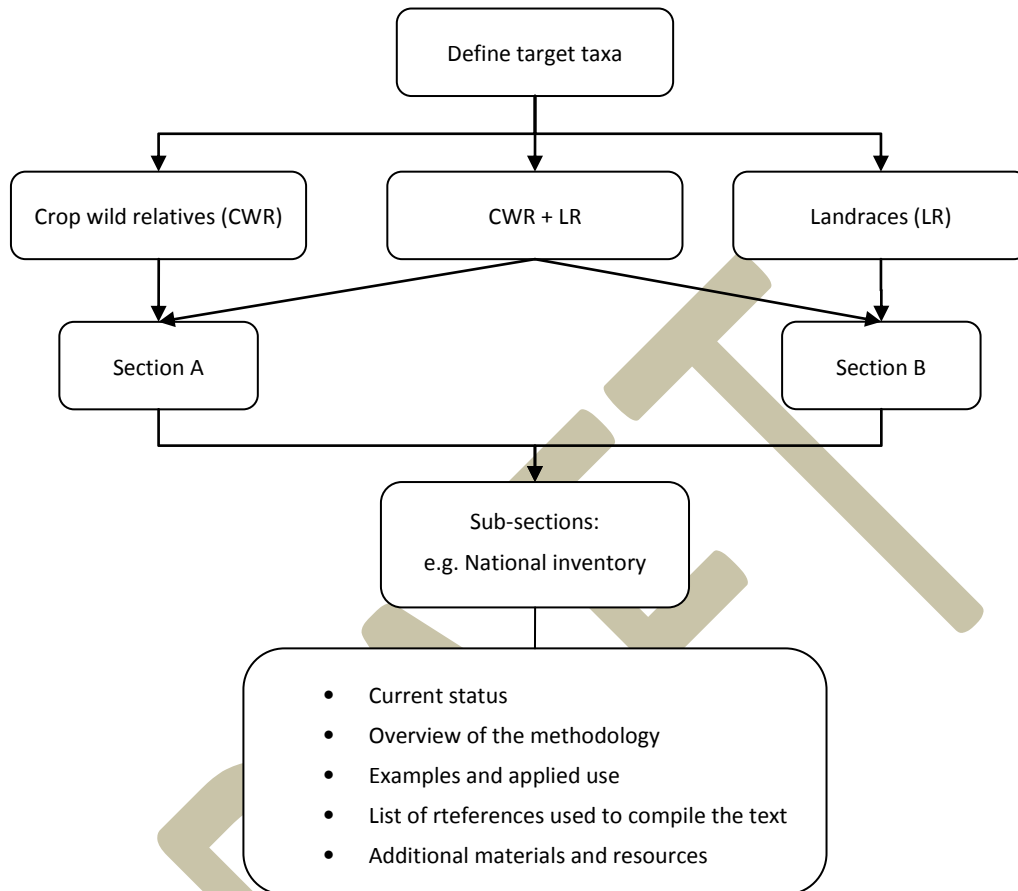


Figure 5 Schematic view of how the Agrobiodiversity Toolkit can be used.

- The first decision the user needs to make regarding the target species is whether the user wants to develop a National Strategy for CWR or LR, or for both.
- From there, the Toolkit is divided into two main sections: section A for CWR and section B for LR.
- Each of these main sections is then divided into sub-sections which are related to the different steps needed to develop a national strategy for the target groups (e.g. A.2.1 Additional materials and resources).
- Each sub-section generally starts with “Overview”, followed by “Overview of the methodology”, “Examples and applied use”, “List of references used to compile the text” and “Additional materials and resources”.
- “Overview” provides a brief explanation of that sub-section, sometimes highlighting some of the developments in that particular area. It also gives a flowchart that may take the form of an expert system (composed of a series of yes/no questions) that helps the user move through the various steps and helps choose which options are more adequate given a particular national context.
- “Methodology” provides a thorough description of the methodology suggested in order to undertake that particular step in the national strategy development process.

- “Examples and applied use” makes reference to case studies where each step of the national strategy development has been applied.
- “List of references used to compile the text” is the list of references used in the preparation of the text. The references in green are those cited in the text.
- “Additional materials and resources” includes extra information (books, scientific papers, grey literature, PowerPoint presentation, software, relevant projects, and web links) (see the icons used below) that not only provide the user with extra practical examples but also help them to visualise and understand how to undertake that particular step; it is generally divided into different topics.



Books, scientific papers, grey literature.



PowerPoint presentations.

WWW Web links.



Software, informatics tools.



Projects.

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SECTION A. CROP WILD RELATIVES

A.1. Introduction

What are crop wild relatives?

Crop wild relatives (CWR) are taxa closely related to crops and are defined by their potential ability to contribute beneficial traits for crop improvement; for example, to confer resistance to pests and diseases, improve tolerance to environmental conditions such as extreme temperatures, drought and flooding, and to improve nutrition, flavour, colour, texture and handling qualities. A working definition of a CWR based on the Gene Pool concept or, in the absence of crossing and genetic diversity information, the Taxon Group concept¹, has been proposed:

“A crop wild relative is a wild plant taxon that has an indirect use derived from its relatively close genetic relationship to a crop; this relationship is defined in terms of the CWR belonging to gene pools 1 or 2, or taxon groups 1 to 4 of the crop”.

Gene pool Figure (with explanation of gene pools)	Taxon group Figure (with explanation of taxon groups)
Example of CWR	Example of CWR

Further background information about CWR is provided in Part 1.

Genetic erosion is a key problem for CWR. What is genetic erosion?

Genetic erosion is a fundamental problem for CWR and has been referred to in the literature as the permanent reduction in richness (total number of alleles) or evenness (i.e. spread of allelic diversity)³ of common local alleles, or the loss of combinations of alleles over time in a defined area⁴. Genetic erosion can affect wild populations conserved *in situ* and *ex situ* collections (i.e. when the *ex situ* collection goes through the regeneration process and are inadvertently selected to suit the regeneration site). It is important to distinguish genetic changes that are detrimental to populations from the ‘normal’ background levels of change⁴.

³ Ford-Lloyd (2006)

⁴ Maxted and Guarino (2006)

Any loss of genetic erosion means the individual is less likely to be able to adapt to their changing environment and means potentially useful traits are unavailable to the breeder.

Why are CWR threatened?

There are numerous factors that negatively impact wild plant populations resulting in genetic erosion, and potentially eventual loss (extinction) of taxa (varieties, subspecies, and species).

The main factors that contribute to the genetic erosion of CWR diversity include:

- Expansion of the human population (which leads to the unequal and unsustainable use of natural resources, and is the basis of all other threats);
- Climate change which is expected to directly affect the cropping patterns and extinction of wild plant species, particularly in drier regions where certain CWR may already be at the edge of their distribution;
- Habitat destruction, degradation, homogenisation and fragmentation;
- Changes in agricultural practices, soil and land use;
- Use of pesticides and herbicides;
- Over-exploitation (excessive extraction from the wild of timber, fuel wood, medicinal and horticultural plants, overgrazing, excessive tourism, etc.);
- Introduction of exotic species (weeds, pests and diseases that compete with, hybridise with, cause physical or biological damage to, or kill native species);
- Natural calamities (floods, landslides, soil erosion, etc.);
- Lack of education and awareness of the importance of CWR and the need to conserve them;
- War and political instability;
- Lack of conservation action for CWR;
- Environmental mismanagement.

Example of threat	Example of threat
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What are the practical consequences of CWR genetic erosion?

- A decline in the short- to medium-term viability of individuals and populations;
- A reduction in the evolutionary potential of populations and species;
- Loss of genetic diversity implies inability to adapt to the changing environmental conditions;
- A decrease in the availability of genes and alleles in providing microhabitat adaptation, disease and pest resistance, yield enhancement traits, etc., for future exploitation (e.g. to develop better or newly adapted varieties) which will restrict breeders options and have a necessary impact on future food security.

Why do CWR need a National Conservation Strategy?

CWR are unique resources for food security and are increasingly used for crop development and improvement⁵. However, they are becoming more threatened and are therefore suffering from genetic erosion. A coordinated, systematic and integrated *in situ* and *ex situ* approach to CWR conservation is essential to secure these critical resources. This is best practically implemented via national conservation strategies because each nation is responsible for the conservation and sustainable use of the natural resources within its political boundaries and as such conservation is predominantly organised on a national basis. The national CWR conservation strategies, as mentioned in Part 1, may be prepared using a floristic or monographic approach; the floristic approach uses as its basis the entire flora of the country and from this identifies the CWR present, while the monographic approach uses a list of the country's crop and that is matched against the flora to identify the CWR present. The national CWR conservation strategies combine at regional and eventually global level into a coordinated holistic approach to ensure that the most important CWR resources are conserved and available for use for crop improvement.

What are the general goals of a National CWR Conservation Strategy?

A National CWR Conservation Strategy aims at the long-term active conservation of the country's CWR taxonomic and genetic diversity, while at the same time promoting its use because experience has shown that through use comes conservation sustainability. Specifically with reference to *in situ* CWR conservation, once *in situ* CWR conservation sites (genetic reserves and informal *in situ* conservation sites) are established, they can be grouped into a coherent national network and provide an opportunity to monitor and assess short and long term changes in CWR diversity. This would help in addressing the CBD Strategic Plan⁶. Also, more specifically, the decision X/2 of the COP 10 (Nagoya, Japan, October 2010), to facilitate the assessment of progress towards the 2020 targets, "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" have been recognised as important elements of biodiversity to maintain "and [by 2020] strategies have been developed and implemented for minimizing genetic erosion and safeguarding their genetic diversity". A network of national CWR *in situ* CWR conservation sites would provide a unique opportunity to assess and meet this CBD 2020 target.

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A.1.2. Additional materials and resources

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WWW Crop Wild Relatives Global Portal: <http://www.cropwildrelatives.org/>

WWW Crop Wild Relatives Discussion Group: <http://tech.groups.yahoo.com/group/CropWildRelativesGroup/>

WWW Agricultural Biodiversity Weblog: <http://agro.biodiver.se/>



Diverseeds Documentary Film. Plant Genetic Resources for Food and Agriculture: <http://www.diverseeds.eu/index.php?page=video> (shows the importance of agricultural biodiversity for food and agriculture, with astonishing pictures from

Europe and Asia)



Unlocking the secrets of Crop Wild Relatives:
<http://www.cropwildrelatives.org/cwr.html>

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A.2. National CWR Conservation Strategy planning – overview

What is a National CWR Conservation Strategy?

A document that sets out a coordinated, systematic and integrated approach to the *in situ* and *ex situ* conservation of a particular country's CWR diversity; that not only evaluates current conservation actions and establishes future CWR conservation objectives, but also reviews the resources required to implement conservations, attributes responsibilities and sets CWR conservation action in the broader environmental and agricultural policy context.

Given the CWR diversity present, the available data, the financial and human resources allocated to conservation, as well as the different levels of commitment by national agencies and governments, the formulation and implementation of a National CWR Conservation Strategy will differ from country to country. Nevertheless, there are likely to be common elements in the development of a National Strategy of this kind that comprise a series of steps aiming at successful conservation of CWR diversity. These steps are:

- (i) Preparation of a national CWR checklist (list of CWR taxa) and inventory⁷ (list of CWR taxa with ancillary information): prepare a national inventory of the country's CWR diversity (floristic approach), or alternatively, an inventory of CWR in priority crop gene pools found within a country (monographic approach).
- (ii) Prioritization of national CWR: prioritise the national CWR inventory to focus conservation resources on the most important taxa; typically, species will be prioritized on the basis of the food security and economic importance of the related crop, the degree of relationship of the wild relative to the crop, and relative level of threat.
- (iii) Ecogeographic diversity analysis of priority CWR: collate and analyse the available geographic, ecological and taxonomic data for priority CWR.
- (iv) Genetic diversity analysis of priority CWR: collate genetic data for priority CWR or, if unavailable, carry out novel genetic analysis.
- (v) Threat assessment of priority CWR: identify threats that affect priority CWR diversity, be aware of previous threat assessment and undertake novel threat assessment for individual species that have not previously been assessed or their assessments are out of date due to the availability of new data.
- (vi) Gap analysis: identify *in situ* and *ex situ* conservation gaps.
- (vii) Formulation of the National CWR Conservation Strategy: establish and implement *in situ* and *ex situ* conservation goals and actions.
- (viii) Monitoring of conservation status: ensure that the conservation actions are maintaining target CWR diversity, either by monitoring *in situ* CWR conservation sites, and possibly changing the population management if diversity is decreasing, and monitoring if *in situ* diversity has changing sufficiently to warrant further *ex situ* sampling.
- (ix) Promotion of the use of CWR: make available characterization and evaluation data to the potential user community to facilitate its sustainable utilization.

The conclusion of this process is the National CWR Conservation Strategy which identifies key sites for *in situ* conservation of CWR and diversity under-represented in *ex situ*

⁷ Note: in this document we distinguish between a checklist and an inventory; checklist is used for the list of CWR names alone and inventory for when more meaningful data has been added to the initial checklist. We also distinguish between a full inventory (all CWR species) and a partial or prioritised inventory (subset of CWR species).

collections. The National Strategy should include provisions for the utilization of conserved CWR diversity by plant breeders, researchers and other potential users.

Figure 6 summarises the model for the development of a National CWR Conservation Strategy as well as the link to international legislation, strategies, habitat and species conservation plans and the utilization of CWR diversity by traditional or local, professional and general users for research, education, and breeding activities. As well as meeting practical national CWR conservation needs and national development schemes, policies and strategies, it is important that the National Strategy should be integrated with other international strategies and legislation.

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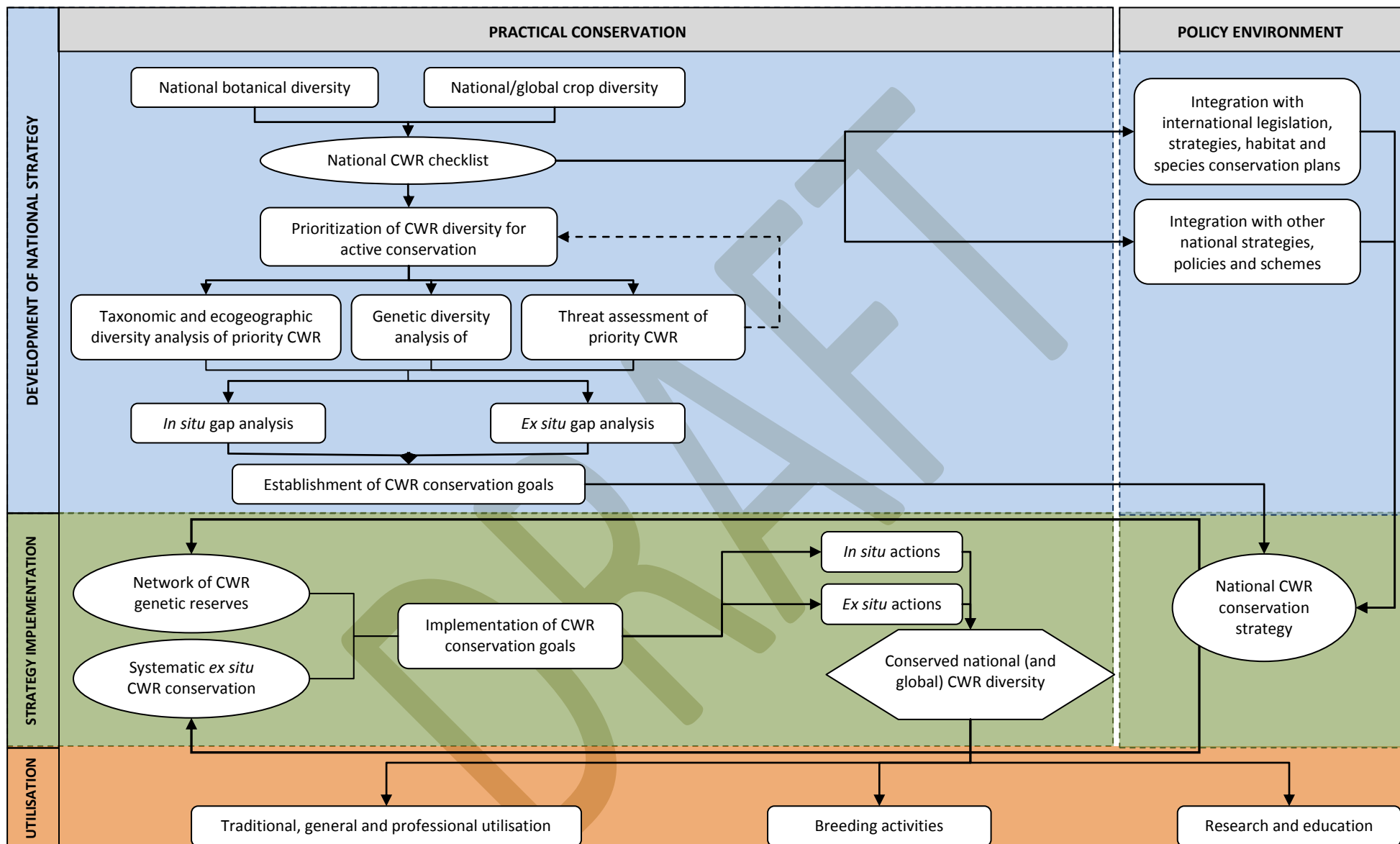


Figure 6. Model for the development of a National CWR Conservation Strategy

A.2.1. Additional materials and resources

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Maxted N, Ford-Lloyd BV, Kell SP, Iriondo J, Dulloo E, Turok J (eds) (2008) Crop wild relative conservation and use. CAB International Wallingford.



Sammour RH (1993) The strategy of conservation of genetic resources. *Journal of Islamic Academy of Sciences* 6(1): 52-55 Available from: <http://www.cropwildrelatives.org/fileadmin/www.cropwildrelatives.org/documents/Sammour.pdf> [Accessed March 2012].



University of Birmingham (2003–2012) *Crop wild relative*. Available from: www.pgrforum.org/Publications.htm (Issues 1–5), www.cwrsg.org/Publications/Newsletters/index.asp (Issues 6 and 7) and www.pgrsecure.org/publications (Issue 8–) [Accessed May 2012].



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http://www.pgrforum.org/Documents/Poster_presentations/WCC_2004.pdf

[Accessed March 2012].



Holubec V and Vymyslický T (2008) Conservation of Biodiversity – hovering between agriculture and botany. IUCN World Conservation Congress, Species Survival Commission, Barcelona, 5-14 October (poster).

Crop Wild Relatives Global Portal: <http://www.cropwildrelatives.org/>. The Portal currently offers access to: CWR National Inventories developed and maintained by the countries that make them available to the portal, external datasets containing important information on CWR, image archive, publications, training resources, and list of experts and institutions working for CWR conservation.

WWW

WWW

CWR *In Situ* Strategy Helpdesk. An Integrated European In Situ Management Work Plan: Implementing Genetic Reserves and On-farm Concepts (AEGRO). Available from: <http://aegro.jki.bund.de/aegro/index.php?id=188> [Accessed May 2012].

WWW eLearning Modules for the *in situ* conservation of CWR:
http://www.cropwildrelatives.org/capacity_building/elearning/elearning.html#c6867

WWW WISM-GPA (<http://www.pgrfa.org/gpa/selectcountry.jsp>), the world information sharing mechanism on the implementation of the Global Plan of Action (GPA) for plant genetic resources for food and agriculture (PGRFA) provides access to National Mechanisms' portals and databases on conservation and sustainable use of PGRFA.

www PGR Secure Crop Wild Relative and Landrace Conservation Helpdesk. Available at: www.pgrsecure.org/helpdesk [Accessed July 2012]. Provides technical assistance through the provision of resources and tools, as well as one-to-one advice on all aspects the CWR and LR conservation strategy planning process. This facility will be available until August 2014.

Regional/national biodiversity conservation strategies that refer to CWR conservation:



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WWW Ireland's National Plant Conservation Strategy. Available from: <http://www.botanicgardens.ie/gspc/inspc.htm> [Accessed May 2012].

National CWR conservation:












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-  Smekalova TN and Chukhina IG (2005) Main aspects of the development of CWR *in situ* conservation strategy for Russia. Available from: http://www.google.pt/url?sa=t&rct=j&q=main%20aspects%20of%20cwr%20in%20situ%20conervation%20strategy%20for%20russia&source=web&cd=1&sqi=2&ved=0C CoQfjAA&url=http%3A%2F%2Fwww.pgrforum.org%2FDocuments%2FWS2_Presentations%2FWS2_Day3%2FSmekalova_et_al.ppt&ei=utRxT-HWFMjF0QWJqqUS&usg=AFQjCNFgTKIyf7gnidqTSd3IKH1pJaTYhw&cad=rja [Accessed May 2012].
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-  Magos Brehm J, Maxted N, Ford-Lloyd BV and Martins-Loução MA (2008) Conservation strategy for Crop Wild Relatives and Wild Harvested Plants in Portugal. Scientific workshop commemorating the 130 years of the Botanical Garden of the National Museum of Natural History (University of Lisbon): Conservation and Biodiversity – the role of the Botanic Gardens. 11 de November, Lisbon, Portugal.
-  Magos Brehm J, Maxted N, Ford-Lloyd BV and Martins-Loução MA (2007) AEGRO and genetic reserves methodologies: 2 - National approach. First meeting of the AEGRO project. 2-3 November, Evershot (UK).
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<http://typo3.fao.org/fileadmin/templates/agphome/documents/PGR/SoW2/CropWild>

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Maxted N, White K, Valkoun J, Konopka J and Hargreaves S (2008) Towards a conservation strategy for *Aegilops* species. *Plant Genetic Resource: Characterization and Utilization* 6(2): 126-141.

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A.3. National CWR checklist and inventory creation

A.3.1. Overview

What are a checklist and an inventory of crop wild relatives?

A national CWR checklist is simply a list of CWR taxa present in a country, while an inventory is the list of CWR taxa present in a country with ancillary information, such as: nomenclature, gene pool or taxon group concept applied, biology, ecogeography, populations, uses, threats and conservation. Here we deliberately distinguish between a checklist and an inventory to reflect the content distinction but in the broader literature the two terms are confused. The preparation of a national CWR checklist will normally precede an inventory of a geographically defined area and both constitute the starting point for preparing a National CWR Conservation Strategy.

We need to know what exists, and where, to determine how we can conserve and use it effectively. Plant checklists and inventories provide the baseline data critical for biodiversity assessment and monitoring, as required by the Convention on Biological Diversity (CBD) (CBD, 1992), the Global Strategy for Plant Conservation (GSPC) (CBD, 2010a), the European Strategy for Plant Conservation (ESPC) (Plantlife International and Council of Europe, 2008) and the International Treaty on Plant Genetic Resources for Food and Agriculture (ITPGRFA) (FAO, 2001). CWR checklists and inventories provide the essential foundations for the formulation of strategies for *in situ* and *ex situ* conservation and on the species' current and potential uses as novel crops or gene donors. Further, checklists and inventories provide the data needed for integrating CWR into existing conservation initiatives and a means of organising information in a logical and retrievable way, preventing duplication of effort when planning conservation. They provide policy makers, conservation practitioners, plant breeders and other user groups with a view of CWR species' distributions and a means of prioritizing conservation activities. CWR checklists and inventories also provide a basis for monitoring biodiversity change internationally, by linking CWR information with information on habitats, policy and legislation and climate change. They also serve to highlight the breadth of CWR diversity available in the target area, which may include important resources for CWR conservation and use in other parts of the world.

There are numerous publications on inter- and intra-crop diversity, both at a global and national level, but the study and report of the wild component of PGRFA has been largely neglected, but in recent years the situation is improving. The Second Report on the State of the World's Plant Genetic Resources for Food and Agriculture reported a substantial increase in the number of CWR national inventories with 28 countries reporting relevant activities compared to only 4 countries in 1996. A few of these inventories comprise the entire CWR national diversity (e.g. Portugal⁸, United Kingdom⁹) but most of them are limited to single crop gene pools or small groups of species, or to certain regions within the countries. Despite this increase in the number of CWR national inventories, the majority of countries still lack a coordinated and systematic inventory of their CWR and this is mainly due to lack of financial and human resources, deficient skills and knowledge, lack of coordination, unclear responsibilities and low national priority, among other factors¹⁰.

⁸ Magos Brehm *et al.* (2008)

⁹ Maxted *et al.* (2007)

¹⁰ FAO (2009)

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CWR

The preparation of a CWR national inventory can be seen as a six stage process: (i) Determine the geographical scope (if not national), (ii) Produce a digitised list of national crop species, (iii) Produce a digitised list of national flora, (iv) Match the crop genera against the floristic checklist and generate the checklist, (v) Prioritise the checklist on those CWR that are to be actively conserved and add extra information on each prioritised CWR to generate the inventory, and (vi) Make the inventory available to users. These steps constitute the general methodology, which is illustrated in Figure 7 and described further below. The importance of creating an inventory of CWR at national instead of regional within a country level should be emphasized, because it provides the best foundation for developing a National CWR Conservation Strategy. However, this approach is not always an option due to resource limitation at the time available to develop such a National Strategy.

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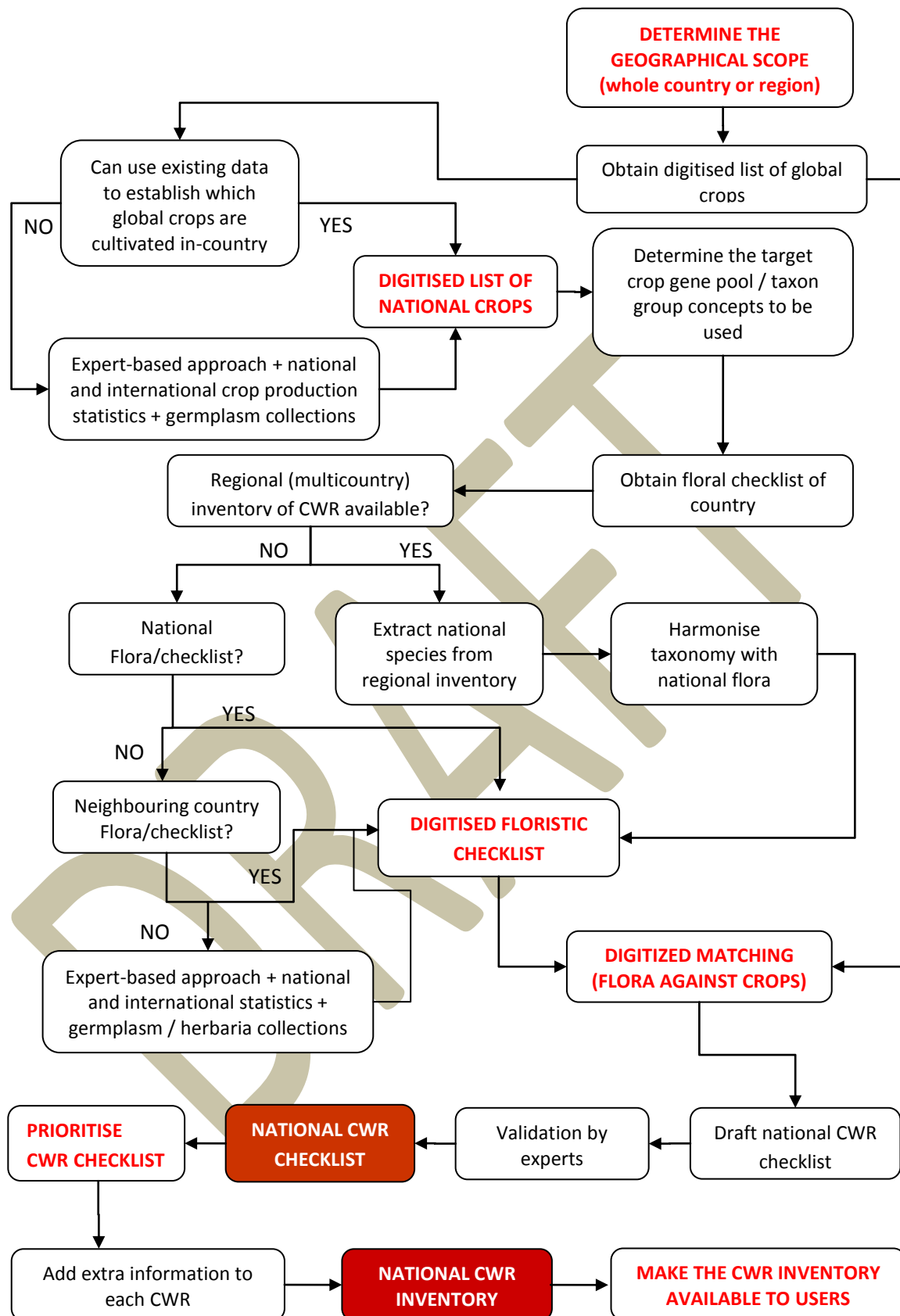


Figure 7. Overview of the creation of a national inventory of crop wild relatives

A.3.2. Methodology national CWR checklist and inventory creation

(i) Determine the geographic scope

Discuss and agree the geographic scope of the inventory (i.e., whether to cover the whole country or a sub-national unit such as a region). CWR inventories of different sub-national units in a country can eventually be compiled to create a national CWR inventory.

(ii) Digitised list of national crops

Several sources may need to be consulted when compiling a list of crops grown in a particular country or area, if that list is not previously available. Key sources are:

- Globally cultivated species publications (e.g., Mansfeld's World Database of Agricultural and Horticultural Crops);
- Regional or national crop checklists/agricultural statistics (e.g., EuroStat);
- Underutilised species/neglected crops lists;
- Individual crop studies;
- National, regional or international agricultural statistics (e.g., FAOSTAT);
- Expert consultation.

The scope of the inventory should be discussed and agreed with the various stakeholder groups to decide the crops and therefore crop gene pools to be included:

- Whether to consider nationally cultivated crops only or to also include crops cultivated in other parts of the world but with CWR that occur in the target country. Given the high level of interdependence among countries with respect to the conservation and use of PGRFA, it is highly advisable that all crops (nationally and globally grown) are considered when preparing the inventory, as all countries depend on CWR diversity that occurs in other countries for the improvement of their crops.
- How broadly to define the crop scope of the inventory. Whether for example to consider major food crops only or to include minor and underutilised crops, forage and fodder crops, or even forestry, industrial, ornamental and medicinal crops.
- Whether introduced CWR will be included in the inventory. This is a pragmatic decision based on these species' importance in the development of national economies. They can be included so the inventory is as comprehensive as possible then assigned a lower priority in the later prioritization step.

At the completion of this stage there should be available a digitised list of the crops that will be included in the inventory.

(iii) Digitised floristic checklist

This floristic checklist may be of two kinds either a complete national floristic checklist or a partial floristic checklist based on the crops with native species present in the country. The choice that will need to be discussed and agreed by the national stakeholders may at least partially be dependent on the availability of a digitised flora, along with financial resources and human capacity to hand, if available the complete national floristic checklist should be used, if not then a partial floristic checklist may be created to cover all crop gene pools or a subset of priority crop gene pools found in the country. Note existing complete national floristic checklists are available for all European and Mediterranean countries but are less common in other continents. These two alternative approaches may be referred to as the:

- **Floristic approach** is used to produce inventories of all CWR that occur in a geographically defined area. CWR inventories of different regions in a country can eventually be compiled to create a national inventory of CWR.

- **Monographic approach** is used to produce an inventory of CWR of one or several selected crop gene pools. The main difference from the floristic approach is therefore the focused selection of particular target crop gene pools for which the inventory is being developed.

In general, the more inclusive the inventory, the greater its use and the likelihood of multiple studies is avoided; therefore, a broad geographic and crop scope is recommended where possible. Nevertheless, the monographic approach may be practical though inevitably its non-comprehensive nature may mean with time the need to be repeated the exercise when sufficient resources are available for a more comprehensive approach.

Where a regional¹¹ CWR checklist exists, as in Europe, it may be filtered for a specific country so generating the national CWR checklist. However, if using this approach, it is important to harmonise the species names obtained from the regional inventory with the existing national Flora/checklist: (a) consult national floristic experts or target taxon specialists and review recent classifications of the group published in revisions and monographs in order to decide which is the appropriate classification to use, (b) collate all the published taxonomic data available for the more obscure groups that may lack a recent revision or monograph, (c) compile all the common synonyms of each taxa and convert all population, accession or other source data to the name used by the accepted classification to avoid nomenclatural confusion (but retaining the initial ascription for reference).

Countries usually have some form of national floristic checklist or Flora. When either of these is unavailable, it may be possible to use the Flora of a neighbouring region (e.g. the Flora of Turkey lists many of the species found in Syria). However, it then needs to be recognized that there may be taxa present in neighbouring countries that are absent in the target country and vice versa. Alternatively, global plant checklists can be used to extract wild species lists for each country.

When the methods above are not feasible or for countries where a digitized flora is not available, an alternative approach based on the knowledge of crop experts and taxonomists who define a list of important crops and a list of wild species within the crop genera may be used. To achieve this: (a) arrange a stakeholder / expert workshop, (b) agree a priority list of crops and known CWR of these crops found within the country, and (c) complement this list of cultivated and wild species with a germplasm and herbaria survey¹² to ensure the list is as comprehensive as possible; the wild species included make the national CWR checklist. This route is a more subjective and less comprehensive approach as some crops and CWR might be missed but it is pragmatic if there is no alternative.

See the 'Additional materials and resources' for concrete references under each key source.

¹¹ Region is defined here as comprising different countries (e.g. Sub-Saharan Africa, Mediterranean region) rather than a sub-unit within a country.

¹² The sole use of germplasm/herbaria survey to create a CWR checklist can be misleading as some taxa might not be represented in these collections; nevertheless it could form the basis for the checklist.

CWR	CWR
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(iv) Digitized matching of flora against crops

Once the digitised list of national crops and the complete or partial national botanical checklist is available the genus name of the crop is matched digitally against the genera found in a country and all the matching species are by definition, when applying the generic definition of CWR, the national CWR present¹³. This approach is comprehensive in that all possible CWR taxa are objectively considered and the national CWR checklist is produced semi-automated¹⁴. Once the draft national CWR checklist has been generated it should be validate through consultation with appropriate floristic and monographic experts in order to resolve minor errors and to engender stakeholder buy-in to the project.

See 'Examples and applied use' for few examples.

(v) Prioritization and population of the CWR checklist

Having generated the national CWR checklist it will commonly be extensive, including a relatively large number of CWR, especially if the generic definition of CWR has been applied, so the next practical step will be to prioritise the checklist to include a more manageable number of CWR that can be actively conserved with the national resources and expertise available. However, some may prefer to populate the entire checklist with ancillary information and then prioritise the completed inventory at a subsequent stage. As there is a large literature on prioritization and much to consider the details of how to prioritise a CWR checklist or CWR inventory will be discussed in the section (see A.4. Setting CWR conservation priorities).

As mentioned above, the distinction between a CWR checklist and a CWR inventory is based on additional information being added to the CWR name. By adding further and relevant information to each CWR the checklist becomes significantly more useful as the inventory. Additional information that may include in an inventory is:

- Scientific name of the related crop
- Economic value of related crop
- Crop gene pool level/taxon group level¹⁵
- Uses/potential uses of the taxon as a gene donor
- Taxon description
- Critical taxonomic notes

¹³ CWR are those taxa found in the same genus as a crop because they are, by definition, taxonomically closest to that crop (Maxted *et al.* 2006).

¹⁴ If either the Flora/checklist or the list of crops is not digitised, it is advisable to digitise them and proceed with the digital matching.

¹⁵ See A.1. Introduction for definitions and explanations.

- Synonyms
- Vernacular names
- Plant life-form¹⁶
- Chromosome number
- Ecology and habitat
- Flowering time
- Economic value of related crop
- Ethnobotanical Direct uses (i.e., not as a gene donor)
- Global and national distribution
- Threat category
- *Ex situ* and *in situ* conservation status
- Legislation applied

Users of the Toolkit are encouraged where possible to use existing data recording standards, i.e. use where possible TDWG standards (<http://www.tdwg.org/standards/>), and specifically in relation to CWR (see <http://pgrsecure.org/>; <http://www.cropwildrelatives.org/>; <http://www.cwrdiversity.org/>).

(vi) Make the CWR inventory available to users

The inventory should be made public and available to users, ideally via a web-enabled database.

A.3.3. Examples and applied use

Box 11. Global inventory of priority CWR

Recently, within the context of the 'Adapting Agriculture to Climate Change: Collecting, Protecting and Preparing Crop Wild Relatives' project led by the Global Crop Diversity Trust and Royal Botanic Gardens, Kew, and sponsored by the Norwegian Government, a web-enabled global priority inventory of CWR taxa was created (<http://www.cwrdiversity.org/checklist/>). The inventory contains background information on 173 food and agricultural crop genepools and 1,667 priority CWR taxa from 37 families, 109 genera, 1392 species and 299 sub-specific taxa. It is referred to as the Harlan and de Wet Global Priority CWR Checklist to acknowledge the pioneering work of Harlan and de Wet (1971) in first proposing the Gene Pool (GP) concept to explain the relative value of species in their potential as gene donors for crop improvement. The taxa included were deemed priority CWRs as defined by their membership in GP1b or GP2, or Taxon Groups (TG) 1b, 2 or 3. There are also a limited number of GP3 and TG4 taxa included if they have previously been shown to be useful in breeding. The Gene Pool concept designated the crop itself as GP1a, while GP1b are the wild or weedy forms of the crop that cross easily with it. GP2 are secondary wild relatives (less closely related species from which gene transfer to the crop is possible but difficult using conventional breeding techniques), and GP3 are tertiary wild relatives (species from which gene transfer to the crop is impossible, or if possible, requires more advanced

¹⁶ The Raunkiær's classification system of main plant life-forms (Raunkiær 1934) includes: phanerophytes (normally woody perennials with resting buds more than 25 cms above soil level), chamaephytes (buds on persistent shoots near the ground, woody plants with perennating buds borne no more than 25 cms above soil surface), hemicryptophytes (buds at the soil surface), cryptophytes (below ground or under water, with resting buds lying either beneath the surface of the ground as a rhizome, bulb, corm, etc., or a resting bud submerged under water; they are divided into: geophytes – resting in dry ground, helophytes – resting in marshy ground, and hydrophytes – resting by being submerged under water), therophytes (annual plants which survive the unfavourable season in the form of seeds and complete their life-cycle during favourable seasons).

techniques, such as embryo rescue, somatic fusion or genetic engineering). Taxa are organised by genera in alphabetical order and according to gene pool or taxon group concepts, and for each crop complex the following information is available: GP or TG concept source citation, Latin and common name, common synonyms, common vernacular names, country geographic distribution, previous or potential reported use in breeding, other uses, ex situ storage behaviour, and main herbaria with representative specimens. The inventory will facilitate global and national conservation planning by for the first time having a pre-existing prioritizing list of priority taxa available for the major and minor crops of the world.

Source: Vincent *et al.* (2012)

Box 12. Using a regional CWR inventory to extract a national CWR checklist

A regional inventory of CWR may be filtered for a specific country, hence extracting the national list of CWR. At present the only regional inventory of CWR is the Crop Wild Relative Catalogue for Europe and the Mediterranean, so currently this approach has only been taken within this region. This approach was successfully implemented in Portugal and a number of other countries. See Box 8 Examples of the floristic approach to cwr conservation (*Floristic approach at national level: Inventory of Portuguese CWR*).

Source: Kell *et al.* (2005) and Magos Brehm *et al.* (2008a)

Box 13. Using a regional botanical checklist to extract a regional CWR checklist

In order to create the CWR Catalogue for Europe and the Mediterranean, four major sources of information were utilized: the Mansfeld's Database of Agricultural and Horticultural Crops (Hanelt and IPK 2001, IPK 2003) for cultivated plants, Schultze-Motel (1966) for forestry genera, the Community Plant Variety Office (CPVO) (Kwakkenbos, pers. comm. 2004) for ornamental genera and the Medicinal and Aromatic Plant Resources of the World Database (MAPROW) (Schippmann, pers. comm. 2004). The genera of crops were identified in these four references and matched with the taxa for these genera found within the Euro+Med PlantBase (version January 2005) (<http://www.euromed.org.uk>).

Source: Kell *et al.* (2005)

Box 14. Using botanical checklist and agricultural statistics to create a CWR inventory

Examples of manual matching to generating a CWR National Inventory are limited and none have thus far been formally published but the grey literature yields two examples where this has been achieved for Bhutan (Tamang 2003) and the Seychelles (Antoine 2003). Both followed the same basic methodology, as follows:

1. Use national agricultural statistics to produce a list of crops grown in the country.
2. Generate a list of national crop generic names.
3. Review national Flora to identify taxa found in same genus as the crop to build CWR list.
4. Define the criteria for prioritising the national CWR checklist, agreed in collaboration with national stakeholders. In Bhutan, the prioritization criteria selected were: national importance of crops (human food, animal food, industrial and ornamental), relative threat of genetic erosion, and already included in national legislation; in the Seychelles they were: national importance of crops (human food, animal food, industrial and ornamental), relative threat of genetic erosion, rarity, native status, existing priorities of national conservation agency, potential for use in crop improvement, biological and cultural importance, and ethical and aesthetic considerations.
5. Apply these criteria to the national CWR checklist to produce a priority list. In Bhutan this generated a priority target list of 230 CWR species and in the Seychelles a priority target list of 139 CWR species.
6. Write Conservation Action Plans for each priority CWR species in collaboration with the lead organizations in the country responsible for its implementation; the Plans included:
 - a. Assessment of current *in situ* / *ex situ* conservation activities for the priority CWR,

- b. Current monitoring activities,
- c. Assessment of current threats to priority taxa,
- d. Assessment of current and potential exploitation of priority taxa,
- e. Gap analysis of priority taxa,
- f. Immediate and future conservation priorities,
- g. Research priorities.

Subsequently, in both cases the National CWR Inventories and Conservation Action Plans have been used by the national conservation authorities to promote CWR conservation and use.

Source: Antoine (2004) and Tamang (2004)

Box 15. Creating a national plant checklist using web-based resources

A plant diversity inventory was successfully compiled for Angola from exclusively free web-based resources. These included on-line checklists (World Checklist of Selected Plant Families, Kew), nomenclatural databases (International Plant Names Index), general taxon/specimen databases (African Plants Initiative, Missouri Botanical Garden TROPICOS, GBIF) and herbaria on-line databases such as that of Royal Botanic Gardens, Kew. The project involved a 1 year full time researcher and 30 collaborators who provided expertise on specific plant families. It resulted in two products: a hard copy of the inventory of the Angolan plants, together with additional information on collectors, synonyms and literature references, and a website (FLAN: Flora of Angola Online, <http://flan.sanbi.org/>) containing the information included in the hard copy.

Source: Figueiredo and Smith (2008) and Smith and Figueiredo (2010)

Box 16. Example of digitized matching

The creation of the CWR Catalogue for Europe and the Mediterranean is a successful example of how a digitized matching can be undertaken. A list of crop genera was generated from Mansfeld's World Database of Agricultural and Horticultural Crops (Hanelt and IPK Gatersleben, 2001; IPK Gatersleben, 2003), the 'Enumeration of cultivated forest plant species' (Schultze-Motel 1966) (for forestry species), the Community Plant Variety Office list of plant varieties (www.cpvo.eu.int) (for ornamental plants) and the Medicinal and Aromatic Plant Resources of the World (MAPROW) (U. Schippmann, pers. comm. Bonn 2004). This was matched against floristic data in Euro+Med PlantBase (version 2006), which is a database of the Euro-Mediterranean flora, including data on the status of occurrence of taxa in countries and/or sub-national units. The CWR Catalogue was generated by extracting the taxa within the genera in Euro+Med PlantBase matching the crop genus names.

Source: Kell *et al.* (2005, 2008) and www.pgrforum.org

Box 17. Germplasm survey-based CWR checklist – *Arachis* CWR

It may also be possible to produce a CWR checklist based on a review of germplasm holdings. As an example ICRISAT produced the checklist of *Arachis* CWR by extracting the country holdings from the catalogue of germplasm accessions of *Arachis* (available at <http://www.icrisat.org/what-we-do/crops/GroundNut/Arachis/Start.htm>). A similar approach could be taken using EURISCO, GENESYS or even GBIF held data, but the sole use of germplasm/herbaria survey to create a CWR inventory could be misleading as some taxa might not be represented in these collections, particularly if only *ex situ* germplasm collection data is used; nevertheless, in the absence of other sources of floristic data, it could form the basis for the inventory.

Source: Stalker *et al.* (2000) and <http://www.icrisat.org/what-we-do/crops/GroundNut/Arachis/Start.htm>

Box 18. Germplasm survey-based CWR inventory – Denmark

The Denmark inventory of CWR was generated from the Nordic Gene Bank Taxon database by combining all previous data associated with CWR collections in Denmark. These species were then assessed for:

- Present or previous cultivation in Denmark
- Present or previous breeding activities in the country
- Future breeding and cultivation potential
- Crop wild relative status
- Exploitation as a wild species
- Exploitation as a spice or medicinal plant.

A list of 450 CWR taxa resulted from the compilation and of these, 100 CWR taxa were selected as priority CWR taxa for active conservation.

Source: Asdal *et al* (2006), Hulden *et al* (1998) and Poulsen (2009)

A.3.4. List of references used to compile the text

Antoine H (2004) Crop wild relative inventory of the Seychelles. Unpublished MSc Thesis, University of Birmingham, Birmingham.

Asdal Å, Olsson K, Wedelsbäck K, Radusiene J, Galambosi B, Bjørn GK, Zukauskas I, Thorvaldsdottir EG and Pihlik U (2006) Spice and medicinal plants in the Nordic and Baltic countries. Conservation of Genetic Resources. Nordic Gene Bank, Sweden.

CBD (1992) Convention on Biological Diversity: Text and Annexes. Secretariat of the Convention on Biological Diversity, Montreal, Canada. www.cbd.int/convention/text/

CBD (2010a) Global Strategy for Plant Conservation. Secretariat of the Convention on Biological Diversity, Montreal. Available from: www.cbd.int/gspc/strategy.shtml [Accessed May 2012].

FAO (2001) International Treaty on Plant Genetic Resources for Food and Agriculture. Food and Agriculture Organization of the United Nations. www.planttreaty.org/

FAO (2009) Second Report on the State of the World's Plant Genetic Resources for Food and Agriculture. Food and Agriculture Organization of the United Nations, Rome, Italy.

Figueiredo E and Smith GF (2008) Plants of Angola/Plantas de Angola. Strelitzia 22. South African National Biodiversity Institute, Pretoria.

IPK Gatersleben (2003) Mansfeld's World Database of Agricultural and Horticultural Crops. Leibniz Institute of Plant Genetics and Crop Plant Research. Available at: <http://mansfeld.ipk-gatersleben.de/> (accessed 3 April 2007)

Hammer K (1990) Botanical checklists prove useful in research programmes on cultivated plants. Diversity 6(3-4): 31-34.

Hammer K (1991) Checklists and germplasm collecting. FAO/IBPGR Plant Genetic Resources Newsletter 85: 15-17.

Hanelt P and IPK Gatersleben (Eds) (2001) Mansfeld's Encyclopaedia of Agricultural and Horticultural Crops. 6 vols. 1st English edition. Springer, Berlin/Heidelberg/New York. 3645 pp.

Hulden M, Lund B, Poulsen GB, Thorn E and Weibull J (1998) The Nordic commitment, regional and international collaboration on plant genetic resources. Plant Varieties and Seeds 11:1-13.

Kell SP, Knüpfner H, Jury SL, Ford-Lloyd BV and Maxted N (2008) "Crops and wild relatives of the Euro-Mediterranean region: making and using a conservation catalogue." In: Maxted N, Ford-Lloyd BV, Kell SP, Iriondo J, Dulloo E and Turok J (eds) Crop Wild Relative Conservation and Use. CABI Publishing, Wallingford, pp. 69-109.

- Kell SP, Knüpfger H, Jury SL, Maxted N and Ford-Lloyd BV (2005) Catalogue of crop wild relatives for Europe and the Mediterranean. University of Birmingham, Birmingham, UK. Available at: <http://www.pgrforum.org/cwris/cwris.asp> and on CD-ROM.
- Knüpfger H and Hammer K (1999) "Agricultural biodiversity: a database for checklists of cultivated plant species." In: Andrews S, Leslie AC and Alexander C (Eds). Taxonomy of Cultivated plants: Third International Symposium. Royal Botanic Gardens, Kew, pp. 215-224.
- Lughadha EN (2004) Towards a working list of all known plant species. Philosophical Transactions of the Royal Society of London B. 359: 681-687.
- Mace GM (2004) The role of taxonomy in species conservation. Philosophical Transactions of the Royal Society of London B. 359: 711-719.
- Magos Brehm J, Maxted N, Ford-Lloyd BV and Martins-Loução MA (2008a) National inventories of crop wild relatives and wild harvested plants: case-study for Portugal. Genetic Resources and Crop Evolution 55: 779-796.
- Maxted N and Kell S (2009) Establishment of a Network for the *In situ* Conservation of Crop Wild Relatives: Status and Needs. Commission on Genetic Resources for Food and Agriculture. Food and Agriculture Organization of the United Nations.
- Maxted N, Scholten MA, Codd R and Ford-Lloyd BV (2007) Creation and use of a national inventory of crop wild relatives. Biological Conservation 140: 142-159.
- Poulsen (2009) Conservation of CWR in Denmark. Crop Wild Relative 7: 13-14. Available from: <http://www.cwrsg.org/Publications/Newsletters/crop%20wild%20relative%20Issue%207.pdf> [Accessed May 2012].
- Planta Europa. 2008. *A Sustainable Future for Europe; the European Strategy for Plant Conservation 2008–2014*. Plantlife International, Salisbury, UK and the Council of Europe, Strasbourg, France.
- RBG (Royal Botanic Gardens, Kew) (2004). Stakeholder consultation on Target 1 of the Global Strategy for Plant Conservation and CBD. Draft report. Secretariat of the Convention on Biological Diversity, Montreal, Canada. Available from: <http://www.cbd.int/doc/meetings/pc/tempc-02/other/tempc-02-target-01-en.pdf> [Accessed May 2012].
- Smith GF and Figueiredo E (2010) E-taxonomy: an affordable tool to fill the biodiversity knowledge gap. Biodiversity and Conservation 19: 829-836.
- Stalker HT, Ferguson ME, Valls JFM, Pittman RN, Simpson CE and Bramel P (2000) Catalogue of *Arachis* germplasm collections. Available from: <http://www.icrisat.org/what-we-do/crops/GroundNut/Arachis/Start.htm> [Accessed May 2012].
- Tamang A (2004) Crop wild relative inventory of Bhutan. Unpublished MSc Thesis, University of Birmingham, Birmingham.
- Vincent H, Wiersema J, Dobbie S, Kell SP, Fielder H, Castañeda N, Eastwood R, Guarino L and Maxted N (2012) Global checklist of priority crop wild relatives. Available from: www.cwrdiversity.org [Accessed May 2012].

A.3.5. Additional materials and resources

Lists of global or regional crop diversity:



Brouk B (1975) Plants consumed by Man. Academic Press, London.



EC (European Commission) (2011a) Common catalogue of varieties of vegetable species. 29th complete edition (2011/C 14 A/01). Official Journal of the European

- Union, 18.01.2011. Available from: <http://eur-lex.europa.eu/LexUriServ/LexUriServ.do?uri=OJ:C:2010:012A:0001:0026:EN:PDF> [Accessed December 2011].
-  EC (European Commission) (2011b) Common catalogue of varieties of agricultural plant species. Third supplement to the 29th complete edition ((2011/C 328 A/01). Official Journal of the European Union, 11.11.2011. Available from: <http://eur-lex.europa.eu/LexUriServ/LexUriServ.do?uri=OJ:C:2010:090A:0001:0020:EN:PDF> [Accessed December 2011].
-  FAO (1997a) The State of the World's Plant Genetic Resources for Food and Agriculture. Food and Agriculture Organization of the United Nations, Rome, Italy. (list of crops considered important for food security and interdependence)
-  FAO (2009) International Treaty on Plant Genetic Resources for Food and Agriculture. Food and Agriculture Organization of the United Nations. Available from: <http://www.planttreaty.org/> [Accessed May 2012]. (globally important food crops)
-  Groombridge B and Jenkins MD (2002) World Atlas of Biodiversity. Prepared by the UNEP World Conservation Monitoring Centre. University of California Press, Berkeley, USA. (list of the major and minor food crop genera)
-  Hanelt P and IPK (Institut für Pflanzengenetik und Kulturpflanzenforschung Gatersleben) (eds) (2001) Mansfeld's Encyclopaedia of Agricultural and Horticultural Crops, 6 vols. 1st Engl. Ed. Springer, Berlin, Heidelberg, New York, 3645 pp.
-  Rehm S and Espig GE (1996) Die Kulturpflanzen der Tropen und Subtropen. Anbau, wirtschaftliche Bedeutung, Verwertung.
-  Sanchez-Monge E (1991) Flora Agricola. T. 1, 2. Ministerio de Agricultura, Madrid.
-  Schultze-Motel J (1966) Verzeichnis forstlich kultivierter Pflanzenarten [Enumeration of cultivated forest plant species]. Kulturpflanze Beiheft 4, 486 pp.
-  Vul'F EV and Maleeva OF (1969) Mirovye resursy poleznykh rastenij [World resources of useful plants]. Nauka, Leningrad.
-  Wiersema JH and Leon D (1999) World Economic Plants. A Standard Reference CRC Press LLC, Washington DC.
-  Zeven AC and de Wet JMJ (1982) Dictionary of cultivated plants and their regions of diversity. Pudoc, Wageningen.
- WWW Global Horticulture Initiative (2007) PROTABASE - Plant Resources of Tropical Africa. Available from: <http://www.globalhort.org/knowledge-base/species/> [Accessed December 2011]
- WWW IPK (Institut für Pflanzengenetik und Kulturpflanzenforschung Gatersleben) (2003) *Mansfeld's World Database of Agricultural and Horticultural Crops*. Leibniz Institute of Plant Genetics and Crop Plant Research. Available from: http://mansfeld.ipk-gatersleben.de/pls/htmldb_pgrc/f?p=185:3:1352060495268324 [Accessed February 2005].
- WWW PROSEA Foundation (n.d.) E-Prosea - Plant Resources of South-East Asia. Available from: <http://proseanet.org/prosea/eprosea.php> [Accessed January 2012] (database of both wild and plant resources of South-East Asia)

WWW World Agroforestry Centre (2011a) Agroforestry Database. Available from: <http://www.worldagroforestry.org/resources/databases/agroforestree> [Accessed December 2011] (data on the management, use and ecology of tree species from all over the World which can be used in agroforestry)



World Agroforestry Centre (2011b) Useful Tree Species for Africa. Available from: http://www.worldagroforestry.org/our_products/databases/useful-tree-species-africa [Accessed December 2011] (this tool enables the selection of useful tree species for planting anywhere in Africa using Google Earth)

Underutilised crops/neglected species lists:



Battle I (2000) Genetic Resources of Minor Fruit and Nut Trees in Europe. In Maggioni, L. (compiler). Report of a Network Coordinating Group on Minor Crops (2nd edition). First meeting. 16 June 1999, Turku, Finland. International Plant Genetic Resources Institute, Rome, Italy.



Della A (2000) Minor Crops in the Mediterranean Region. In Maggioni L (compiler) Report of a Network Coordinating Group on Minor Crops (2nd edition). First meeting. 16 June 1999, Turku, Finland. International Plant Genetic Resources Institute, Rome, Italy.



Hammer K and Spahillari M (2000) Crops of European origin. In: Maggioni L (compiler) Report of a Network Coordinating Group on Minor Crops (2nd edition). First meeting. 16 June 1999, Turku, Finland. International Plant Genetic Resources Institute, Rome, Italy.



Michalová A (2000) Minor Cereals and Pseudocereals in Europe. In Maggioni L (compiler) Report of a Network Coordinating Group on Minor Crops (2nd edition). First meeting. 16 June 1999, Turku, Finland. International Plant Genetic Resources Institute, Rome, Italy.



Pistrick K (2002) Notes on neglected and underutilized crops. Current taxonomical overview of cultivated plants in the families Umbelliferae and Labiatae. Genetic Resources and Crop Evolution, 49: 211-225.



Promoting the Conservation and Use of Underutilized and Neglected Crops Series which have monographic inventories available from <http://www.biodiversityinternational.org/>

WWW Freedman B (2011) Famine foods database. Available from: http://www.hort.purdue.edu/newcrop/faminefoods/ff_home.html [Accessed January 2012] (list of plants that are not normally considered as crops but that are consumed in times of famine)

WWW Global Facilitation Unit for Underutilized Species (n.d.) GFU Underutilized Species GFU Database. Available from: http://www.underutilized-species.org/species/species_mask.asp [Accessed December 2011]

WWW Plants for a Future (1996-2010) Plants for a Future Database. Available from: <http://www.pfaf.org/user/plantsearch.aspx> [Accessed December 2011] (a resource centre edible, medicinal and other uses unusual plants)

National crop diversity studies:



Albania:

Hammer K and Spahillari M (1998) Burimet gjenetike te bimevedhe agrobiodiversiteti. Buletini i Shkencave Bujqesore, 3: 29-36.

Cuba:

Esquivel M, Castiñeiras L, Knüpffer H and Hammer K (1989) A checklist of the cultivated plants of Cuba. Kulturpflanze, 37: 211–357.



Esquivel M, Knüpffer H and Hammer K (1992) "Inventory of the cultivated plants." In Hammer K, Esquivel M and Knüpffer H (eds) (1992-1994). "...y tienen fazones y fabas muy diversos de los nuestros..." – Origin, Evolution and Diversity of Cuban Plant Genetic Resources. 3 vols., 824 pp. IPK, Gatersleben.

Knüpffer H, Esquivel M and Hammer K (unknown date) A database for the cultivated plants of Cuba. Rev. Jard. Bot. Nac., Habana. In Hammer K (1991). Checklists and germplasm collecting. FAO/IBPGR Plant Genetic Resources Newsletter, 85: 15-17.

Korea:



Baik M-C, Hoang H-Dz and Hammer K (1986) A check-list of the Korean cultivated plants. Kulturpflanzen, 34: 69-144.

Hoang H-Dz, Knüpffer H and Hammer K (1997) Additional notes to the checklist of Korean cultivated plants (5). Consolidated summary and indexes. Genetic Resources and Crop Evolution, 44: 349-391.

Libya:



Hammer K and Perrino P (1985) A check-list of the cultivated plants of the Ghat oases. Kulturpflanze, 33: 269–286.

Hammer K, Lehman CO and Perrino P (1988) A check-list of the Libyan cultivated plants including an inventory of the germplasm collected in the years 1981, 1982 and 1983. Kulturpflanze, 36: 475-527.

Russia:



Smekalova T (2009) "Cultivated plants inventory of Russia". In: Veteläinen M, Negri V and Maxted N (eds) European Landraces: On-Farm Conservation, Management and Use. Bioversity Technical Bulletin, No 15. pp.143-154.

South Italy and Sicily:

Hammer K, Knüpffer H and Perrino P (1990). A checklist of the South Italian cultivated plants. Kulturpflanze, 38: 191–310



Hammer K, Knüpffer H, Laghetti G and Perrino P (1992) Seeds form the past. A catalogue of crop germplasm in south Italy and Sicily. Istituto del Germoplasma del Consiglio Nazionale delle Ricerche, Bari. 173 p.

Central and North Italy:

Hammer K, Knüpffer H, Laghetti G and Perrino P (1999) Seeds form the past. A catalogue of crop germplasm in central and north Italy. Istituto del Germoplasma del Consiglio Nazionale delle Ricerche, Bari. 253 p.

International agricultural statistics:

WWW FAOSTAT. Available from: <http://faostat.fao.org/> (data on global production and value for crops that may be queried at a national level)




WWW EUROSTAT. Available from: <http://epp.eurostat.ec.europa.eu> (provides information

for European Union countries)

Global/regional plant checklists:

- WWW Botanic Garden and Botanical Museum Berlin-Dahlem (2006-2011) Euro+Med PlantBase - the information resource for Euro-Mediterranean plant diversity: <http://ww2.bgbm.org/EuroPlusMed/query.asp> [Accessed May 2012]. (available for 132 plant families)
- WWW Catalogue of Life. Available from: <http://www.catalogueoflife.org/> [Accessed May 2012].
- WWW eFloras.org. Available from: <http://efloras.org/> [Accessed May 2012]. (links to flora information from various geographic units (Andes of Ecuador, Chile, China, Madagascar, Nepal, North America, Pakistan))
- WWW Plants of Southern Africa. Available from: <http://www.plantzafrica.com/> [Accessed May 2012]. (Online information about plants native to southern Africa and related topics).
- WWW SABI (2005-2010) Plants of Southern Africa (POSA) – an online checklist. **POSA** ver. 3.0 June 2009. Available from: <http://posa.sanbi.org/searchspp.php> [Accessed May 2012]. (access to plant names and floristic details for southern African plant species)
- WWW SIBIS: SABIF South African Biodiversity Information Facility. SIBIS version 2 Build 6. Available from: <http://sibis.sanbi.org/> [Accessed May 2012]. (threatened species information, distribution maps, area checklists, general species details)
- WWW The Plant List - a working list of all plant species. Available from: <http://www.theplantlist.org/> [Accessed May 2012].
- WWW Tropicos.org - Missouri Tropical Garden. Available from: <http://www.tropicos.org/> [Accessed May 2012]. (present species distribution maps)
- WWW USDA, ARS, National Genetic Resources Program. Germplasm Resources Information Network - (GRIN) [Online Database]. National Germplasm Resources Laboratory, Beltsville, Maryland. Available from: <http://www.ars-grin.gov/cgi-bin/npgs/html/index.pl> [Accessed May 2012].

Global/regional checklists/inventories of CWR:

- Global CWR database for all major and minor crop complexes:
- WWW Vincent H, Wiersema J, Dobbie S, Kell SP, Fielder H, Castañeda N, Eastwood R, Guarino L and Maxted N (2012) Global checklist of priority crop wild relatives. Available from: www.cwrdiversity.org [Accessed May 2012].
-  Heywood VH and Zohary D (1995) A catalogue of the wild relatives of cultivated plants native to Europe. *Flora Mediterranea* 5: 375-415.
-  Kell SP, Knüpffer H, Jury SL, Ford-Lloyd BV and Maxted N (2008) "Crops and wild relatives of the Euro-Mediterranean region: making and using a conservation catalogue." In: Maxted N, Ford-Lloyd BV, Kell SP, Iriondo J, Dulloo E and Turok J (eds) *Crop Wild Relative Conservation and Use*. CABI Publishing, Wallingford, pp. 69-109.
-  WWF and IUCN (1994) *Centres of plant diversity. A guide and strategy for their conservation*. 1st volume. IUCN Publications Unit, Cambridge.

WWW Kell SP, Knüpffer H, Jury SL, Maxted N and Ford-Lloyd BV (2005) Catalogue of crop wild relatives for Europe and the Mediterranean. University of Birmingham, Birmingham, UK. Available at: <http://www.pgrforum.org/cwr/cwr.asp> and on CD-ROM.

National CWR checklists/inventories:

Armenia:



Gabrielian E and Zohary D (2004) Wild relatives of food crops native to Armenia and Nakhichevan. *Flora Mediterranea* 14: 5-80.



Hunter D and Heywood V (eds.) (2011) *Crop wild relatives, a manual of in situ conservation*. Issues in Agricultural Biodiversity. Earthscan, London, Washington.



Hovhannisyanyan M (n.d.) State of national inventories on *in situ*/on farm in Armenia. National online CWR inventory: http://www.cropwildrelatives.org/national_inventories.html (floristic approach)

WWW

Bolivia:



Hunter D and Heywood V (eds.) (2011) *Crop wild relatives, a manual of in situ conservation*. Issues in Agricultural Biodiversity. Earthscan, London, Washington.

Bhutan:



Tamang A (2004) *Crop wild relative inventory of Bhutan*. Unpublished MSc Thesis, University of Birmingham, Birmingham.



China: (in prep.)

Qin, H., Chen, B. and Kell, S. (in prep.) *Crop Wild Relative Inventory of China*.

Denmark:



Poulsen G (2009) Conservation of CWR in Denmark. *Crop Wild Relative* 7: 13-14. Available from: <http://www.cwrs.org/Publications/Newsletters/crop%20wild%20relative%20Issue%207.pdf> [Accessed May 2012].

Finland:



Takaluoma S (2005) Viljelykasvien luonnonvaraisten sukulaisten uhanalaisuus Suomessa [Conservation status of crop wild relatives in Finland]. MSc thesis, University of Helsinki, Finland.

France:



Chauvet M, Lefort M and Mitteau M (1999) "The French national Network for *in situ* conservation of wild relatives." In: Gass T, Frese L and Lipman E (compilers) *Implementation of the Global Plan of Action in Europe – Conservation and Sustainable Utilisation of Plant Genetic Resources for Food and Agriculture*. Proceedings of the European Symposium, 30 June – 3 July 1998, Braunschwig, Germany. International Plant Genetic Resources Institute, Rome, pp. 38-43.

Germany:

WWW PGRDEU - Germany online CWR inventory. Available from: <http://pgrdeu.genres.de/index.php?tpl=home> [Accessed May 2012].

WWW Guatemala:

USDA, ARS. Atlas of Guatemalan Crop Wild Relatives (*Atlas Guatemalteco de Parientes Silvestres de las Plantas Cultivadas*). Available from: <http://www.ars.usda.gov/Services/docs.htm?docid=22225> [Accessed May 2012].

Ireland:



FitzPatrick Ú and Lupton D (2010) Establishment of a national crop wild relative (CWR) database. Final report to Department of Agriculture, Fisheries and Food. Conservation of Genetic Resources Grant Aid Scheme for 2010 [Dept. of Agriculture, Fisheries and Food Ref: 10/GR/10]. National Biodiversity Data Centre. Available from: <http://www.biodiversityireland.ie/wp-content/uploads/Establishment-of-a-national-crop-wild-relative-database-Final-report-Dec-2010.pdf> [Accessed May 2012].

WWW Genetic Resources (2010) Portal for information on Crop Wild Relatives in Ireland. Available from: <http://geneticresources.biodiversityireland.ie/crop-wild-relatives/> [Accessed May 2012]. (Monographic approach).



Italy:

Mazzola P, Raimondo F M and Scuderi G (1997) The occurrence of wild relatives of cultivated plants in Italian protected areas. *Boccone* 7: 241-248.

Madagascar:

WWW Madagascar CWR inventory. Available from: http://mg.chm-cbd.net/cwr_mada [Accessed May 2012]. (monographic approach)



Portugal:

Magos Brehm J, Maxted N, Ford-Lloyd BV and Martins-Loução MA (2008a) National inventories of crop wild relatives and wild harvested plants: case-study for Portugal. *Genetic Resources and Crop Evolution* 55: 779-796. (floristic approach)

Russia:



Smekalova T (2008) "National crop wild relative *in situ* conservation strategy for Russia." In: Maxted N, Kell SP, Ford-Lloyd BV, Dulloo E and Iriondo J (eds) *Crop Wild Relative Conservation and Use*. CABI Publishing, Wallingford, pp. 143-151.

WWW Afonin AN, Greene SL, Dzyubenko NI and Frolov AN (eds) (2008) *Interactive Agricultural Ecological Atlas of Russia and Neighbouring Countries (AgroAtlas)*. Economic Plants and their Diseases, Pests and Weeds [Online]. Available from: <http://www.agroatlas.ru> [Accessed May 2012].



Seychelles:

Antoine H (2004) Crop wild relative inventory of the Seychelles. Unpublished MSc Thesis, University of Birmingham, Birmingham.



Spain:

Rubio Teso ML, Torres ME, Parra-Quijano M and Iriondo JM (2012) Prioritization of crop wild relatives in Spain. *Crop Wild Relative* 8: 18-21.



Sri Lanka:

Hunter D and Heywood V (eds.) (2011) *Crop wild relatives, a manual of in situ conservation*. Issues in Agricultural Biodiversity. Earthscan, London, Washington.

WWW Sri Lanka CWR inventory: <http://www.agridept.gov.lk/index.php/en/crop-wild-relatives> (monographic approach)

Switzerland:



Häner R and Schierscher B (2009) First step towards CWR conservation in Switzerland. *Crop Wild Relative* 7: 14-16. Available from: <http://www.cwrs.org/Publications/Newsletters/crop%20wild%20relative%20Issue%207.pdf> [Accessed May 2012].

WWW

Swiss Commission for Cultivated Plant Conservation (2000-2012) *Crop Wild Relative*. Available from: <http://www.bdn.ch/pages/cwr/> [Accessed May 2012]. (floristic approach)

The Netherlands:



Hoekstra R, van Veller MGP and Odé B (2008) "Crop wild relatives in the Netherlands: actors and protection measures." In: Maxted N, Ford-Lloyd BV, Kell SP, Iriondo JM, Dulloo ME and Turok J (eds) *Crop Wild Relative Conservation and Use*. CABI Publishing, Wallingford, pp. 165–177.

United Kingdom:



Maxted N, Scholten MA, Codd R and Ford-Lloyd BV (2007) Creation and use of a national inventory of crop wild relatives. *Biological Conservation* 140: 142-159. (floristic approach)

United States of America:



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WWW

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Hunter D and Heywood V (eds.) (2011) *Crop wild relatives, a manual of in situ conservation*. Issues in Agricultural Biodiversity. Earthscan, London, Washington.

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WWW

Moore *et al.* (2005-2008) Crop Wild Relative Information Schema. Available from: <http://www.pgrforum.org/CWRML.xsd> and <http://www.pgrforum.org/CWRML.htm> [Accessed May 2012].

www

UNEP/GEF Crop Wild Relatives Project descriptor lists: Developed and used within the framework of the UNEP/GEF funded project 'In situ conservation of crop wild relatives through enhanced information management and field application' (2004–2010) http://www.pgrsecure.bham.ac.uk/sites/default/files/documents/helpdesk/UNEP-GEF_CWR_Project_descriptors.zip [Accessed July 2012]

A.4. Setting CWR conservation priorities

A.4.1. Overview

Why do we need to have conservation priorities?

The creation of a CWR national checklist is likely to identify a greater number of taxa than can be actively conserved due to resource limitations, especially if applying the broad concept of CWR (all the taxa within the same genus as a crop). Therefore, the process of establishing priorities for CWR conservation is an obvious and essential step in the development of the National CWR Conservation Strategy.

Economists have developed a number of methods for assessing the economic value of biodiversity and genetic resources^{17,18,19}; however, the main focus has been on the valuation of ecosystem services rather than genetic resources *per se*.

There has been considerable debate over which criteria should be utilised when undertaking a scheme of species prioritization^{20,21}. Criteria such as threat of genetic erosion, endemism, rarity and population decline^{22,23,24}, quality of habitat and intrinsic biological vulnerability²⁵, species abundance in relation to their geographical range size²⁶, “responsibility for the conservation of a species” (estimate of the geographic proportion of a species distribution in a certain country against the worldwide distribution)²⁷, recovery potential, feasibility and sustainability of conservation²⁸, taxonomic uniqueness^{29,30} and genetic distinctiveness, phylogenetic criteria and the ability of a species to speciate within “new” environments³¹, cultural importance^{32,33}, economic factors³⁴ and socio-economic use, current conservation status, ecogeographic distribution, biological importance, legislation, ethical and aesthetic considerations, and priorities of the conservation agency. Specifically regarding the establishment of conservation priorities for CWR, several different categories of criteria have been used (see A.4.1 Overview).

Distinct criteria and numerous methods that vary in complexity have been used (see Box 19) in establishing species priorities but when deciding which ones to use it depends on the needs and available resources of individual countries and/or the conservation agencies within the countries that are undertaking the prioritization exercise. Specifically concerning CWR, there is some consensus for

¹⁷ Flint (1991)

¹⁸ Shands (1994)

¹⁹ Drucker *et al.* (2001)

²⁰ See e.g. Fitter and Fitter (1987)

²¹ See Maxted *et al.* (1997c)

²² Whitten (1990)

²³ Department of Environment (1996)

²⁴ Sapir *et al.* (2003)

²⁵ Tambutii *et al.* (2001)

²⁶ Hoffmann and Welk (1999)

²⁷ Schnittler and Günther (1999)

²⁸ Whitten (1990)

²⁹ Vane-Wright *et al.* (1991)

³⁰ Faith (1992)

³¹ Linder (1995)

³² Norton (1994)

³³ Dhar *et al.* (2000)

³⁴ Bishop (1978)

an initial, simple prioritization on the basis of potential economic value of the related crop, the degree of relationship of the wild relative to the crop / ease of crossing with the crop, and relative level of threat^{35,36}. A combination of all three criteria is usually used.

However, whatever prioritization methodology and criteria are used, the total number of target CWR should be adjusted to a number that can be actively conserved using the available financial and human resources. There is no precise way of estimating the number of target CWR and so the estimate will be subjective.

An alternative more flexible approach would be to assign different levels of conservation priority depending on the groups of conservationists going to be undertaking the CWR conservation and how much tax seems reasonable for each of them to consider implementing active conservation. In this way, a more extensive list is more easily objectively justified, maintained and updated, and taxa that are not of immediate priority may be given conservation attention at a later date. Further using this approach, some of the taxa that are of less immediate conservation action may occur within the same sites as those of highest priority, so they could be captured in the same *in situ* CWR conservation sites and targeted when collecting higher priority for *ex situ* conservation. The critical point being there is no exact number of national priority CWR that should be set down or set as a target for each national CWR inventory.

The process of setting priorities for CWR conservation can be complex and time-consuming depending on the methodology and criteria used. Methodologically, the starting point of prioritization is the CWR national checklist, the list of all CWR found in the country, and a list that is too long to be considered for active conservation. Whatever the approach, floristic or monographic, prioritization essentially consists of three main steps: (i) Definition of the valuation criteria to be applied, (ii) Definition of the prioritization methodology, and (iii) Application of both the criteria and the methodology to obtain the priority CWR. Associated with these steps there will also be a need to consider how many priority CWR will be flagged for immediate conservation action (see Figure 8).

³⁵ Barazani *et al.* (2008)

³⁶ Ford-Lloyd *et al.* (2008)

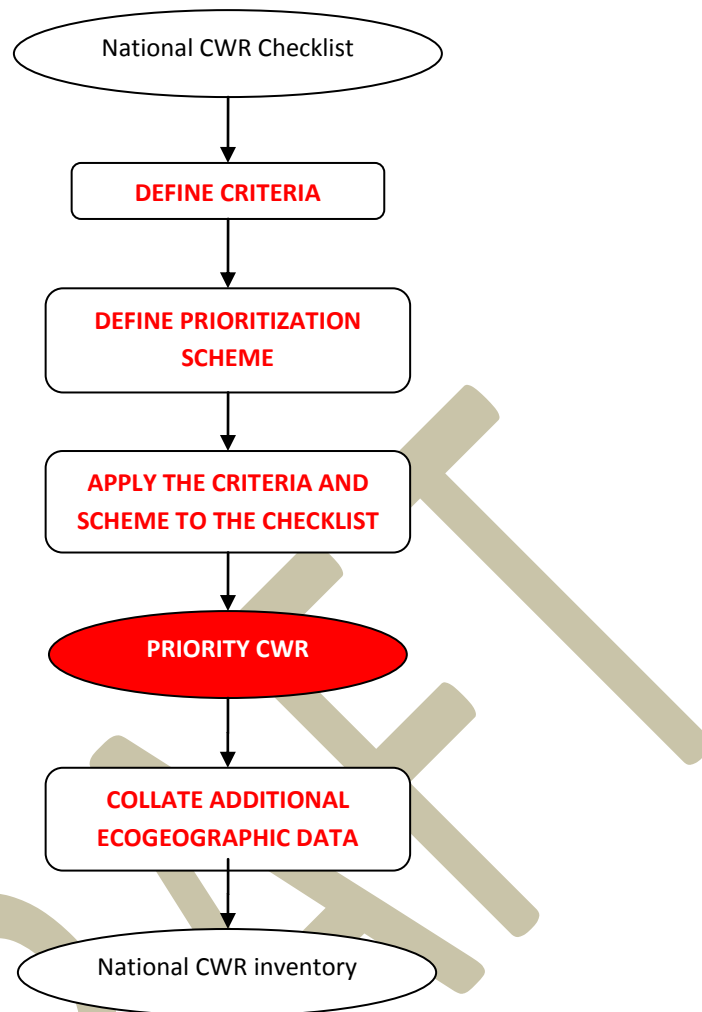


Figure 8. Process of establishing conservation priorities from a CWR national inventory

Box 19. Systems and methods for setting species priorities

Numerous systems and methods have been used to set priorities for conservation. One of the first attempts was presented by Rabinowitz (1981) and Rabinowitz *et al.* (1986) where an eight-celled table based on range, habitat specificity and local abundance was developed in order to evaluate different ‘types of rarity’. Other types of prioritization procedures include rule-based systems, scoring schemes, and ranking systems. An example of a rule-based system is the IUCN Red List Categories and Criteria (IUCN 2001) and consists of a series of rules that a species has to agree with in order to fit in to a certain category. Scoring schemes use multiple scoring over a range of criteria to derive total scores for each species (Given and Norton 1993). This system has been applied to a wide range of taxa of both plants (e.g. Perring and Farrell 1983, Briggs and Leigh 1988, CALM 1994, Dhar *et al.* 2000, Sapir *et al.* 2003, Kala *et al.* 2004), and animals (Millsap *et al.* 1990, Carter and Barker 1993, Hunter *et al.* 1993, Lunney *et al.* 1996, Carter *et al.* 2000, Ray *et al.* 2005, Rosenberg and Wells 2005) from all over the world. Scoring systems have also been complemented with multivariate analysis in order to look at the arrangement of these species so as to identify groups of species with similar profiles (e.g. Given and Norton 1993), uncertainty values associated with some of the criteria, reflecting the extent of the existing knowledge, and thus their confidence in the estimates presented (e.g. Hunter *et al.* 1993, Carter and Barker 1993), and user-friendly interactive databases (Hunter *et al.* 1993). The weighting of the criteria is a variant of this type of method (e.g. Carter and Barker 1993, Lunney *et al.* 1996). The Department of Environment (1996) suggested the use of “individual weighting on each criterion in order to give some indication of the relative importance of that factor in measuring the extent of threat”. Amongst the most widely applied systems is the biodiversity status-ranking system developed and used by the Natural Heritage Network and The Nature Conservancy (Master 1991, Morse

1993, Stein 1993). This priority-ranking system was primarily applied to vertebrates and plants (Master 1991). The species ranks were based on information about each species for a series of criteria relating to species' rarity (number of individuals, number of populations or occurrences, rarity of habitat, and size of geographic range), population trends, and threats; a scale ranging from (1) critically imperilled to (5) demonstrably secure was then used to assign a rank to each species at three separate levels – global, national, and state or province (Stein *et al.* 1995). When these three levels were combined, the system allowed for a rapid assessment of the species' known or probable threat of extinction (Master 1991). Other approaches include that suggested by Coates and Atkins (2001) who developed a priority setting process for Western Australian flora where risk of extinction at population, taxon and ecological community levels were the primary determinant for setting priorities. The authors considered, however, that if financial resources are severely limited then further prioritization has to be undertaken based on taxonomic distinctiveness and ability to recover. Pärtel *et al.* (2005) proposed a new combined approach that focuses on species groups with similar conservation needs instead of individual species.

Source: Magos Brehm *et al.* (2010)

A.4.2. Methodology

(i) Definition of the CWR prioritization criteria. The main criteria to consider are:

- **Economic value of the related crop:** CWR have their main potential application in genetic improvement of existing varieties or the creation of new ones; the economic importance of the related crop species is thus a good indicator of their wild relative value. The selection of priority crops will vary according to scale of prioritization (i.e., global, regional, national or local) and may even vary according to the implementing agency. However, the highest priority crops are likely to be food crops (important for nutrition and food security), crops of economic value and crops with multiple use values. Note should be made that a single genus may contain more than one crop as for *Solanum* (e.g. *Solanum tuberosum* L. – potato, and *Solanum melongena* L. – aubergine). Several sub-criteria concerning the national economic value of the related crop can be taken into consideration such as: quantity produced, surface area of cultivation, number of varieties grown at national level, and value to local populations or regions of the target country.
- **Genetic potential as a gene donor:** the wild taxa in a crop gene pool are genetically related by degree, some being more closely related to the crop than others. Where genetic information is available, taxa can be classified using the Gene Pool concept³⁷ and for some crops, the Gene Pool concept has already been defined. However, if genetic data are not available and the Gene Pool concept has not been previously defined, the Taxon Group concept³⁸ which provides a proxy for taxon genetic relatedness can be applied. In general, the closest wild relatives in GP1B and GP2 or TG1B and TG2 are given priority. However, tertiary wild relatives that are already known as gene donors or have shown promise for crop improvement should also be assigned high priority. If neither Gene Pool nor Taxon Group concepts can be applied, then the available information on genetic and/or taxonomic distance should be analysed to make reasoned assumptions about the most closely related taxa. Gene Pool or Taxon Group concepts have been compiled for approximately 174 food crop gene pools and are available

³⁷ Gene Pool concept: GP1A-cultivated forms of the crop, GP1B-wild or weedy forms of the crop, GP2-secondary wild relatives (less closely related species from which gene transfer to the crop is possible but difficult using conventional breeding techniques), GP3-tertiary wild relatives (species from which gene transfer to the crop is impossible, or if possible, requires sophisticated techniques, such as embryo rescue, somatic fusion or genetic engineering) (Harlan and de Wet 1971).

³⁸ Taxon Group concept: TG1a-crop, TG1b-same species as crop, TG2-same series or section as crop, TG3-same subgenus as crop, TG4-same genus (Maxted *et al.* 2006).

online³⁹. For other crops, a literature survey will be required in order to ascertain if Gene Pool or Taxon Group concepts have already been established or if taxonomic classification are available to establish new Taxon Group concepts and so establish the degree of relationship of each wild relative to its associated crop (see 'Additional materials and resources').

- **Status of occurrence:** whether the CWR is native to the country, introduced⁴⁰, and if it is known to be invasive.
- **Threat status:** relative threat is probably the most obvious criterion used in establishing conservation priorities: the more threatened (i.e. increased likelihood of genetic erosion or actual extinction of the species) the greater the conservation priority. Therefore, the collation of existing threat assessments will give us an indication of the extinction risk of the species but also will allow us to use that information when prioritising taxa for conservation. As the knowledge about plant taxa has increased, so national Red Lists and Red Books (see 'Additional materials and resources') are published based on the IUCN Red List Categories and Criteria—the most commonly applied means of assessing threat to wild taxa.

Threat assessment can be carried out at different geographical scales (i.e., global, regional, national). Both national and global assessments should be taken into account but the meaning and implications of threat status depends on the scale of the assessment and this should be taken into account when applying the criterion of relative threat in the prioritization process.

The collation of existing threat assessments is a four stage process: (i) Identification of potential sources of information on threat to CWR, (ii) establish if CWR have been Red List assessed, (iii) for the CWR not already assessed gather the necessary data and undertake novel red list assessment, and (iv) Collation of existing threat assessments (at national and global level) (see Figure 9). Information on threat assessment of CWR can be obtained from national and regional Red Lists and Red Data Books (see 'Additional materials and resources'), the IUCN Red List of Threatened Species (for global Red List assessments, searchable at <http://www.iucnredlist.org/>), as well as peer-reviewed papers and reports, and expert knowledge.

In the absence of Red List assessments, endemism and relative distribution can be used as an indicator of relative threat. Inferences from known threats to/loss of habitats/land use types can also be applied, as well as local expert knowledge. (See A.7. Novel threat assessment of priority CWR).

³⁹ www.cwrdiversity.org/checklist/

⁴⁰ According to Kornas (1990), an introduced species can be roughly classified according to its approximate date of introduction: archaeophyte (before 1500s) or neophyte (after 1500s) and diaphyte (established in a non-permanent way).

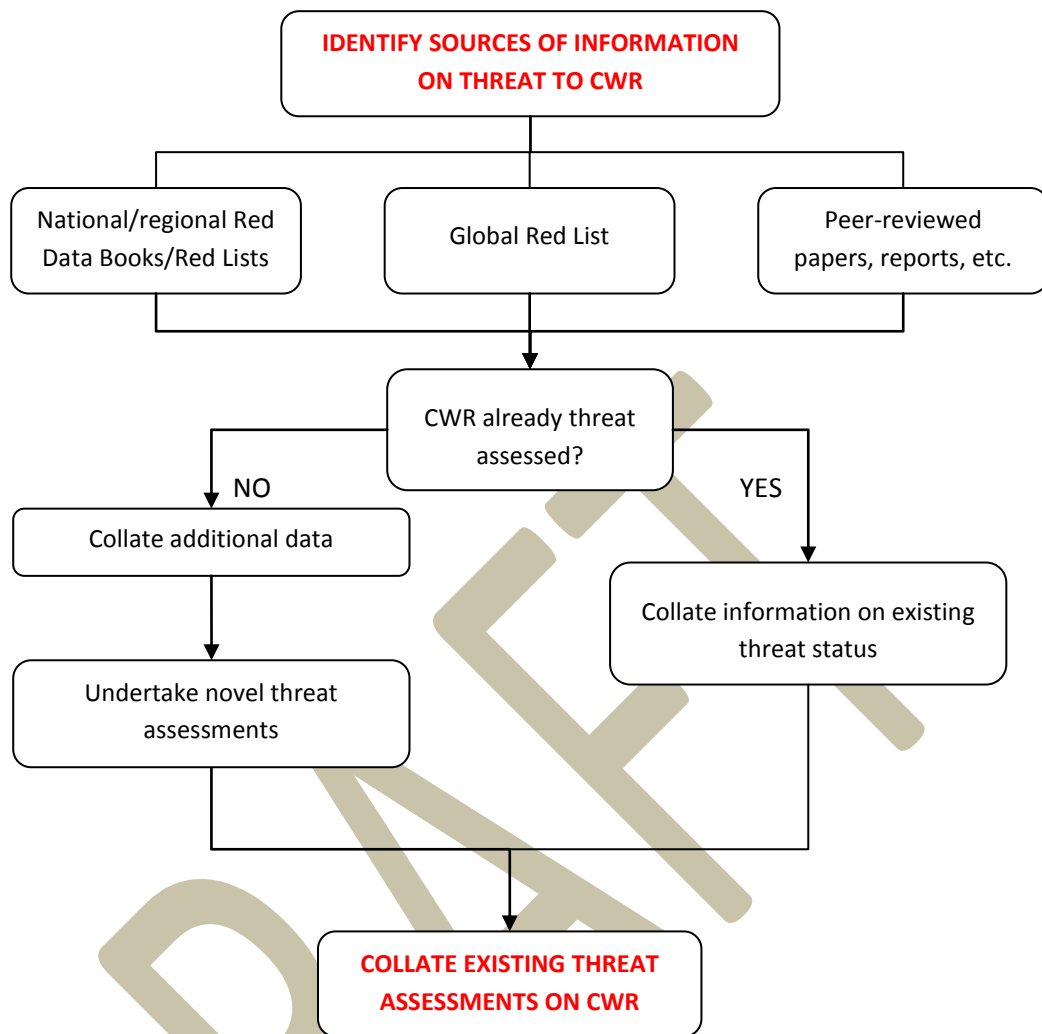


Figure 9. Collation of existing threat assessment information for CWR diversity

- **Conservation status:** before a taxon can be given high priority for conservation, related current conservation activities should be reviewed. If sufficient genetic diversity is already being conserved by *in situ* and/or *ex situ*, additional conservation efforts may not be justified, and resources should focus on those species that are not being conserved.
 - a. *Ex situ*: careful attention to the information obtained from current *ex situ* conservation holdings should be paid because: the material held in gene banks might be incorrectly determined, dead, in poor conditions or unavailable to potential users, the number of accessions might be misleading because of duplicates, and/or the *ex situ* accessions might not be representative of the overall genetic diversity of a species.
 - b. *In situ*: just because a species is found in a protected area does not necessarily mean that it is adequately protected; for example, the population size may be declining due to the focus of the management plan being on other species and therefore the management actions having a negative impact on the CWR population. Two types of *in situ* conservation can be distinguished: passive, when species and genetic diversity is not being monitored and managed, and active conservation, when species and genetic diversity is afforded long-term monitoring and management. Given these concepts, actively conserved species are given lower priority for conservation than passively

conserved species, and the latter is given lower priority than those taxa that do not occur in PA.

Box 20. Collation of threat assessments for Portuguese CWR

The national inventory of Portuguese CWR was produced in a MS Access Database. Different types of information were collated for each taxon in the inventory (see Magos Brehm *et al.* 2008a), including threat status. To achieve this, existing threat assessments were collated and when sufficient and reliable information was available, novel Red List assessments were carried out for the taxa that had not previously been assessed (see Magos Brehm *et al.* 2008b, Magos Brehm 2009).

The collated threat assessments were based on publications from 1985 to 2004 where pre-1994 (e.g. Ramos Lopes and Carvalho 1990; Dray 1985; SNPRCN 1985) and 1994 IUCN Categories and Criteria (IUCN 1994) (e.g. Govaerts 1994) were used as well as the latest 2001 version of these Categories and Criteria (IUCN 2001) (e.g. Aguiar *et al.* 2001a, b; Mitchell 2004) and other types of assessment such as the threat assessment vulnerability index by Maxted *et al.* (2004) (e.g. Magos Brehm 2004) and information on species endangered by overexploitation (e.g. Ramos Lopes and Carvalho 1991). Threat assessment information was then used to establish conservation priorities among the Portuguese CWR (see Magos Brehm *et al.* 2010). Preferably, the more recent threat assessments were used, but for most of the species 2001 IUCN Red Listing was missing and older assessments were therefore used.

Source: Aguiar *et al.* (2001a, b), Dray (1985), Govaerts (1994), Magos Brehm (2004, 2009), Magos Brehm *et al.* (2008a, b), Maxted *et al.* (2004), Mitchell (2004), Ramos Lopes and Carvalho (1990, 1991), SNPRCN (1985).

<i>Ex situ</i> conservation of CWR	<i>In situ</i> conservation of CWR

- **Legislation:** whether the taxon is under any kind of regional, national or local legislative protection; if so, it will automatically require conservation attention because national governments are under a legal obligation to protect them. It is important to note however that these species may already be afforded some level of conservation action due to their legislative protection status. Whether this is the case or not will be ascertained when the gap analysis is undertaken (see section A9, 'Gap analysis of priority CWR').
- **Species distribution:** in general, priority increases inversely to geographic range, such that species with a more restricted distribution (e.g. national endemics) should be given higher priority than species occurring worldwide. The reason relative distribution may be used for prioritization is that geographically restricted species are potentially more adversely impact by localized threats and extinction events and loss of any single population or group of populations may impact the entire viability of the species.
 - a. *Global distribution:* the distribution of the taxon worldwide. Species endemic to a country or that occur in only a few countries are likely to be prioritized above those that occur in several countries. However, it should be noted that a species can occur in several countries and still be of priority at national level because of its nationally restricted range or based on other prioritization criteria. Also, the size of the countries

(i.e. Russia versus Lesotho) that the species occurs in must be taken into account, as well as the species distribution within those countries.

- b. *National distribution*: the distribution of the taxon within the country (e.g. the number of provinces where each taxon occurs). It may be considered as an indicator of rarity, a species occurring in few regions within the country is considered rarer than a species occurring throughout the country.

However, when deciding priorities on the basis of the geographical range of the taxa a degree of objectivity is required, since there is no clear dividing line between a taxon with a limited range and one with a distribution that is deemed to enable 'classification' of the taxon as one not in immediate need of conservation action, unless very detailed information is already available about genetic erosion of the taxa. However, where the range of a taxon is known, the methodology proposed by Ford-Lloyd *et al.* (2008, 2009) can be used as a guide when establishing taxon conservation priorities at regional level (e.g., across sub-Saharan Africa). Generally speaking, taxa that are known to be endemic to a country or subnational unit or those that occur in only a few countries or subnational units are more likely to be under threat at regional level. Similarly, at national or subnational level, available information must be gathered on the range of the taxa in order to establish which are most likely to be threatened by their limited distribution range.

- Use requirement: As the *raison d'être* for the conservation of CWR is primarily their use by breeders, their involvement in establishing the list of species to be actively conserved should be encouraged. This potential involvement of breeders in defining conservation targets has the additional benefit of also encouraging closer links between conservationists and germplasm users, therefore promoting use and it reinforces the maxim 'through use comes conservation sustainability'.
- Other: other criteria that might be useful or considered important include population data (though such data are generally scarce), species and area management, genetic diversity, relative costs of conservation, etc.

The definition of the criteria applied in the CWR prioritization process should be made by the national agency or researcher that is undertaking this task. Although CWR prioritization can be carried out at different geographical (i.e., global, regional, national, subnational) and taxonomic (e.g., crop genus) scales and can be simple to complex, depending on scale, time, resources and conservation goals. The methods used vary depending on a number of factors—the number of taxa, the resources available for their conservation, the differing needs of the target area and the priorities/interests of the implementing body. Recent studies have shown how CWR can be prioritized globally (Maxted and Kell, 2009), regionally (Ford-Lloyd *et al.* 2008; Kell *et al.* 2012) and nationally (e.g., Maxted *et al.* 2007; Magos Brehm *et al.* 2010). However, it should be emphasized that at each scale the economic value of the related crop (hence breeder demand), genetic potential for contributing traits and relative threat are the most widely used criteria.

- (ii) Definition of the prioritization scheme. Similar to the selection of the prioritization criteria, the choice of the scheme (or methodology) should be a decision made by the national agency that is undertaking this task. The complexity of the scheme will depend on time available, financial resources and data availability, etc. Prioritization schemes often include rule-based and scoring systems, with or without weighting of the criteria, and different combinations of criteria (see Box 21).
- (iii) Application of both the criteria and the prioritization scheme to the checklist. This will culminate in the list of priority CWR to which data may be added to produce the inventory.

Box 21. Systems and methods for setting species priorities

Numerous systems and methods have been used to set species priorities for conservation. One of the first attempts was presented by Rabinowitz (1981) and Rabinowitz *et al.* (1986) where an eight-celled table based on range, habitat specificity and local abundance to evaluate different 'types of rarity'. Rule-based systems and scoring schemes (or ranking systems) are probably the most commonly used prioritization methods.

A rule-based system is used by IUCN (2001) and consists of a series of rules that a species has to agree with in order to fit in to a certain category. This method can have two variants: it can be used to select those species that fulfil ALL criteria selected allowing us to select those species that fulfil SIMULTANEOUSLY ALL CRITERIA (e.g. CWR AND threatened species AND species not conserved both *in situ* and *ex situ*), or to select those species that fulfil SOME of the criteria allowing us to be more flexible (e.g. ALL CWR THAT ARE EITHER threatened species OR species not conserved both *in situ* and *ex situ*).

Scoring schemes use multiple scoring over a range of criteria to derive total scores for each species (Given and Norton 1993), resulting in a ranked list of species. This system has been applied to a wide range of taxa of plant species (e.g. Perring and Farrell 1983, Briggs and Leigh 1988, CALM 1994, Dhar *et al.* 2000, Sapir *et al.* 2003, and Kala *et al.* 2004) worldwide. A scoring system was also by Kala *et al.* (2004) to establish conservation priorities of medicinal plants in Uttarakhand (India). Medicinal plants were given scores for specific criteria: endemism (to the Himalayan region), mode of harvesting (shoots, roots or both), use values (the number of diseases cured by a species), and rarity status, as follows:

Category of criteria	Sub-category	Scores
Endemism	Endemic to the Himalaya	1
	Non-endemic	0
Mode of harvesting	Shoot or aboveground plant part	1
	Roots	2
	Both roots and shoots	3
Use value	Used in 1-5 ailments	1
	Used in 6-10 ailments	2
	Used in 11-15 ailments	3
	Used in >16 ailments	4
Rarity status	Rare	1
	Vulnerable	2
	Endangered	3
	Critically endangered	4

Species scores were summed up for each species without any weighting to give total scores. The maximum score a species could get was 12. A priority list of 17 medicinal plants was then obtained, where higher scores correspond to highest priority.

Scoring systems have also been complemented with multivariate analysis in order to look at the arrangement of these species so as to identify groups of species with similar profiles (e.g. Given and Norton 1993), uncertainty values associated with some of the criteria, reflecting the extent of the existing knowledge, and thus their confidence in the estimates presented (e.g. Hunter *et al.* 1993, Carter and Barker 1993), and user-friendly interactive databases (Hunter *et al.* 1993).

The weighting of criteria is a variant of the scoring system (e.g. Carter and Barker 1993, Lunney *et al.* 1996). The Department of Environment (1996) suggested the use of "individual weighting on each criterion in order to give some indication of the relative importance of that factor in measuring the extent of threat". However, according to Carter and Barker (1993) in the absence of information suggesting which criteria may be more important in determining conservation priority for a species, it is better to keep the weights equal across criteria.

Amongst the most widely applied systems is the biodiversity status-ranking system (a variant of a scoring system) developed and used by the Natural Heritage Network and The Nature Conservancy in the US (Master 1991, Morse 1993, Stein 1993). The species ranks are based on information about each species for a series of criteria relating to species' rarity (number of individuals, number of populations or occurrences, rarity of habitat, and size of geographic range), population trends, and threats; a scale ranging from (1) critically imperilled to (5)

demonstrably secure was then used to assign a rank to each species at three separate levels – global, national, and state or province (Stein *et al.* 1995). When these three levels were combined, the system allowed for a rapid assessment of the species' known or probable threat of extinction (Master 1991).

Other approaches include that suggested by Coates and Atkins (2001) who developed a priority setting process for Western Australian flora where risk of extinction at population, taxon and ecological community levels were the primary determinant for setting priorities. The authors considered, however, that if financial resources are severely limited then further prioritization has to be undertaken based on taxonomic distinctiveness and ability to recover. Pärtel *et al.* (2005) proposed a new combined approach where species with conservation need are grouped according to the similar activities needed for their conservation. These species were linked to eight qualitative conservation characteristics, four reflecting natural causes of rarity (restricted global distribution, restricted local distribution within a country, with small populations, and occurring in very rare habitat types), and four connected with nature management (species needing the management of semi-natural grasslands, species needing local disturbances like forest fires, species needing traditional extensive agriculture, and species which may be threatened by collecting). This procedure allows one to focus on species groups with similar conservation needs instead of individual species.

A.4.3. Examples and applied use

Box 22. Criteria used in prioritizing CWR – examples

A number of studies have applied different criteria for CWR prioritization. Mitteau and Soupizet (2000) prepared a list of priority CWR for *in situ* conservation in France and a group of experts defined the relevant criteria. These were: level of knowledge, state of present research, threats, importance as a genetic resource, protection status, and distribution within natural reserves. Later, Flor *et al.* (2004) suggested five criteria to prioritise European CWR: threat (IUCN Red List category, biological susceptibility), conservation status (*in situ* and *ex situ*), genetics (data on gene pool, genetic erosion and pollution), economics (trade), and utilization (frequency, uses). Ford-Lloyd *et al.* (2008) suggested a straightforward methodology to be used with limited information and/or at the supra-national context when several countries are involved. The criteria these authors suggested include: the number of countries in which taxa occur (as a proxy indicator of abundance/threat) and the 'use' categories of the related crop (food, fodder/forage, industrial, forestry, spice/condiment, medicinal, ornamental, cultural value).

At national level, Maxted *et al.* (2007) used a combination of economic value of the related crop and CWR threat status to select species for conservation in the United Kingdom, and Magos Brehm *et al.* (2010) used economic value, native status, national and global distribution, *in situ* and *ex situ* conservation status, threat, and legislation in order to set priorities for Portuguese CWR.

For prioritization of CWR taxa within gene pools (i.e., when using the monographic approach), Maxted and Kell (2009) proposed that the degree of relationship of the wild relatives to the crop taxon using the Gene Pool or Taxon Group concepts should be used in combination with the relative threat status of the wild relatives in the gene pool. When developing a conservation strategy for a crop gene pool, these two criteria may be used sequentially in either order, depending on the size of the gene pool (number of taxa) or the availability of data for the taxa in the gene pool (Kell *et al.* 2012a).

The selection of native European CWR for inclusion in the European Red List (http://ec.europa.eu/environment/nature/conservation/species/redlist/index_en.htm) was based on the economic value of the related crops in Europe combined with wild relatives of food crop genera and forage/fodder species listed in Annex I of the International Treaty on Plant Genetic Resources for Food and Agriculture (FAO 2001) (Bilz *et al.* 2011, Kell *et al.* 2012b). For some of the larger genera (e.g., *Lathyrus*, *Vicia*), only the species in Gene Pools or Taxon Groups 1B and 2 were included due to insufficient resources to assess the Red List status of all the species. However, for the majority of the crop gene pools, all species were assessed, thus providing an opportunity to evaluate which gene pools in Europe are most threatened and to provide an indication of relative threat of all priority European CWR species, whether closely or more distantly related to the crops (Bilz *et al.* 2011, Kell *et al.* 2012b).

Box 23. Establishing conservation priorities for the CWR of India

CWR conservation priorities were established under the *Biodiversity Conservation Prioritization Project* of WWF-India which aimed at researching knowledge on the status of CWR in India and to identify *in situ* conservation priorities.

CWR were defined as those taxa that were within a genus that contained a taxon reported to be under cultivation. Information on their distributional range, consumptive usage etc., were collated.

A first prioritization shortlisted those taxa that were identified to: (i) be morphologically and genetically closest to their related crops, (ii) have a limited distributional range, (iii) be rare and/or endemic, (iv) be threatened due to overexploitation, (v) be taxa of high socio-economic significance, and (vi) be those species for which adequate information could not be obtained.

Final priorities were assigned to taxa depending on whether they:

1. Were endemic to a particular region,
2. Were restricted distribution in one to two biogeographic zones,
3. Were Critically Endangered due to overexploitation or habitat destruction,
4. Have contributed genes of resistances to modern cultivars and facing threats due to anthropogenic factors,
5. Have potential sources of useful traits,
6. Were of high socio-economic significance (e.g. used for medicinal purposes, as substitutes for food crops during stress periods like drought and famine, and in religious ceremonies, etc.).

Over 100 species related to 27 crops (e.g. rice, maize, millets, etc.) were prioritised.

Source: Rana *et al.* (2001).

Indian priority CWR	Indian priority CWR
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Box 24. Establishing conservation priorities for the CWR of Spain

A comprehensive list of genera containing food crops included in Annex 1 of the FAO International Treaty on Plant Genetic Resources for Food and Agriculture (FAO 2001) and the Spanish Annual Agriculture Statistics (Ministerio de Medio Ambiente, Medio Rural y Marino, 2010) was combined with crop genera included in the Annual Report of the Community Plant Variety Office in Europe (2010), the list of the International Union for the Protection of New Varieties of Plants (UPOV) (2010), and other bibliographic references. The list was then discussed with agrobiodiversity expert and revised. Given the large number of taxa from 202 genera included, priorities established based on the most important crops for Spain and world food security using the following criteria:

Genera listed in Annex 1 of the ITPGRFA or Spanish Annual Agricultural Statistics; AND with at least one species native to Spain; AND it has registered crop varieties in Spain.

Additional genera were also prioritised due to their national socio-economic importance.

Fifty genera were then listed and subsequently classified into four categories (33 food crop genera, 10 fodder and forage crop genera, 5 ornamental crop genera and 6 genera containing crops with other uses) and all the

species within each genus were obtained using *Flora Iberica* (Castroviejo *et al.* 1986–2011), the Anthos project (Anthos 2011), and the List of *Wild Animal and Plant Species of the Canary Islands* (Acebes Ginovés *et al.* 2010).

The CWR of the 33 food crop genera were then further prioritised using the following criteria:

1. Taxa belonging to Gene Pools 1B and 2, or classified into Taxon Groups 1B, 2 or 3; or
2. Threatened (or near threatened taxon according to IUCN Red List Categories); or
3. Endemic to Spain.

The prioritization exercise finally resulted in a list of 149 food-related CWR.

Source: Rubio Teso *et al.* (2012).

Spanish priority CWR	Spanish priority CWR
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A.4.5. Additional materials and resources

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http://typo3.fao.org/fileadmin/templates/agphome/documents/PGR/SoW2/CropWildRelatives_2011_final.pdf Includes information prioritization at national and gene pool level. Fourteen crop gene pools are included: finger millet (*Eleusine*), barley (*Hordeum*), sweet potato (*Ipomoea*), yam (*Manihot*), banana/plantain (*Musa*), rice (*Oryza*), pearl millet (*Pennisetum*), garden pea (*Pisum*), potato (*Solanum*), sorghum (*Sorghum*), wheat (*Triticum*), faba bean (*Vicia*), cowpea (*Vigna*) and maize (*Zea*).



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http://www.pgrsecure.bham.ac.uk/sites/default/files/meetings/palanga/WG1_04_Options_for_CWR_Prioritization_Kell.pdf

WWW

CWR In Situ Strategy Helpdesk. Available at: <http://aegro.jki.bund.de/aegro/index.php?id=188> [Accessed July 2012]. A guide and information facility for national programmes, research institutes, NGOs, protected area managers or individuals involved in the development of a CWR in situ conservation strategy. Includes guidance on CWR prioritization at national level and within gene pools.

National CWR prioritization:



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Crop Gene Pool prioritization:



Singh RJ and Jauhar PP (eds) (2005) Genetic resources, chromosome engineering, and crop improvement. Vol I, Grain legumes. Taylor & Francis pp. 390. (information on 3 crop gene pools complexes: *Cajanus*, *Cicer* and *Lens*)



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Smartt J (1980) Evolution and evolutionary problems in food legumes. Economic Botany 34(3): 219-235. (information on *Phaseolus* crop gene pool)

WWW The Harlan and de Wet Crop Wild Relative Checklist: <http://www.cwrdiversity.org/home/checklist/>

WWW Bioversity International, IRRI and CIAT (2009) Gap analysis. Available at: <http://gisweb.ciat.cgiar.org/gapanalysis/> [Accessed June 2012] (information on 12 crop gene pools complexes: *Cicer*, *Phaseolus*, *Hordeum*, *Vigna*, *Triticum* and *Aegilops*, *Zea*, *Sorghum*, *Eleusine*, *Pennisetum*, *Cajanus*, *Vicia*, and *Lens*)

Global and regional examples of Red Lists and Red Data Books:

WWW IUCN Red List of Threatened Species. <http://www.iucnredlist.org/>



Walters KS and Gillett HJ (1998) 1997 IUCN Red List of Threatened Plants. Compiled by the World Conservation Monitoring Centre. IUCN - The World Conservation Union, Gland, Switzerland and Cambridge, UK. pp. 1-862.

WWW Global Red Lists searchable at: <http://www.iucnredlist.org/>

WWW Black Sea:

Black Sea Red Data Book: <http://www.grid.unep.ch/bsein/redbook/index.htm>

WWW Europe:



Bilz M, Kell SP, Maxted N and Lansdown RV (2011) European Red List of Vascular Plants. Luxembourg: Publications Office of the European Union. Available at: http://ec.europa.eu/environment/nature/conservation/species/redlist/downloads/European_vascular_plants.pdf [Accessed June 2012].

WWW European Red List searchable at: http://ec.europa.eu/environment/nature/conservation/species/redlist/index_en.htm

WWW South Africa:

Online version of SANBI's Red List of South African plants. <http://redlist.sanbi.org/>

National examples of Red Lists and Red Data Books:

WWW IUCN National Red Lists portal, searchable for regional and national red listed species: <http://www.regionalredlist.com/site.aspx>.

Australia:

WWW Threatened Flora of Australia: <http://www.environment.gov.au/cgi-bin/sprat/public/publicthreatenedlist.pl?wanted=flora>



Bolivia:

VMABCC-Bioersity 2009

WWW Libro Rojo de Parientes Silvestres de Cultivos de Bolivia:
http://www.cropwildrelatives.org/fileadmin/www.cropwildrelatives.org/documents/Red%20List_Bolivia_optim.pdf

Canada:

WWW Canadian Red List: http://www.cosewic.gc.ca/eng/sct5/index_e.cfm

Colombia:

WWW Phaneograms Red Data book of Colombia [*Libro rojo de plantas fanerógamas de Colombia*]: http://www.humboldt.org.co/conservacion/libros_rojos/LR_plantas.htm (in Spanish)

Croatia:

WWW Red Book of Vascular Flora of Croatia: <http://www.dzrp.hr/eng/publications/red-books/red-book-of-vascular-flora-of-croatia-395.html>

Denmark:

WWW Red List of Plant and Animal Species in Denmark:
<http://www.sns.dk/udgivelser/1997/rodliste/rodlis.pdf> (in Danish, with summary in English).


Luxembourg:

WWW Red List of the vascular plants of Luxembourg:
<http://flore.dunord.free.fr/IMG/pdf/ListeRougeLux.pdf>

Russia:

WWW List of the vascular plants in the Red Data Book of Russia:
<http://www.biodat.ru/db/oopt/doc/ListRB.zip>

Spain:

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<http://www.uam.es/otros/consveg/documentos/listaroja08baja.pdf> [Accessed June 2012]. (in Spanish)

Ukraine:

WWW Red Data Book of Ukraine: (plants in Volume I)
http://enrin.grida.no/biodiv/biodiv/national/ukraine/legis/l2_3.htm

United States of America:

WWW California Natural Diversity Database (CNDDDB):
<http://www.dfg.ca.gov/biogeodata/cnddb/>

WWW British Columbia Red List- Provincial Red and Blue lists for species in British Columbia:
<http://www.env.gov.bc.ca/atrisk/red-blue.htm>

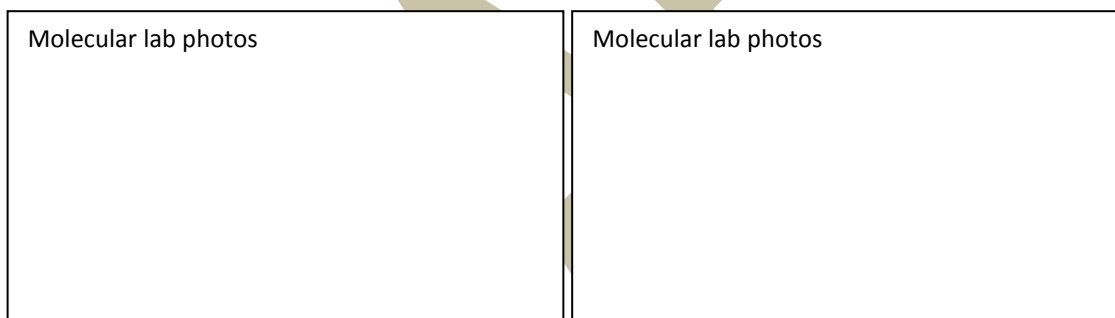
A.5. Genetic data analysis of priority species

A.5.1. Overview

Why it is important to undertake genetic diversity studies on CWR?

Genetic diversity studies are important to (a) to understand the richness and evenness of diversity across the geographic breadth of the species, (b) to obtain genetic baseline information against which to detect changes in diversity and identify genetic erosion, (c) to establish population priorities for conservation within each taxon, and (d) to identify traits of interest for crop improvement.

(i) *Assessment of genetic diversity within a target taxon.* Typically, conservation biology aims at conserving the maximum number of species and numbers of individuals within a species. However, the conservation of intrinsic genetic diversity within a taxon has also been identified as equally important. The genetic diversity available within a species represents not only a potential exploitable resource for human utilization but also encompasses the species' evolutionary potential to evolve and adapt within a changing environment. Therefore, when assessing genetic diversity is important to identify the allelic richness (relative number of different alleles) and evenness (frequency of different alleles) across the geographic breadth of the species.



(ii) *Establishing a genetic baseline*

An understanding of the pattern of allelic richness and evenness across the geographic breadth of the species establishes a relative baseline against which change can be measured, just as population ecologists measure demographic changes in population number so population geneticists measure changes in allelic richness and evenness over time. Again like demographic changes in population number so population changes in allelic richness and evenness over time are natural and so by monitoring genetic change natural changes can be distinguished from changes associated with adverse population management that result in genetic erosion and would ultimately lead to population extinction. Establishing the genetic baseline and assess genetic diversity regularly over time enables these deleterious changes to be detected early and population management changes implemented before there is significant genetic erosion (see A.12. Monitoring).

(iii) *Establishing population priorities for conservation within a target CWR.* The amount and patterns of genetic diversity both within and between populations of a species, genetic population structure, and common and localised alleles (see Box 25) are some of the data that can be useful when prioritising populations for conservation. For instance, if a particular CWR is genetically homogenous or if the partitioning of genetic diversity is considerably higher

within rather than between populations, then a limited number or even a single genetic reserve may be enough to efficiently conserve the species (the population with higher genetic diversity and with highest number of common and localised alleles, for instance). However, if different populations of the same CWR are genetically different or if the between populations' partitioning of genetic diversity is high, indicating significant differentiation among populations, multiple genetic reserves would probably be needed to ensure that all genetic diversity within that particular CWR is conserved. It is important to also take into account that even in cases where there is only a small fraction of genetic differentiation between populations, this diversity can be very important as it may contain adaptive traits which are critical for the species' ability to inhabit different environmental conditions. This factor can be particularly important when considering the conservation of populations in the margins of a species' range, especially considering the need for species to adapt to changing environmental conditions brought about by climate change.

(iv) *Identifying traits of interest for crop improvement.* Two distinct but complementary components of genetic variation have been identified. The first is related to the functional diversity which has resulted from adaptive evolution due to natural selection (which acts on a limited set of loci). The second relates to neutral alleles which result from neutral evolutionary forces such as gene flow, mutation and genetic drift which affect genetic variation at all loci to the same extent. The relative importance of adaptive versus neutral variation in conservation genetics has been vastly debated over the years⁴¹. Adaptive variation refers to alleles (or quantitative traits) that affect fitness. They are the primary targets of natural selection and reflect the species' potential ability to adapt to changing environments⁴². Adaptive genetic variation is evaluated in quantitative genetic experiments under controlled and uniform environmental conditions. Nevertheless, the assessment of adaptive variation assessment is very time consuming and quantitative traits involved in adaptation are sometimes difficult to find. Moreover, since that adaptive quantitative variation is the result of environmental and genetic factors, large sample sizes are required (which might not be available in rare or threatened populations) in order to understand the contribution of these components to the overall variation. Recent developments in high-throughput sequencing now provide an opportunity to discover the genetic signatures of selection at a genome-wide level⁴³. Although finding individual genes under selection based on genetic variation patterns between adaptively differentiated populations is conceptually simple, it requires wide genomic sampling. A further challenge is to link patterns of adaptive variation at specific loci in natural populations to environmental factors affecting these patterns (i.e., how is adaptation to different ecologies/habitats driven from the molecular level?)

Neutral genetic diversity, on the other hand, refers to those alleles that have no direct effect on a species' fitness and which are not affected by natural selection. They do not provide information on the adaptive or evolutionary potential of populations or species. This type of genetic diversity can be assessed using a wide range of molecular markers. They include microsatellites and AFLP (Amplified Fragment Length Polymorphism). The assessment of neutral genetic variation has been frequently used as a shortcut to infer global genetic

⁴¹ e.g. Bowen (1999), Fraser and Bernatchez (2001), Merilä and Crnokrak (2001), Reed and Frankham (2001), McKay and Latta (2002), Holderegger *et al.* (2006)

⁴² e.g. Falconer and Mackay (1996), McKay and Latta (2002), van Tienderen *et al.* (2002)

⁴³ Brieuc and Naish (2011)

diversity and to support strategies for the conservation of threatened taxa⁴⁴. The use of molecular markers is a fast and relatively cheap technique which allows the study of gene flow, migration and dispersal.

The topic on whether a correlation between neutral and adaptive variation exists has been debated and conclusions do not always agree. Some authors have found that neutral and adaptive genetic diversity and differentiation are positively correlated⁴⁵, whereas other studies indicate that measurements of neutral diversity have a very limited prediction ability of quantitative variation⁴⁶ and thus cannot be used as a surrogate for adaptive genetic data, at least for some traits. However, despite the controversy, neutral genetic markers can provide highly useful information for the conservation of genetic resources. They can be used to characterize various evolutionary forces that impact the maintenance of genetic diversity⁴⁷. For example, based on neutral marker data, it is possible to reveal the extent of genetic drift, gene flow and inbreeding, or the presence of past population bottlenecks. Within the context of genetic conservation, especially under a climate change threat, gene conservation strategies should focus on the adaptive capacity of populations (and species) by considering their “individual plasticity” (i.e. their ability to respond to different environmental conditions), their adaptive genetic diversity and the occurrence of natural selection that acts upon them, as well as their ability to disperse⁴⁸. Adaptive variation assessment is therefore particularly important since it allows the identification of the components of genetic diversity responsible for the adaptation of populations to different conditions. Nevertheless, adaptive studies are still more time consuming and expensive but are becoming more achievable. In summary, ideally, an adaptive diversity study should be undertaken. If for reasons of limited financial resources, time available or lack of skilled staff it is not possible to undertake such studies, and assuming there is a positive correlation between neutral and adaptive genetic diversity, then neutral genetic diversity results could be used as a proxy of adaptive genetic diversity.

Box 25. Allele types according to their distribution in populations

Marshall and Brown (1975) developed a two-way classification system of alleles based on their frequency in populations (common or rare) and distribution across populations (widespread over many populations, or localized to just a few). Marshall and Brown (1975) and Brown and Hardner (2000) defined any allele occurring in $\geq 25\%$ of populations as a widespread allele and those occurring in $< 25\%$ of populations as a localized allele. Marshall and Brown (1975) also suggested the classification of the alleles according to their average frequency in a population as common ($P \geq 0.05$) or rare ($P < 0.05$). Four classes of alleles were then defined: (i) common and widespread (population frequency $P \geq 0.05$, and occurring in $\geq 25\%$ of populations); (ii) common and local (population frequency $P \geq 0.05$, and occurring in $< 25\%$ of populations); (iii) rare and widespread (population frequency $P < 0.05$, and occurring in $\geq 25\%$ of populations); (iv) rare and local (population frequency $P < 0.05$, and occurring in $< 25\%$ of populations). From these four categories, the authors argued that the “common and local” category is the most important in terms of conservation because it includes those alleles that confer adaptation to local conditions. On the other hand, “common and widespread” alleles are everywhere so they will inevitably be conserved regardless of the conservation strategy; “rare and widespread” alleles will be conserved depending on the total number of sampled plants if *ex situ* accessions are to be sampled, or if the

⁴⁴ e.g. Palacios and González-Candelas (1999), Rottenberg and Parker (2003), Eckstein *et al.* (2006), Watson-Jones *et al.* (2006)

⁴⁵ e.g. Merilä and Crnokrak (2001), Pearman (2001)

⁴⁶ e.g. Reed and Frankham (2001, 2002)

⁴⁷ Ahuja (2011)

⁴⁸ Lefèvre (2007)

conservation area includes most of the population in an *in situ* approach; the “rare and local” class includes very rare variants and recent or deleterious mutants which are extremely difficult to collect but a fraction will always be included in any conservation strategy.

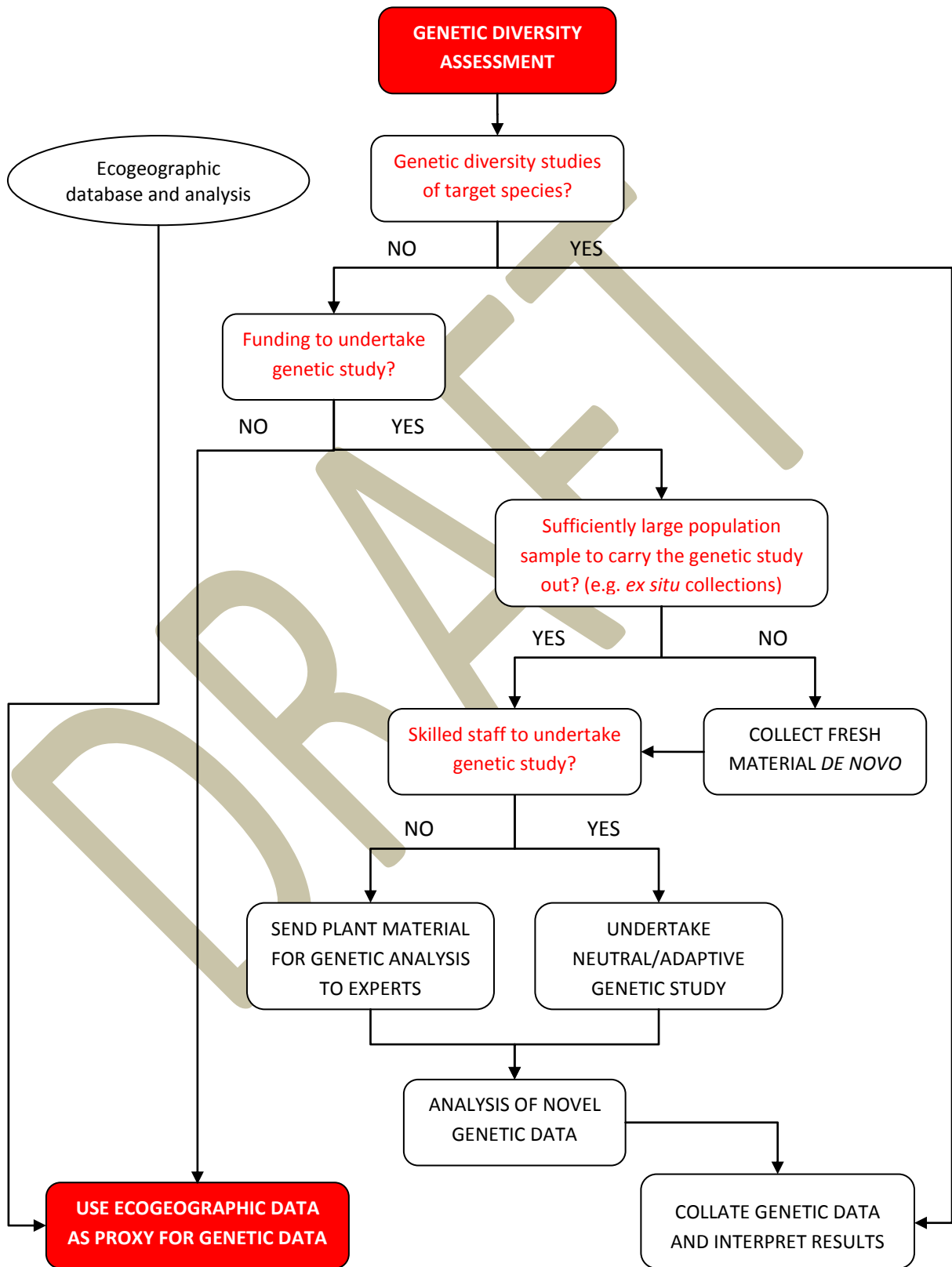


Figure 10. Collation of genetic diversity data of CWR

Along with taxonomic, ecogeographic, characterization and evaluation data, a National CWR Conservation Strategy should, whenever possible, include genetic information of the CWR not only to genetically characterise them, but also to detect which priority CWR populations should be targeted for *in situ* and *ex situ* conservation (i.e. those with greatest amount of genetic diversity, with interesting adaptive alleles etc.), and help detecting and thus preventing CWR diversity from genetic erosion. Where genetic analysis has not been undertaken or where resources are unavailable to undertake genetic analyses, as will often be the case when preparing a National CWR Conservation Strategy, ecogeographic diversity can be used as a proxy for genetic diversity, the premise being that conserving the widest possible ecogeographic range of populations of a species will maximise the overall genetic diversity of the species conserved. Figure 10 illustrates the process of collating genetic diversity data for CWR. It is necessary to know whether: (i) there are pre-existing genetic studies on the CWR, (ii) there are financial resources to undertake (further) genetic studies, (iii) there is a sufficiently large population sample to carry the genetic study out, (iv) there is skilled staff to carry out the genetic study, or alternatively, (v) whether ecogeographic diversity within the CWR can be used as a proxy of genetic diversity. Finally, a genetic erosion monitoring scheme should be implemented in order to detect changes in genetic diversity of the CWR (see A.12. Monitoring *in situ* CWR conservation sites).

A.5.2. Methodology

The main practical questions that need to be answered in regard to the collation of genetic data are:

- (i) Are there any genetic studies and genetic information already available for the target CWR? If so, collate all the information obtained which can be useful to understand the species genetic characteristics. Information on breeding system and seed dispersal mechanism as well as on other life history traits should also be gathered as they are crucial in determining the patterns of genetic diversity among and between populations (see Box 26 **Error! Reference source not found.** and Table 1). If no genetic information is available, then if possible a genetic study (on adaptive or neutral diversity) should be carried out.
- (ii) Are there sufficient financial resources to undertake a genetic study (either on adaptive or neutral genetic diversity)?
- (iii) Are there enough population samples available to undertake the genetic study? These may be either material of the species already present in available *ex situ* collections or through fresh collection from throughout the ecogeographic range of the species.
- (iv) Are there skilled staff able to undertake such a study? If financial resources and expertise are available, a genetic study is thus desirable. If financial resources are available but no skilled staff, plant samples should be collected, then sent to skilled experts to analyse.
- (v) However, if resources are limited and not available to carry out a genetic diversity study, ecogeographic diversity (together with information on reproduction and dispersal systems) can be used as a proxy for genetic diversity (different ecogeographic characteristics entail different genetic characteristics). In other words, if a priority CWR species is distributed throughout a country then it is assumed, unless there is evidence to the contrary, that genetic diversity or distance is partitioned in relation to ecogeographic diversity, and sampling from the maximum diversity of locations will result in the most genetically diverse samples. Disparate ecogeographic locations can

then be identified for the establishment of *in situ* CWR conservation sites or the sampling of populations for *ex situ* conservation.

Box 26. Genetic diversity in relation to life history traits in plant species

Hamrick (1983) and Loveless and Hamrick (1984) used several life history and ecological traits to determine whether inter-population genetic heterogeneity was related to the species' characteristics. They found that life form, geographic range, breeding system and taxonomic status had significant effects on the partitioning of genetic diversity within and among plant populations. For detailed information on how breeding system, floral morphology, mode of reproduction, pollination mechanism, seed dispersal, seed dormancy, phenology, life cycle, timing of reproduction, successional stage, geographic range, population size and density, and population spatial distribution may affect the genetic variation within populations as well as the genetic structure among and within populations, see a literature review of several case studies undertaken by Loveless and Hamrick (1984).

In addition, Hamrick and Godt (1996) perform two-trait combination analyses on five different life history characteristics (breeding systems, seed dispersal mechanism, life form, geographic range, and taxonomic status) in order to study how genetic diversity varies in seed plants. They analysed interspecific variation of allozyme genetic diversity regarding the percentage of polymorphic loci within the species (P), genetic diversity within the species (Hardy-Weinberg expected heterozygosity - H_{es} - Weir 1990), and the proportion of total genetic diversity among populations (G_{ST}).

The categories of each of the life history traits studied were:

- breeding systems: outcrossing, selfing and mixed mating;
- seed dispersal mechanism: attached, gravity, animal, wind;
- life form: annual, short-lived and long-lived perennial taxa;
- geographic range: endemic, regional, narrow and widespread;
- taxonomic status: gymnosperm, dicotyledon, monocotyledon.

The authors concluded that all examined traits have significant effects on the genetic parameters considered but life form and breeding system have the most significant influence on the levels and distribution of genetic diversity. Their main conclusions were:

- regardless of other traits, outcrossing species tend to be more genetically diverse and have less genetic differentiation among populations;
- woody plants have less among population differentiation and somewhat more genetic diversity than non-woody species with similar life history traits;
- species within families with predominately outcrossing and woody species had more genetic diversity and less inter-population differentiation than species within families with predominately herbaceous species;
- species with low inter-population genetic differentiation tend to have more overall genetic diversity;
- woody plants have lower G_{ST} values and somewhat higher P , and H_{es} values than herbaceous plants with the same combinations of life history traits, regardless of their phylogenetic relationship.

Table 1. Ecological factors affecting genetic variation and population structure ^{49, 50}

ECOLOGICAL FACTOR	GENETIC VARIATION WITHIN POPULATIONS	GENETIC STRUCTURE AMONG POPULATIONS	GENETIC STRUCTURE WITHIN POPULATIONS
Breeding system			
Primarily inbreeding	Lower than other species, low heterozygosity	Increased divergence due to drift and reduced gene flow	Reduced heterozygosity and within family genotypic diversity; low N_e ; restricted gene migration and high population subdivision
Mixed mating	More variability	Potential for differentiation; depends on selfing and may vary in time	Potentially subdivided; depends on balance between selfing and outcrossing
Predominantly outbreeding	Higher than other species, high heterozygosity	Reduced divergence due to increased pollen flow	Increased N_e and N_A , reduced subdivision
Floral morphology			
Hermaphrodite	Moderate levels if mixed mating; lower if selfing	Depends on breeding system; selfing promotes divergence	Potential for subdivision; depends on mating system and pollen movement; floral morphology affects pollination and pollen carryover, altering N_e and N_A up or down
Monoecious or dichogamous	Potentially high, if predominantly outcrossed	Increased outbreeding and pollen flow reduce differentiation	Depends on mating system and pollinators; likely to have reduced subdivision and increased homogeneity
Dioecious or heterostylous	High	Enforced outcrossing and pollen movement reduce differentiation	Enforced outbreeding reduces subdivision; assortive mating and unequal sex ratios can reduce N_e and generate differentiation
Mode of reproduction			
Obligate apomixis	Low but depends on the number of genets	Founder effects and drift promote divergence; lack of recombination leads to loss of genotypic	Homogeneous clones; population highly subdivided

⁴⁹ Adapted from Loveless and Hamrick (1984)

⁵⁰ N_e =effective population size, N_A =neighbourhood area

ECOLOGICAL FACTOR	GENETIC VARIATION WITHIN POPULATIONS	GENETIC STRUCTURE AMONG POPULATIONS	GENETIC STRUCTURE WITHIN POPULATIONS
		variability	
Facultative apomixis	Moderate; depends on breeding system and other factors	Founder effect may limit number of genets, thus enhance differentiation	Potentially subdivided; depends on breeding system and amount of sexual reproduction
Sexual reproduction	Potentially high	Depends on other factors	Depends on other factors
Pollination mechanism			
Small bee	Insect-pollinated species have reduced amounts of variability	Limited pollen movement and local foraging (especially by small insects) increase differentiation Rare long-distance pollen dispersal, long-distance trap-lining, or low background pollen levels (wind) prevent divergence	Limited, leptokurtic or nearest neighbour pollen movement reduces N_e , promotes subdivision, family structure and inbreeding Animal vectors with high variance in pollen carryover and delivery will increase N_e Large, vagile vectors will visit more plants, reduce subdivision, give moderate to large N_e and large N_A
General entomophily			
Large bee			
Butterfly/moth			
Bird/bat			
Wind	High		Wind pollination gives large N_e and N_A and reduces subdivision
Seed dispersal			
Gravity	Intermediate	Limited dispersal promotes differentiation	Limited seed movement reduces N_e , promotes family structure, inbreeding, increased homozygosity and subdivision
Explosive/capsule	Intermediate	Small amounts of long-distance migration can prevent divergence	
Winged/plumose (wind)	High		
Animal-ingested	Intermediate	Regular long distance transport promotes homogeneity	Large variance in dispersal distance increases N_e , decreases subdivision Dispersal by wind and animals may reduce clumping and family structure
Animal-attached	Low		

ECOLOGICAL FACTOR	GENETIC VARIATION WITHIN POPULATIONS	GENETIC STRUCTURE AMONG POPULATIONS	GENETIC STRUCTURE WITHIN POPULATIONS
Seed dormancy			
Absent	Determined by other factors	Determined by other factors	Determined by other factors
Present	Increases potential genetic variation	Reduces divergence; retards loss of alleles by drift and isolation	Retards loss of alleles; increases generation time of genotypes, increases N_e , and inhibits subdivision; may be countered by differential fecundities or other factors
Phenology			
Populations asynchronous	No prediction	Prevents gene exchange; promotes divergence	Restricts mating, reduces N_e and promotes subdivision
Populations seasonal and synchronous	No prediction	Potential for extensive gene flow reduces probability of divergence	Large potential N_e ; may be restricted by pollinator behaviour or family structure, but potentially homogeneous
Extended, low level flowering	No prediction	Long-distance pollinator movement prevents divergence	Reduces selfing, increases pollen flow, increases N_A and prevents subdivision
Life cycle			
Annual	Reduced variability; less heterozygosity	Increases chances of subdivision	Increases susceptibility to drift due to bottleneck effects and variable fecundities; smaller N_e promotes local subdivision
Short-lived perennial			
Long-lived perennial	Increased variability	Reduces effects of drift, increases chances of migration, and thus hinders divergence	Retards loss of variation; increases N_e , increases mating opportunities, and retards subdivision
Timing of reproduction			
Monocarpic	No prediction	Promotes drift and divergence between populations	Restricts mating possibilities, shortens effective generation time; reduces N_e which promotes differentiation in time and space but reduces flowering

ECOLOGICAL FACTOR	GENETIC VARIATION WITHIN POPULATIONS	GENETIC STRUCTURE AMONG POPULATIONS	GENETIC STRUCTURE WITHIN POPULATIONS
			density, which may increase N_e
Polycarpic	No prediction	May inhibit divergence; depends on other factors	Increases N_e by increasing mating pool and generation time, reducing probability of subdivision
Successional stage			
Early	Reduced variability	Founder and drift effects, short population lifespan promotes differentiation	Depends on other factors: generation time, breeding system and dispersal may have conflicting effects on N_e
Late	Increased variability	Stable, long-lived population structure promotes migration, reduces drift and reduces differentiation	Depends on other factors; longer generation time reduces population subdivision
Geographic range			
Endemic	Genetically depauperate	Small, local populations will show more divergence due to drift and isolation	Possibly homogenous, due to size fluctuations, lack of variability
Narrow	Moderate levels		
Regional	Maximum variation	Patterns in more widespread species determined by other factors	Patterns influenced by other factors
Widespread	Less variability		
Population size			
Large and stable	High	Trade-off in populations of all sizes between drift and migration effects: small populations promote divergence due to drift but are more heavily influenced by small numbers of migrant propagules; structure will depend on amount of migration	Potentially subdivided, depending on pollinator behaviour
Small and stable	Lower, due to drift		More likely to be homogeneous, depending on scale of gene flow and magnitude of drift
Fluctuating size	Low, due to drift		Homogeneous due to loss of variability and inbreeding during periods of small size; net N_e is weighted towards length of time spent at small population sizes
Population density			
High	No prediction	Trade-offs analogous to those for population size	Animal-dispersed pollen movement is more susceptible

ECOLOGICAL FACTOR	GENETIC VARIATION WITHIN POPULATIONS	GENETIC STRUCTURE AMONG POPULATIONS	GENETIC STRUCTURE WITHIN POPULATIONS
			to density; high densities restrict pollen flow and increase subdivision
Low	No prediction	Low density may promote long-distance pollen flow, increasing homogeneity	Low densities may increase pollen movement (increase N_A) or may reduce pollinator visits (decrease N_A and N_e)
Population spatial distribution			
Patchy	No prediction	Increasing isolation reduces gene flow and enhances differentiation	Patchiness may affect pollinator behaviour in complex ways; in general, spatial patchiness increases inbreeding, reduces gene flow and N_e , and enhances genetic patchiness and subdivision
Uniform	No prediction	Promotes migration and homogeneity	Promotes gene flow and reduces subdivision
Population shape	No prediction	Divergence enhanced in linear arrays of populations	Subdivision is increased in linear habitats

A.5.3. Examples and applied use

Box 27. Genetic diversity of *Dianthus cintranus* subsp. *barbatus* in Portugal

A genetic diversity study using AFLP was undertaken for *Dianthus cintranus* Boiss. & Reut. subsp. *barbatus* R. Fern. & Franco—a priority CWR for conservation in Portugal. The AFLP analysis showed that *D. cintranus* subsp. *cintranus* presents low but significant among population differentiation ($F_{ST}=0.038$). The AMOVA showed that the within population component of the genetic variance is extremely high (92%). The populations of the taxon are characterized by the high number of private alleles. Additionally, a significant pattern of isolation-by-distance between the populations of *A. victorialis* ($R^2=0.692$, $P=0.032$) and *D. cintranus* subsp. *cintranus* ($R^2=0.286$, $P=0.034$) was observed, indicating restricted gene flow over a small geographic scale. Given that the taxon did not show isolation by distance, a Bayesian clustering analysis was performed and the results obtained on population genetic structure complemented the analyses. Two genetic clusters were identified for *D. cintranus* subsp. *barbatus*.

Genetic (namely, expected heterozygosity, total number of polymorphic alleles, common and localized alleles, and inter-population genetic distance), demographic (population size) and threat data were used in order to prioritise populations for *in situ* conservation of the studied species. Results showed that one population of the target taxon should be conserved *in situ* and *ex situ*.

Source: Magos Brehm *et al.* (2012)

<i>Dianthus cintranus</i> subsp. <i>barbatus</i> in Portugal	Population of <i>Dianthus cintranus</i> subsp. <i>barbatus</i> in Portugal
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Box 28. Islands as refugia of *Trifolium repens* genetic diversity

A genetic diversity study using AFLP was carried out in order to compare mainland wild and landrace populations of *Trifolium repens* compared with wild populations collected from the islands surrounding the UK. Results showed that the population from the now uninhabited island of St Kilda (Outer Hebrides) is highly differentiated from UK mainland populations and genetically distinct from cultivated varieties, retaining high diversity through limited human influence, thus representing a unique conservation resource. In contrast, the mainland UK wild populations are relatively genetically similar to the cultivated forms, with geographic barriers preventing complete homogenisation.

Source: Hargreaves *et al.* (2010)

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Technical documents on genetic diversity analysis:



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WWW Bioversity International training modules on molecular analysis of diversity:
http://www.bioversityinternational.org/training/training_materials.html#c10719

DRAFT

A.6. Ecogeographic analysis of priority species

A.6.1. Overview

What is an ecogeographic survey and why it is needed?

An ecogeographic survey is the process of collating diversity and ecogeographic data. It is defined as “an ecological, geographical, taxonomic and genetic information gathering and synthesis process, where the results are predictive and can be used to assist in the formulation of collection and conservation priorities”⁵¹⁵². It is generally based on the collation of information from herbarium specimens, gene bank accessions, databases, literature, and all other possible data sources and, if possible, should be complemented by the collection of novel data if the taxon is poorly known.

An ecogeographic survey is needed in the development of any conservation strategy in order to obtain baseline information regarding the species taxonomy, distribution and ecology which will then help in formulating, establishing and implementing conservation priorities.

Ecogeographic analysis has become routinely applied, increasingly sophisticated and detailed due to the development of tools such as Geographic Information Systems (GIS) (see Box 29), but it should always be stressed that using ecogeographic analysis is always sub-optimal, where ever possible it is better to genetic diversity analysis rather than ecogeography as a proxy for genetic diversity.

In the literature the terms ecogeographic study and survey are used, the difference between the two is one of degree, a study involves a more detailed data analysis and interpretation phase than a survey and a survey is quicker and based on easily available existing information.

Box 29. Ecogeographic studies using GIS – potentialities

Studies using GIS to analyse ecogeographic data include those investigating:

- Habitat and environmental characterization of species' collecting sites;
- Optimization of germplasm collecting missions oriented to gathering representative samples of genetic diversity for *ex situ* conservation;
- Ecogeographic characterization of land/populations/species (in order to help interpret geographic, ecological and taxonomic patterns);
- Ecogeographic representativeness and bias in existing *ex situ* collections;
- Establishment of core collections ;
- Where to establish genetic reserves,
- Predicted climate change impact on natural populations, etc.

Source: Bennet and Bullita (2003), Bennet and Maxted (1997), Berger *et al.* (2003), Draper *et al.* (2003), Ferguson *et al.* (2005), Greene *et al.* (1999), Grenier *et al.* (2001), Hijmans *et al.* (2000), Igartua *et al.* (1998), Jarvis *et al.* (2008), Lobo Burle *et al.* (2003), Parra-Quijano *et al.* (2008, 2011a, 2012b), Ramírez-Villegas *et al.* (2010)

Figure 11 illustrates the ecogeographic study methodology. It comprises three main phases: project design, data collection and analysis, and the ecogeographic products. The project design includes: (i) Identification of taxon or crop expert, (ii) Selection of target taxon/crop taxonomy, and (iii) Design and creation of the database structure. The data collection and

⁵¹ Maxted *et al.* (1995)

⁵² Castañeda Álvarez *et al.* (2011)

analysis include: (iv) Survey of passport, management, site and environment, and existing characterization and evaluation data, (v) Collation of data into database, (vi) Data verification, and (vii) Data analysis. The ecogeographic products includes: (viii) CWR database (which contains raw data, (ix) Conspectus (that summarizes the taxonomic, geographical and ecological data for the target taxon), and (x) Report (which interprets the data obtained). Note some of these elements have been addressed in previous sections of the Toolkit (see A.3 National CWR checklist and inventory creation).

The culmination of the ecogeographic survey and analysis is:

- (i) the ecogeographic characterization of priority CWR,
- (ii) the identification of areas for *in situ* conservation of priority CWR⁵³,
- (iii) the identification of populations of priority CWR that contain unique genetic diversity that is not already conserved *ex situ*, and once identified, this material may be collected and conserved in the appropriate gene banks.

A.6.2. Methodology

- (i) Identification of taxon expertise. Taxon experts and people with specialist knowledge of the flora of a target area may give you accurate species location and ecological information as well as recommend relevant grey literature, Floras, monographs, taxonomic databases, which herbaria and gene banks should be visited, and also put the conservationist in contact with other specialists. Experts to contact may include:
 - Botanical, agrobiodiversity and biodiversity conservation, taxonomic, genetic, geographic, breeding, researchers;
 - Herbaria and gene bank curators;
 - NGOs working in conservation in the target region or target crops.
- (ii) Selection of target taxon/taxonomy. The generally accepted taxonomic classification can be determined with the help of:
 - Target taxon experts;
 - National or global Floras;
 - Taxonomic monographs;

⁵³ If these areas were selected based on high concentrations of CWR they might be considered analogous to the broader biodiversity hotspots (Mittermeier *et al.* 1999, Myers *et al.* 2000) or taxonomic Important Plant Areas (Target 5 of the CBD Global Strategy for Plant Conservation - www.biodiv.org/programmes/cross-cutting/plant/) and in this case areas with high concentrations of CWR diversity might be referred to as Important CWR Areas.

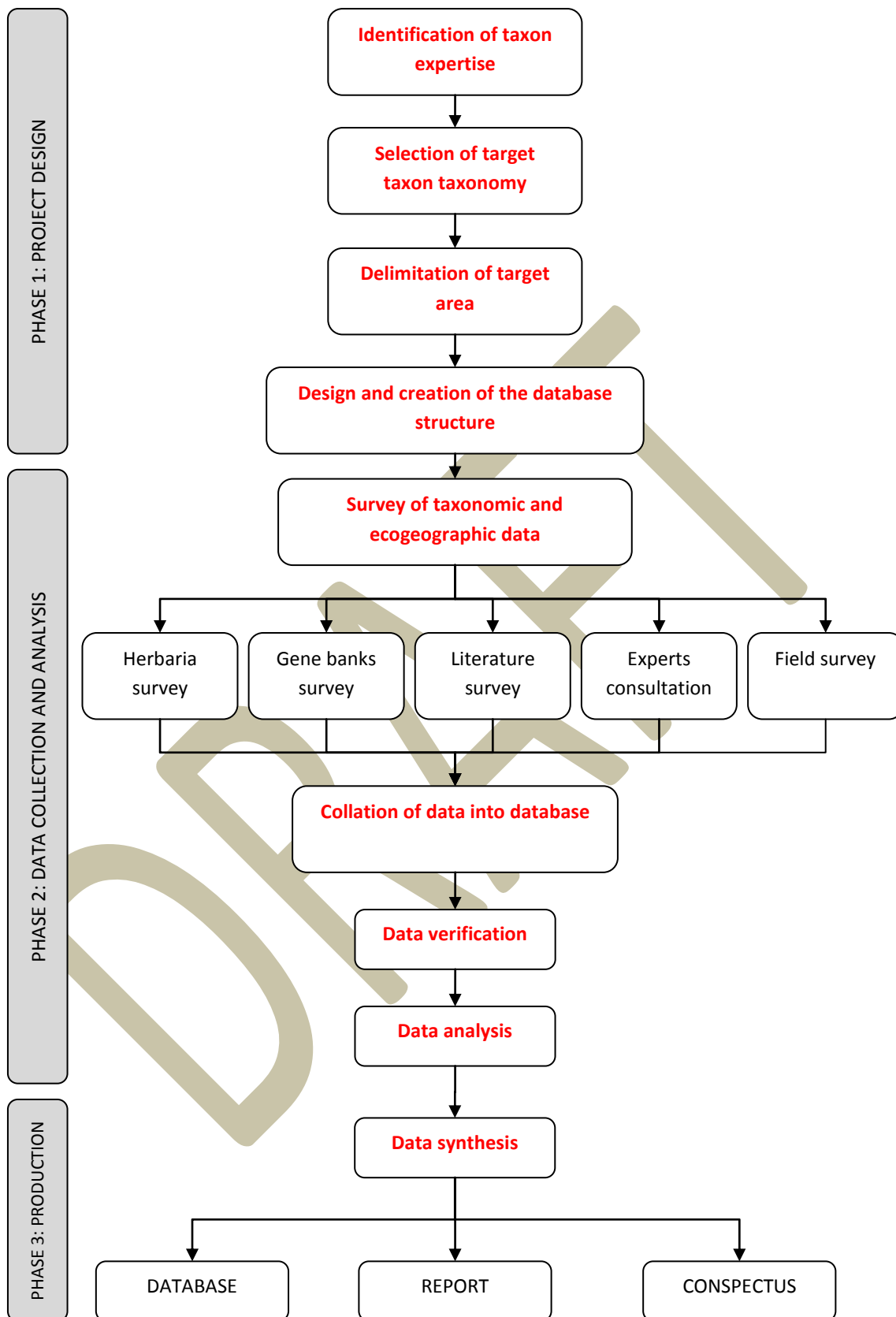


Figure 11. Ecogeographic study model for CWR⁵⁴

⁵⁴ Modified from Maxted *et al.* (1995)

- Recent taxonomic revisions;
- Taxonomic databases, etc.

It is important to detect existing synonyms so to avoid missing specimens that may be identified under synonymous names and to prevent separate treatments of the same taxon. In the context of the development of a National CWR Conservation Strategy, this step would already have been undertaken as part of the creation of the CWR checklist (prior to taxon prioritization).

- (iii) Delimitation of the target area. Normally an ecogeographic study should include the whole range of the species distribution so as to avoid the problem of non-compatible data sets that can be inherent in multiple surveys of the same taxon. However, given that the conservation strategy is at national level, the whole country should be the target area.
- (iv) Design and creation of the ecogeographic database structure.
- A careful reflection on the types of data to be included in the database should precede its creation. The collecting form (when field work is to be undertaken) should be strongly linked to this database (i.e., all fields in the collecting form should be included in the database structure);
 - Types of data include: accession descriptors, collecting descriptors, nomenclatural data, socio-economic data, site and environment data See Box 31 for different kinds of data to include in the database;
 - Data descriptors and data standards should be determined;
 - The database software package should be both user-friendly and able to accommodate the complexity of a database of this kind. Several database software packages are available (Microsoft Access, MySQL, etc.).
 - The data format should be standardised;
 - The ecogeographic database should be directly linked to the CWR national inventory through a unique identifier (CWR taxon ID). Typically, the database may comprise two linked tables—the taxon information table and the ecogeographic data table (as suggested below). However, for practical reasons, more than one table may be used to manage the ecogeographic data which is likely to contain many data fields. :
 - a. *Taxon information table:* links the CWR checklist to taxon level data collected during the survey. Data are usually obtained from bibliographic references (Floras, monographs, etc.) and may include: taxon name, synonyms, authorities, vernacular names, plant life-form¹⁶, reproductive system, habitat, flowering time, altitude, chromosome number, national and global distribution, actual and potential uses, etc.
 - b. *Ecogeographic data table:* links the CWR checklist to accession level data collected from the herbarium specimens, germplasm accessions, personal communications, bibliographic references and field surveys; each taxon in the inventory is likely to have several accessions which may or may not be collected in different locations, giving an approximation of the taxon distribution. Passport data include: institution acronym, accession number, location, coordinates, altitude, date of collection, collectors' name, if specimen

was flowering or fruiting, ecological notes (climate, soil type, etc.)⁵⁵, associated species, taxonomic revision notes, population and threat data, etc. The basic types of data recorded at the accession level are summarised within the FAO/Bioversity Multi-crop Passport Descriptors (MCPD) ver. 2 (Alercia *et al.* 2012 at http://www.bioversityinternational.org/fileadmin/bioversity/publications/pdfs/1526_FAO-Bioversity_multi_crop_passport_descriptors_V.2_Final_rev.pdf) (see Annex 4).

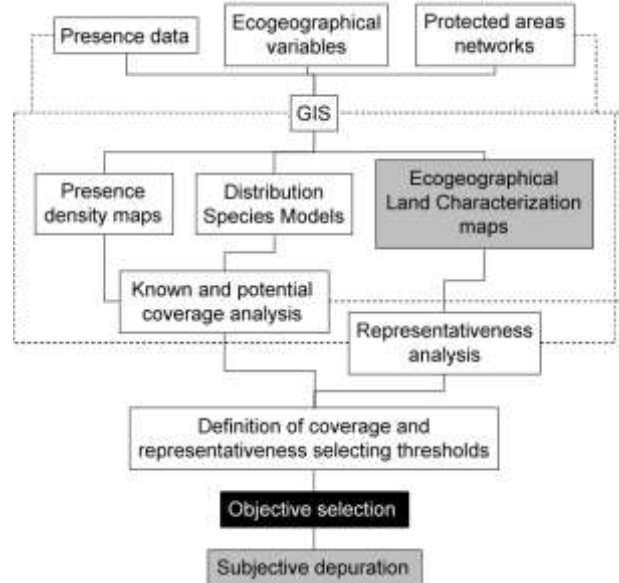
- (v) Survey and collation of diversity and ecogeographic data into the database. Sources of data are likely to include:
- Herbaria and gene banks (also on-line): see Box 32 for issues to take into consideration when using *ex situ* data;
 - Scientific and 'grey' literature: Floras, monographs, recent taxon studies, reports of Environmental Impact Assessment studies⁵⁶, databases, gazetteers, scientific papers, soil, vegetation and climate maps, atlases, etc., available both in conventional printed paper and in digital files;
 - GIS layers: ecogeographic analysis is increasingly linked to some form of spatial analysis and this analysis requires GIS maps to compare to the accession data, recently ecogeographic land characterization maps have been generated that combine multiple feature of interest (see Box 30);
 - Expert knowledge: contact with taxonomic or geographic experts is likely to provide significant additional data to facilitate the analysis and will also provide an opportunity to gain feedback on the analysis results;
 - Field survey data: where ecogeographic data is scarce there may be insufficient data to undertake meaningful ecogeographic analysis and it will then be necessary to collate fresh data from field observation of the target taxa.

Box 30. Ecogeographic land characterization mapping

Ecogeographic land characterization (ELC) maps have been proposed as a suitable technique to assess the adequacy of ecogeographic representativeness of germplasm in *ex situ* collections. The map reflects as many categories as environmental adaptive scenarios occurring over a particular area, based on bioclimatic, geophysical and edaphic characteristics to form a combined ecogeographic map, the process is summarised in the following model.

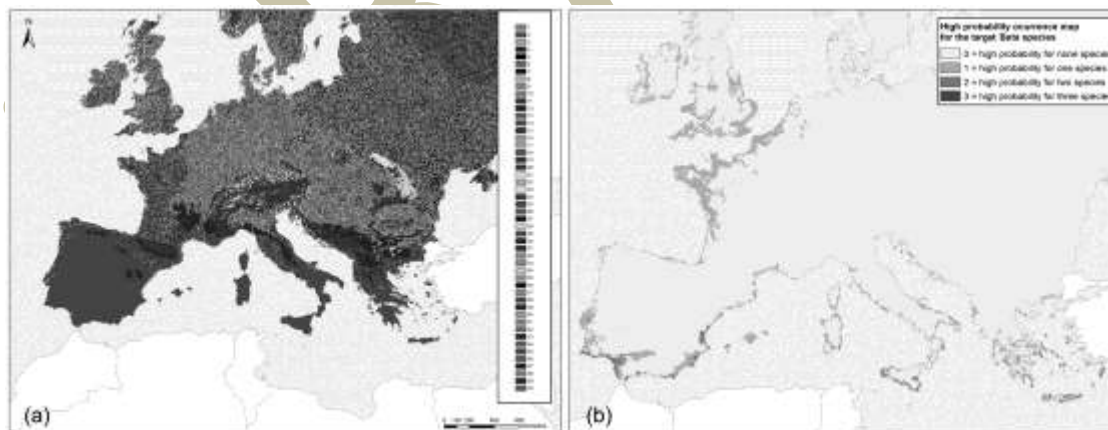
⁵⁵ Ecological notes include information registered as passport data. However, posterior information (e.g. on temperature, rainfall, air humidity, frost, soil type, soil pH, soil rock, etc.) can be extracted at each known location using a GIS.

⁵⁶ Environmental Impact Assessment (EIA) have been defined by the IAIA and IEA (1999) as "the process of identifying, predicting, evaluating and mitigating the biophysical, social, and other relevant effects of development proposals prior to major decisions being taken and commitments made." In other words, they permit assessing the possible negative and positive impacts that a project (e.g. highway, dam, building, etc.) may have on the natural, social and economic aspects. Regarding the biophysical aspect, EIA reports generally provide species lists of Flora (and Fauna) that occur in the area where the project is to be developed thus constituting important sources of species distributional data.



The authors used this approach to suggest genetic reserves for beet CWR in Europe using population density maps, ecogeographic data and species distribution models as follows:

1. A map of population density of the selected species was elaborated as a starting point.
2. Locations were refined by choosing site with potential richness of at least two species.
3. Areas with most representative ecogeographic units for group of species were selected.
4. Sites located within existing protected areas, with the greatest number of populations, representing common and marginal ecogeographic units for the target taxa. The premise of this approach is that the conservation of the species' greatest ecogeographic variability implies the conservation of the greatest genetic diversity of adaptive importance and, possibly, the most interesting allelic variation in the genes of interest for crop improvement. Below (a) shows an Ecogeographic Land Characterization map for *Beta* species with 50 ecogeographic categories and (b) shows the potential species richness map for three *Beta* species.



Source: Parra-Quijano *et al.* 2008, Parra-Quijano *et al.* 2011, Parra-Quijano *et al.* 2012b

Box 31 lists the different types of data to include in the ecogeographic database. Existing descriptors and data standards should be used where possible in order to improve options for data sharing (see section A.3.2.). The passport data should be available for every accession of every CWR included; though it should be stressed that georeferencing is often required to ensure the necessary data is complete. The characterization and evaluation data are frequently not available and may require specific trials. The broader the sampling of

ecogeographic data associated with herbarium specimens and germplasm accessions the more geographically and ecologically representative the data will be.

Box 31. Types of data to include in the ecogeographic database

- Nomenclature data: genus, species, authority, infra-specific epithet, infra-specific epithet authority, taxonomic rank, synonyms, vernacular names;
- Taxon biology: descriptive information, phenology, pollination, autoecology, synecology;
- Related crop: related crop, degree of relationship to crop, how relationship defined whether gene pool or taxon group knowledge was used, which gene pool source used;
- Distribution data: location, coordinates,
- Population characteristics: size, age structure, genetic diversity, dynamics;
- Environmental data: altitude, aspect, slope, soil texture, soil drainage, soil pH, temperature, rainfall, habitat;
- Population site-related information: as vegetation type, associated species, human pressures;
- Land use data: urbanization, agriculture, forestry, wilderness.
- Conservation data: threat status, legislation, *in situ* and *ex situ* conservation status, method of selection of seed saved, method of seed storage, maintainer exchange frequency, whether it is adequately managed *in situ*, threat of genetic erosion, length of seed saving, etc.
- Ex situ characterization data: e.g. leaf shape, flower colour, plant habit, seed colour, chromosome number, etc.;
- Ex situ evaluation data: plant height, days to maturity, etc.;
- Photographs/illustrations/links to digital specimens
- Utilization potential: previous use as trait donor, potential use as trait donor, other uses.

(vi) Ecogeographic data verification (Figure 12).

- Check for duplicates. Namely regarding the gene bank and herbaria survey, those records with the exact same data should be highlighted as duplicates so to avoid a false impression of the intensity of CWR collection.
- Check for spelling errors and standardise data format.
- Georeference all the entries, if possible. All data should also be georeferenced by using (online) gazetteers, maps, Google Earth, etc.
- Assign a level of geographic precision. Different levels of precision should be assigned to each record (see Table 2 as an example of geographic precision for CWR).
- Check for outlier locations. Distribution maps should be created (with a GIS if possible) to look for outlier collection sites. All individual records should then be corrected for these mistakes or deleted if correction is not possible.

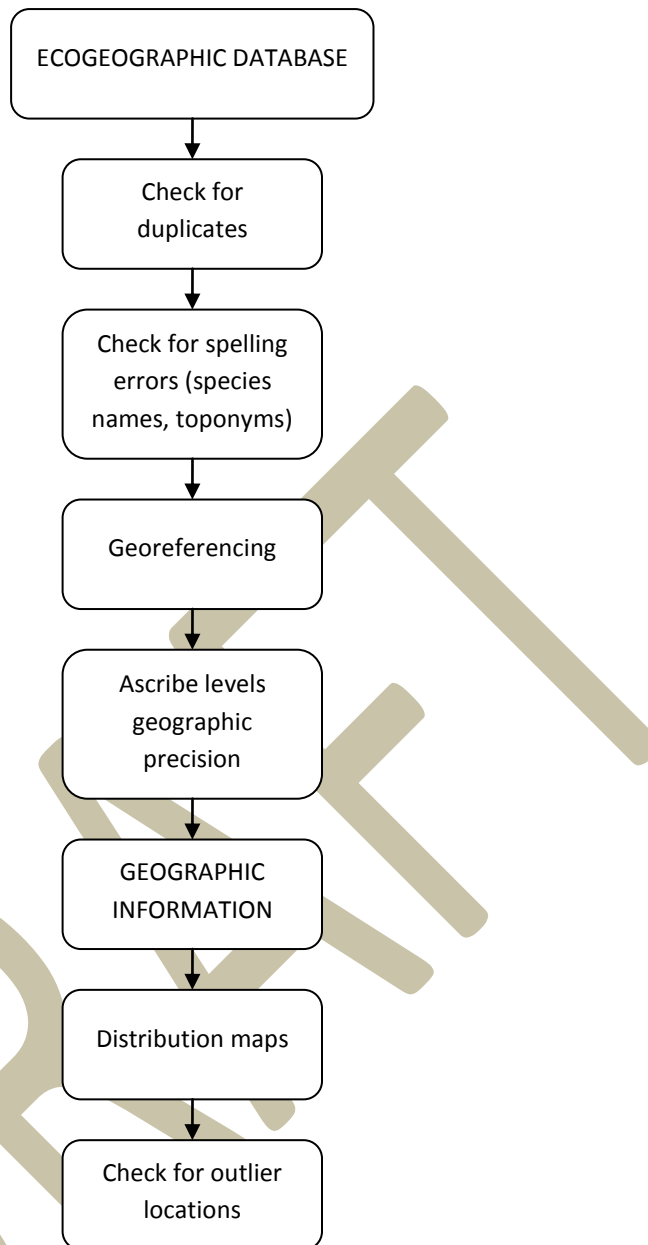


Figure 12. Schematic representation of ecogeographic data verification

Table 2. Examples of location data and their corresponding level of geographic precision⁵⁷.

LEVEL OF PRECISION	LOCATION DATA
1	Exact place (e.g. 21 km along the road between location x and location y).
2	Within a defined area of 1 km ² .
3	Within a defined area of 10 km ² .
4	Within a defined area of 20 km ² .
5	Within a defined area of 100 km ² .

⁵⁷ Adapted from Magos Brehm (2009)

(vii) Analysis of collated data. Data analysis may include:

- The distribution of CWR;
- The ecogeographic characterization of CWR;
- The distribution of specific characterization and evaluation traits (e.g. pest resistance, frost tolerance, yield characteristics) within the CWR;
- The mapping and detection of ecogeographic patterns (e.g. phenology of the species in different areas, whether a particular CWR occurs on a particular soil type, or whether the frequency of a character state changes along an environmental gradient);
- The identification of representative populations of the full range of diversity of each target taxon and/or with traits of specific interest;
- The identification of populations for *ex situ* sampling and conservation for individual taxa and hotspots for groups of taxa
- The identification of hotspots for groups of taxa for *in situ* conservation
- Climate change analysis to identify threatened population that required *ex situ* conservation or population suitable for long-term *in situ* conservation.

(viii) Data synthesis. The products that synthesise the data collated include the ecogeographic database (which contains raw data), the conspectus (that summarizes all data collated for each CWR) and the report (which interprets the data obtained).

Box 32. Factors to take into consideration when using *ex situ* data

Care must be taken when interpreting information on current germplasm conserved *ex situ*. In many cases the coordinates are wholly or partly missing, imprecise or wrong. Moreover, the material held might be incorrectly identified, it might not be representative of the genetic diversity of the sampled population, it might be duplicated in several institutions giving a false idea of the actual genetic diversity being conserved, it may for various reasons be unavailable to potential users, some collections might not be efficiently managed and therefore records may contain errors, and the germplasm might not be managed to international gene bank standards. The requirement for germplasm users to routinely sign Material Transfer Agreements as part of ITPGRFA obligations may for certain uses (e.g. commercial breeding companies) limit access to material as the user may not wish to draw attention to the material they are accessing from gene banks.

Source: Maxted *et al.* (1995), Hijmans *et al.* (1999).

A.6.3. Examples and applied use

Box 33. Ecogeographic characterization of *Lupinus luteus*

Lupinus luteus populations in Spain were characterised ecogeographically as follows:

1. Good quality georeferenced presence data were selected.
2. Ecogeographical GIS layers/variables (from passport data and by extracting information from georeferencing collecting sites) were compiled.
3. The most relevant ecogeographic variables were selected both through consultation with experts and by analysing their relative statistical significance.
4. A Principal Component Analysis (PCA) was performed in order to reduce the number of variables.

5. Tables with accessions and their corresponding ecological descriptors were created.
6. Ecogeographical distances between all pairs of accessions were estimated (by using the Gower similarity coefficient).
7. Cluster analysis on the distance matrix and UPGMA agglomerative method was performed and dendrograms that represented ecogeographic similarities between accessions were obtained.
8. Ecogeographic groups (EG) were then obtained from the cluster analysis using the new variables obtained with the PCA (PCA1 related to thermopluviometric factors, PCA2 related to temperature, PCA3 related to edaphic factors).
9. To each accession its corresponding EG was assigned and visualized in a map.

Source: Parra-Quijano et al. (2008).

Box 34. Strategies for the development of core collections based on ecogeographic data

The authors determined the suitability of core collections based solely on ecogeographic data. Sixteen ecogeographic core collections were evaluated for six *Lupinus* spp. occurring in peninsular Spain and the Balearic Islands. A Ward-Modified Location Model (Ward-MLM) and a two-step clustering (TSC) with proportional allocation strategy (P) produced the most representative core collections for the target taxa. In addition, a highly representative ecogeographic core collection was obtained by a simpler procedure of grouping according to ecogeographic land characterization maps (CEM) with P allocation. Ecogeographic data were thus used to create representative core collections with similar strategies to those used with genotypic or phenotypic data or simpler ones such as CEM, which is easy to apply and update.

Source: Parra-Quijano et al. (2011).

A.6.4. List of references used to compile the text

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http://www.pgrsecure.bham.ac.uk/sites/default/files/meetings/palanga/WG1_08_Ecogeographic_Data_Analysis_Iriondo.pdf [Accessed July 2012]

WWW CWR Portal resources – presentations on conservation:
<http://www.cropwildrelatives.org/resources/presentations.html#c6854>

Technical documents on ecogeographic survey and analysis:



Schledeman X and van Zonneveld M (2010) Training Manual on Spatial Analysis of Plant Diversity and Distribution. Bioversity International, Rome, Italy. Available at:
http://www.bioversityinternational.org/training/training_materials/gis_manual/gis_download.html

WWW Bioversity International training modules on ecogeographic surveys and spatial analysis:
http://www.bioversityinternational.org/training/training_materials.html#c10725

Environmental data:

WWW Bioclimatic variables: WorldClim – Global Climate Data: <http://www.worldclim.org/>

WWW Climate Change Forecasts (IPCC): Future climate projections http://www.ipcc-data.org/ddc_climscen.html

WWW Climatic Research Unit: <http://www.cru.uea.ac.uk/cru/data/>

WWW EUNIS: European Nature Information System <http://eunis.eea.europa.eu/>

WWW Glob cover: European Space Agency Global Land Cover map, latest version = 2009
<http://ionia1.esrin.esa.int/>

WWW Global Land Cover Characterization: <http://edc2.usgs.gov/glcc/glcc.php>

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

WWW STRM DEM: 90m digital elevation dataset <http://srtm.csi.cgiar.org/index.asp>

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

WWW UNEP WCMC World Database of Protected Areas: World Database on Protected Areas (polygons) <http://www.protectedplanet.net/>

WWW World Soil Database: Harmonized World Soil Database v 1.2
<http://www.iiasa.ac.at/Research/LUC/External-World-soil-database/HTML/>

WWW World Reference Base for Soil Resources: <http://www.fao.org/ag/agl/agll/wrb/>

WWW Worldclim Global Climate layers: 1km resolution grids of climate and derived bioclimatic datasets <http://www.worldclim.org/>

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

Biodiversity occurrence data:

WWW BioCASE: Biological Collection Access Service for Europe <http://search.biocase.org/>

WWW Botanical Garden Conservation International: Botanic garden holdings information
<http://www.rbgekew.org.uk/BGCI/http://www.biodiv.org/>

- WWW CWRIS-AEGRO-PLIS: <http://aegro.jki.bund.de/aegro/index.php?id=168>
- WWW EURISCO European Internet Search Catalogue of *Ex Situ* PGR Accessions
<http://eurisco.ecpgr.org/>
- WWW European Native Seed Conservation Network (ENSCOBASE): European database of major *ex situ* botanic garden gene bank holdings <http://enscobase.maich.gr/>
- WWW FAOSTAT: Agricultural statistics and data <http://www.faostat.fao.org/>
- WWW Gap Analysis Project: *Ex situ* gap analysis results of 13 crop gene pools
gisweb.ciat.cgiar.org/gapanalysis/
- WWW GENESYS: Global database of major *ex situ* gene bank holdings <http://www.genesys-pgr.org/>
- WWW Global Biodiversity Information Facility: <http://www.gbif.org/>
- WWW Inter-American Biodiversity Information Network (IABIN):
<http://www.oas.org/en/sedi/dsd/iabin/>
- WWW Harlan and de Wet Global Priority CWR Inventory: Global checklist and database of priority CWR taxa in 173 crop gene pools <http://www.cwrdiversity.org>
- WWW IUCN Red List: Database of red list (extinction threat) assessments
<http://www.iucnredlist.org/>
- WWW JSTOR: herbariaHerbaria resources <http://plants.jstor.org/>
- WWW Kew Bibliographic Databases: provides a link to the Kew Record of Taxonomic Literature, Economic Botany and Plant Micromorphology
<http://kbd.kew.org/kbd/searchpage.do>
- WWW Mansfeld's World Database of Agricultural and Horticultural Crops: Global database of crop related information <http://mansfeld.ipk-gatersleben.de/>
- WWW Plant list: Working list of all known plant species <http://www.theplantlist.org/>
- WWW Tropicos (Missouri Botanical Gardens, USA): Herbaria resources
<http://www.tropicos.org>
- WWW US Genetic Resources Information Network (GRIN): Database of USDA *ex situ* gene bank holdings http://www.ars-grin.gov/npgs/acc/acc_queries.html

WWW

Gazetteers and other ways of searching place names:



Chambers (1988) Chambers World Gazetteer: An A-Z of Geographical Information. 5th edition. Larousse Kingfisher Chambers, London.



Times Books (1999) Atlas of the World, ed. 10. Times Books, London.

WWW Google Maps: <http://maps.google.com>

WWW BioGeomancer: <http://www.biogeomancer.org/software.html>

WWW GeoNames: <http://www.geonames.org/>

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

WWW Global Gazetteer Version 2.2: <http://www.fallingrain.com/world/>; Falling Rain Genomics, 2010



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



GEOLocate: <http://www.museum.tulane.edu/geolocate/>

GIS software:

WWW BGIS (Biodiversity GIS) - The main SANBI resource for GIS with interactive mapping, biodiversity data, training and legislation:
<http://bgis.sanbi.org/index.asp?screenwidth=1366>



Arc-GIS /Arc info: www.esri.com



DIVA-GIS (geographic information system software, tutorials, documentation, spatial data, discussion forum): <http://www.diva-gis.org/> (freely available)



GRASS GIS: grass.osgeo.org (freely available)



gvSIG: www.gvsig.org/web (freely available)



IDRISI: www.clarklabs.org



Marxan: www.uq.edu.au/marxan



R: www.r-project.org (with some GIS functionalities)

A.7. Novel threat assessment of priority CWR

A.7.1. Overview

Why is threat assessment part of CWR conservation?

CWR are like any other wild plant species they are increasingly subject to anthropogenic threats and as a result suffer genetic erosion and even extinction. Yet the genetic erosion and extinction of these species has direct economic and social impact on humankind; if their genetic diversity is unavailable for exploitation humankind is more food insecure. The process of CWR conservation if it is to be effective will require the collation of large and complex data sets to plan and implement the conservation. Once collated these conservation data sets, which are the same as are required for threat assessment, may also be used for ancillary threat assessment. Therefore, novel threat assessment can run parallel to conservation planning and implementation and in fact be used to further prioritise / enhance the CWR conservation.

Part of the process of selecting priority CWR for conservation action involves the collation of existing information on the relative degree of threat to the CWR in the national checklist (see section A4.2). At this stage, it is rarely the case that resources would be available to undertake novel threat assessment of all the CWR in the checklist; however, once the priority CWR have been selected on the basis of their utilization potential and existing information on their relative threatened status (whether based on published Red List assessments or using proxy measures such as known pressures on their habitats) of priority taxa for which the threatened status is currently unknown may be undertaken. This will help to identify taxa in greatest need of immediate conservation action, understand more about their specific conservation requirements, and establish a baseline for monitoring their threatened status over time.

The assessment of threat to diversity can be carried out at two levels: the individual taxon level (commonly species but also at infra-specific level) and the genetic level. Assessing the threatened status of individual taxa can assist in species prioritization for conservation—the most threatened species having higher conservation priority. Further, threats to a specific region may be assessed in relation to conservation planning (i.e. to identify areas with high numbers of threatened CWR), but in this case it would require undertaking a large amount of individual species assessments and comparing the levels of threats in different regions as there is no means of assessing all the species together in a particular area.

At the genetic level, genetic erosion and pollution threatening CWR should be examined because it can eventually lead to population and even taxon extinction. A decrease in genetic diversity availability means that genes and alleles will not be available for future exploitation which will obviously have an impact on future food security. Additionally, the loss of genetic diversity implies an inability of taxa to adapt to the rapid changes in environmental conditions the planet is undergoing and thus the lack of availability of particular adaptive elements of gene pools to develop new crop varieties able to withstand these new conditions.

The *IUCN Red List Categories and Criteria*⁵⁸ have been widely used (see <http://www.iucnredlist.org/>) for assessing species' extinction risk (or threatened status). They were developed to improve objectivity and transparency in the threat assessment process, and therefore to improve consistency and understanding among users. Assessment of the

⁵⁸ IUCN (2001)

threatened status of species using the IUCN Red List Categories and Criteria is essentially a two-step process⁵⁹:

1. Data of seven types are collated and documented: (i) taxonomic; (ii) distribution; (iii) population; (iv) habitat and ecology; (v) use and trade; (vi) threats; and (vii) conservation actions (see Box 35). These data are gathered from a number of sources, including taxon experts, published and grey literature, databases and websites.
2. The taxon is evaluated against the IUCN Red List Criteria and the Red List Category is selected.

There are five main Red List Criteria: (A) population reduction, (B) geographic range (see Box 35), (C) small population size and decline, (D) very small or restricted population and (E) quantitative analysis indicating the probability of extinction. Each main criterion includes a number of sub-criteria against which the species is evaluated (Table 3). If the species meets the criteria in at least one of the main classes, it is assigned one of the threatened categories, Critically Endangered (CR), Endangered (EN) or Vulnerable (VU). If the species meets the criteria in more than one main class, it is assigned the highest category of threat but the less threatened category according to the other criterion or criteria is also documented. If the species does not meet any of the criteria A–E needed to evaluate it as threatened, another category is selected; these are Extinct (EX), Extinct in the Wild (EW), Regionally Extinct (RE), Near Threatened (NT), Least Concern (LC), Data Deficient (DD) or Not Applicable (NA) (for definitions of the categories, see IUCN, 2001). Figure 13 is a schematic representation of the IUCN Red List Categories.

Box 35. Summary of data types collated to undertake CWR red list assessments

Taxonomy

- Nomenclature (taxon name, authority, synonyms etc.).
- Recent taxonomic changes, any current taxonomic doubts or debates about the validity or identity of the species, or issues of synonymy.
- Note of any subspecific taxa.
- Crop(s) the species is related to (common and scientific names) and information on the degree of relationship of the wild relative to the crop (where known) using the Gene Pool concept (Harlan and de Wet 1971) or Taxon Group concept (Maxted *et al.* 2006).

Distribution and occurrence

- A summary of the current information available for the geographic range of the species.
- Country occurrences (and sub-national unit(s) where applicable) recorded using built-in descriptors in IUCN's Species Information Service (SIS).
- Extent of occurrence and/or area of occupancy (see Box 36).
- A map showing the distribution of the species.

Population

- A summary of the information available for size and trend (i.e., increasing, decreasing or stable) of the overall population of the species. If the population is severely fragmented, this is also recorded.
- Information about sizes and trends of subpopulations or populations of subspecific taxa, or trends in particular areas of the species' range can also be included when available.

⁵⁹ Kell *et al.* 2012

- Where no quantitative information on population sizes or trends are available, if possible it is noted whether the species is common, abundant, or rare, etc. If there really is no information at all about the population, this should be noted.

Habitats and ecology

- A summary account of the suitable habitats and ecological requirements of the species, highlighting any potential traits that may of interest for crop improvement (e.g., drought resistance, salt tolerance).
- Comments on the area, extent and/or quality of habitat; in particular, whether the habitat is thought to be stable or declining.
- The habitat(s) in which the species occurs are also documented using IUCN's Habitats Classification Scheme.

Use and trade

- A summary account of the information available for any utilization and/or trade of the taxon (local, national and international trade).
- A note of any known or potential uses of the species as a gene donor for crop improvement.

Threats

- Major threats that have affected the species in the past, those that are affecting the species now, or those that are likely to affect the species in the future.
- The main reason for the threat, the scale of the threat, and the stress placed on the species are also recorded where the information is available.
- Threats are also documented using IUCN's Threats Classification Scheme.

Conservation

- Conservation actions currently in place (if any) and realistic actions needed to mitigate the threats causing declines (if any). This includes information on both *in situ* and *ex situ* conservation measures.
- Conservation actions are also documented using IUCN's Conservation Actions Classification Scheme.

Source: Adapted from Kell *et al.* (2012)

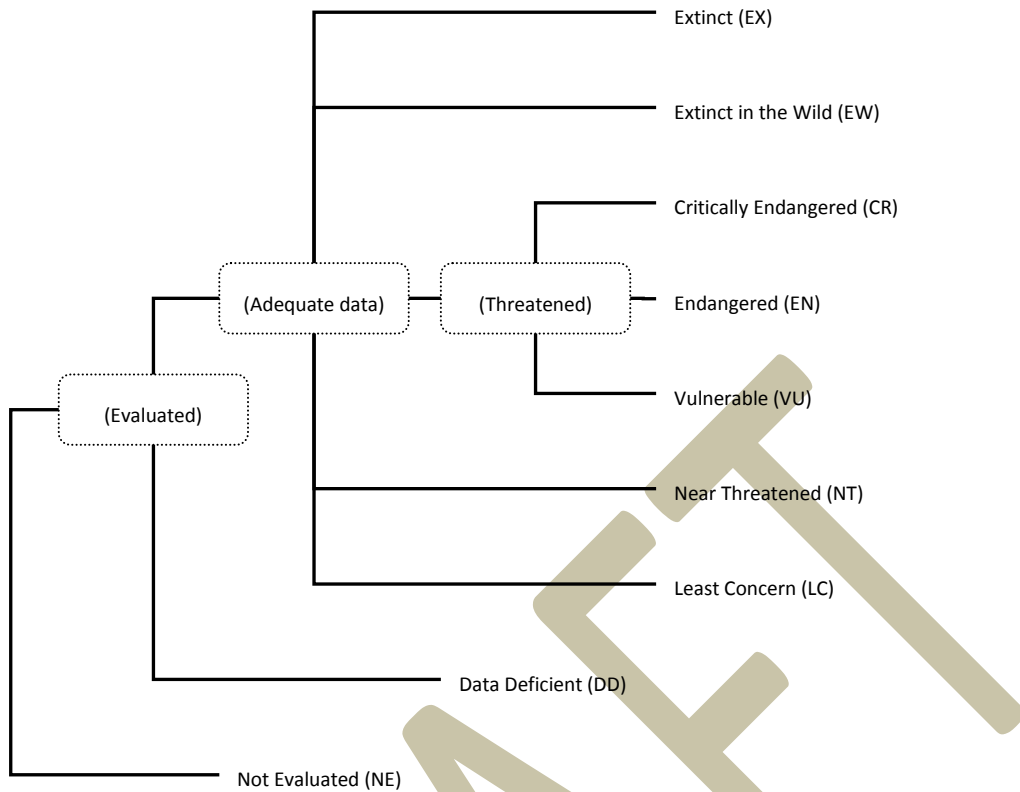


Figure 13. Structure of the IUCN Red List Categories⁵⁸

Given that national boundaries are irrelevant to wild populations, when a particular species goes beyond the limits of a geopolitical border, there might be genetic flow to or from other conspecific populations beyond that border; this will obviously affect the stability, hence the extinction risk of that species. Therefore, when the threatened status of a species is being assessed at national or regional level, unless that species is endemic to the nation or region, the thresholds under each criterion of the 2001 IUCN Red List Categories and Criteria will be erroneous because only part of the overall population of the species is being assessed. For example, taxa classified as Least Concern globally might be Critically Endangered within a particular region where numbers are very small or declining; and conversely, taxa classified as Vulnerable on the basis of their global declines in numbers or range might be Least Concern within a particular region where their populations are stable⁵⁸.

Box 36. Geographic range measurements used in IUCN Red List Criterion B

Location

“The term ‘location’ defines a geographically or ecologically distinct area in which a single threatening event can rapidly affect all individuals of the taxon present. The size of the location depends on the area covered by the threatening event and may include part of one or many subpopulations. Where a taxon is affected by more than one threatening event, location should be defined by considering the most serious plausible threat.”

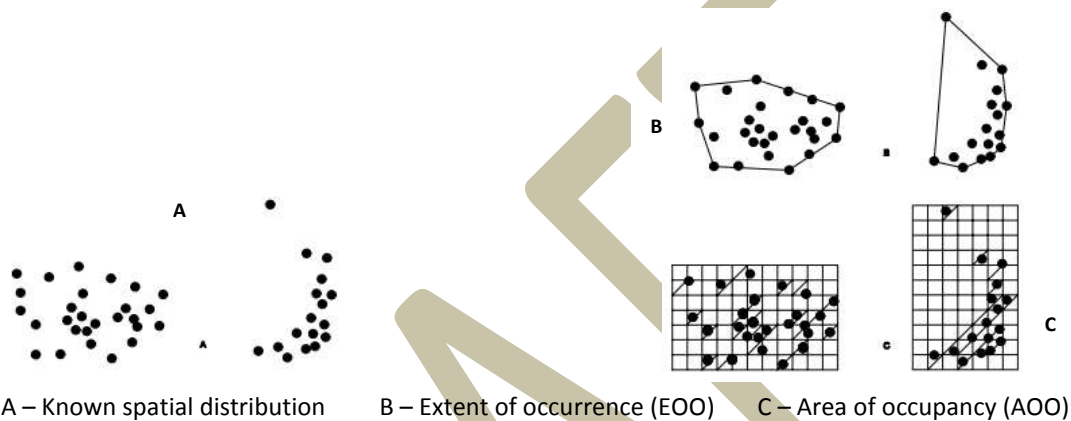
Extent of occurrence (EOO)

“Extent of occurrence is defined as the area contained within the shortest continuous imaginary boundary which can be drawn to encompass all the known, inferred or projected sites of present occurrence of a taxon, excluding cases of vagrancy. This measure may exclude discontinuities or

disjunctions within the overall distributions of taxa (e.g. large areas of obviously unsuitable habitat). Extent of occurrence can often be measured by a minimum convex polygon (the smallest polygon in which no internal angle exceeds 180 degrees and which contains all the sites of occurrence).” (See Figure below).

Area of occupancy (AOO)

“Area of occupancy is defined as the area within its 'extent of occurrence' (see above), which is occupied by a taxon, excluding cases of vagrancy. The measure reflects the fact that a taxon will not usually occur throughout the area of its extent of occurrence, which may contain unsuitable or unoccupied habitats. In some cases, (e.g. irreplaceable colonial nesting sites, crucial feeding sites for migratory taxa) the area of occupancy is the smallest area essential at any stage to the survival of existing populations of a taxon. The size of the area of occupancy will be a function of the scale at which it is measured, and should be at a scale appropriate to relevant biological aspects of the taxon, the nature of threats and the available data.” (See Figure below).



To take this into account, the *Guidelines for Application of IUCN Red List Criteria at Regional Levels*⁶⁰ were developed to re-assess the species’ risk of extinction in a particular region⁶¹ within the light of its overall distribution. However, when the regional population is isolated from conspecific populations, global criteria can be used without modification. The regional categories are the same as the global but there are two additional categories: Regionally Extinct (RE) and Not Applicable (NA). The category NA is applied for species whose population in the region only marginal or when a species is considered not to be native to the region. The regional assessments are the result of downgrades (or very rarely upgrades) from global assessments and they are based on a series of questions essentially concerning conspecific populations outside the region and the status of regional populations as sinks.

Table 3. IUCN Red List Categories and Criteria

Parameters of the subcriteria against which species are evaluated (*requires data from at least two time points)⁶² (For EOO = extent of occurrence; AOO = area of occupancy see Box 36).

⁶⁰ IUCN (2003)

⁶¹ ‘Region’ is defined by IUCN (2003) as any sub-global geographically defined area (e.g. continent, country, or province).

⁶² From Magos Brehm *et al.* (2008b)

Population reduction (% reduction over time)	Geographic range	Locations ⁶³	Extreme fluctuations	Population size	Decline	Biology
Past*	EOO	Number	EOO*	Number of mature individuals	AOO*	Seed dormancy/ viability
Present*			AOO*		EOO*	Generation time/ lifespan
Observed*, estimated*, projected*, inferred or suspected	AOO	Fragmentation	Mature Individuals*	Numbers at subpopulation level	Mature individuals*	Habit
			Number of locations*		Habitat quality*	Migration (how and where to and from)

Box 37. Alternative methods for threat assessment

The fact that IUCN Red List Assessment is so widely applied indicates its success, however it must be admitted that a significant amount of data is required to make a publishable assessment. The required data is by definition more readily available for highly studied species and for species found in areas where the flora is less well known applying the IUCN Red List Criteria is challenging or impossible. But these may be the species that most require Red Listing to aid conservation planning. Therefore where there are insufficient data available to assess a species using the IUCN Red List Categories and Criteria, alternative methods may be used.

An alternative approach was given by Burgman *et al.* (1995; 2000) who used the quantification of the number of observations (both herbarium specimens and germplasm accessions) in order to give an approximation of the taxon vulnerability assessment. However, their work was based on the assumption that threat and rates of material collection were directly related, which might not reflect the actual threat situation. Salem (2003) scored different attributes (status, commonness, life form and use) in order to calculate the conservation values for each species. The author then assigned a relative conservation rank to each taxon and calculated an average conservation value for the overall species within particular PA in order to establish priorities to allocate conservation efforts. While Maxted *et al.* (2004) used a point scoring method based on several criteria: rarity, distributional range, gross representation in *ex situ* collections, geographic coverage of *ex situ* collections, taxon coverage of *ex situ* collections, taxon utility, and taxon extinction assessment (based on Burgman *et al.* 1995).

Most recently Miller *et al.* (2012) compared two alternative methods to full IUCN Red List Assessment. The first NY method use the available georeferenced data to calculate the Extent of Occurrence (EOO) for all plant species in Puerto Rico, excluding unsuitable habitats like lakes, then all species with an EOO greater than 20,000km² (IUCN upper limit for a vulnerability assessment) were assigned to the “Not At Risk” category, and excluded from further study. For species with EOO values below the 20,000 km² threshold all specimens were georeferenced, so the georeferencing of common species was avoided. After georeferencing, EOO values were recalculated, and those species with EOO values above 20,000

⁶³ “The term ‘location’ defines a geographically or ecologically distinct area in which a single threatening event can rapidly affect all individuals of the taxon present. The size of the location depends on the area covered by the threatening event and may include part of one or many subpopulations. Where a taxon is affected by more than one threatening event, location should be defined by considering the most serious plausible threat.” IUCN (2001)

km² were considered “Not At Risk” and if EOO’s were still less than 20,000 km² species were categorized as “At Risk.” Thus the “At Risk” species that would be considered threatened under IUCN’s criterion B1. The second US method included four steps: Step one analyses the age of collections to determine how recently occurrence is documented, if a species has not been collected since 1900 it is considered to be “At Risk”. Step two assess geographic distribution by determining if species are known from six or more provinces or municipalities with an area greater than 9,000 km², or smaller individual islands and those known from six or more locations are considered to be “Not At Risk”, and remaining species documented from five or fewer locations continue on to step three. Step three assess rarity from the comparative abundance of herbarium specimens, determining whether a given species is represented by less than or equal to the median number of 28 specimens per species, so if a species is known from 28 or fewer specimens then it is “At Risk,” and if known from more than 28 specimens, it is analysed in step four. Step four assesses decline of a species by determining whether the species is known from less than or equal to the median number of 7 specimens collected since 1st January 1960 then the species may be in decline and is considered “At Risk”. The authors conclude that both methods are likely to over-estimate threat but while not replacing IUCN Red List Assessment do provide a quick, easy to apply methodology where full assessment datasets are and are likely to remain unavailable.

The process of novel threat assessment of CWR essentially consists of two main steps: (i) collation of relevant information for the assessment (see Box 35), (ii) evaluation of the taxon against the IUCN Red List Criteria and selection of the Red List Category. If the taxon is being assessed at regional (not global) level, a third step is to assess whether it is necessary to downgrade (or rarely to upgrade) the taxon’s Red List Category (see Figure 14).

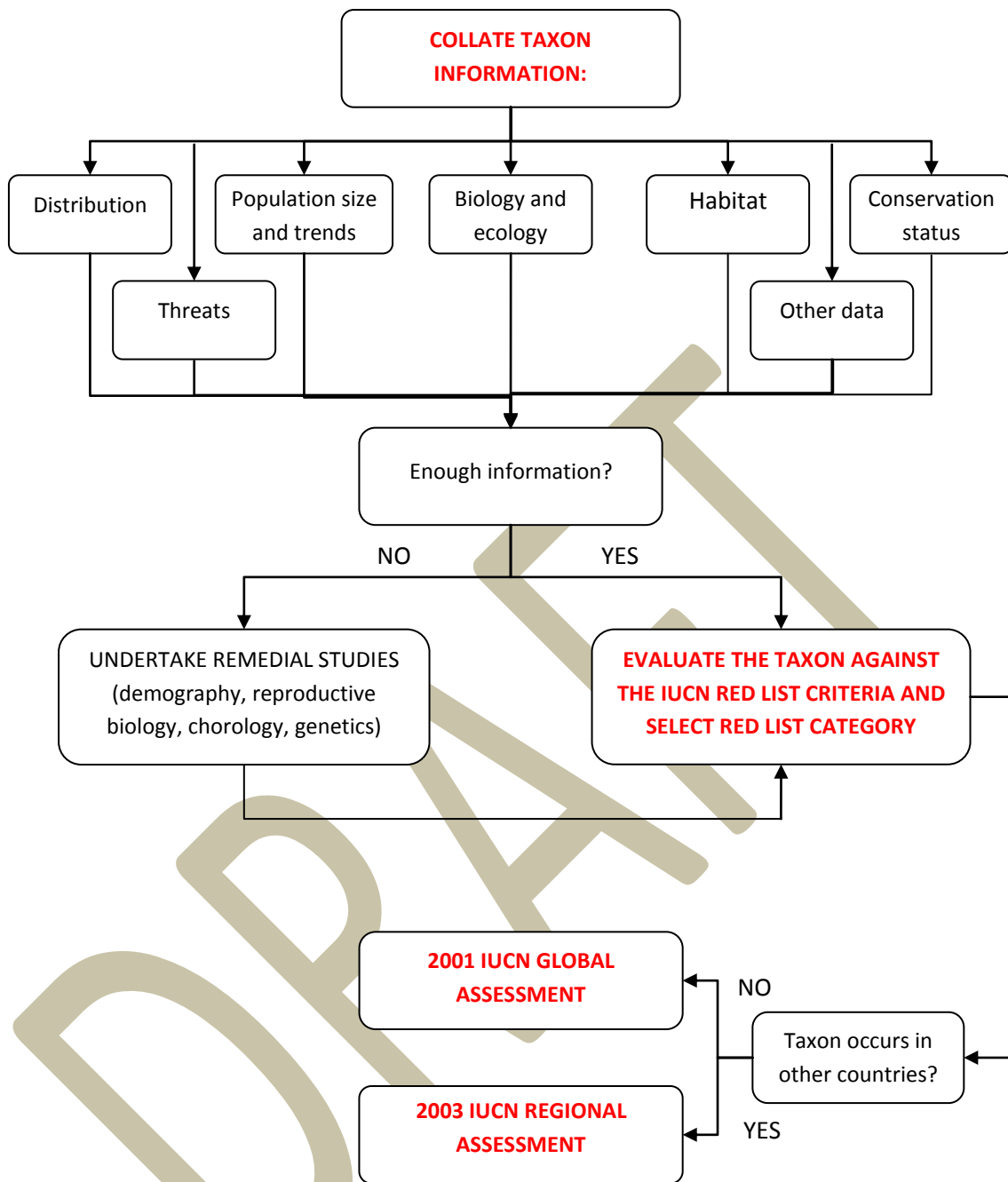


Figure 14. Novel threat assessment of CWR taxa

A.7.2. Methodology

Before undertaking Red List assessments using the IUCN Red List Categories and Criteria, users are advised to consult the IUCN Red List website for detailed information about the assessment process: <http://www.iucnredlist.org/technical-documents/assessment-process>. A range of training materials are also available at: <http://www.iucnredlist.org/technical-documents/red-list-training>. The basic process of undertaking Red List assessments is outlined below.

- (i) Collate taxon information. A literature, database, website, expert, herbarium and gene bank survey is undertaken in order to collect data on distribution, population size and trends, biology and ecology, habitat, conservation status, threats, etc. If needed and

possible, field data should also be obtained. See Box 38 for the limitations on using herbarium data in the Red List assessment process.

- (ii) Evaluation of the taxon against the IUCN Red List Criteria⁶⁴ and selection of the Red List Category. If the compiled data are insufficient to make a reasoned judgement about the threatened status of a taxon, the taxon is assessed as Data Deficient (DD). These species should be prioritised for further study in order to gather the required data. See 'Additional materials and resources' for tools that can be used to estimate some of the parameters needed to carry out Red List assessments.
- (iii) For regional assessments (e.g., national assessments of non-endemic species): collate relevant information about populations of the species in neighbouring countries. Information may be sourced from Red List assessments and conservation status data from the neighbouring countries, or from expert knowledge and available literature about the taxon. For a regional Red List assessment the taxon is subjected to a series of questions which aim to determine whether this taxon's Red List Category should remain the same, be downgraded or (rarely) upgraded from the global assessment (see Figure 14). For detailed guidance on the information required to undertake a regional Red List assessment, see Table 3 'Checklist for judging whether extra-regional populations may affect the extinction risk of the regional population' and Figure 15 'Conceptual scheme of the procedure for assigning an IUCN Red List Category at the regional level' in the IUCN Guidelines for Application of IUCN Red List Criteria at Regional Levels: Version 3.0⁶⁰. For plant populations, in most cases a regional assessment can be based on expert knowledge or on general knowledge of the taxon's breeding and dispersal system, combined with its distribution in the region.

Global Red List assessments (e.g., assessments of national endemic species) can be submitted for publication in the IUCN Red List of Threatened Species (see <http://www.iucnredlist.org/technical-documents/assessment-process>).

IUCN has developed the Species Information Service (SIS), which is web application and standalone database for conducting and managing species assessments for the IUCN Red List of Threatened Species. The system is intended for use by IUCN SSC Specialist Group members and other IUCN partners working on global Red List assessments as well as regional assessment initiatives led by IUCN. As such, access to SIS is controlled but where possible use of SIS will facilitate Red List assessment. For further information about using SIS, users should consult the IUCN Red List website where the relevant contact details can be found: www.iucnredlist.org/

Box 38. Use of herbarium data in red listing

Application of the IUCN Red List Categories and Criteria (IUCN 2001) requires the application of 'the best available evidence'. Often, for plants herbarium and gene bank collections provide the only source of information for the threat assessment and must therefore qualify as 'best available evidence' (Willis *et al.* 2003), even though they can provide little help in estimating population changes over time. Schatz *et al.* (2000) and Golding (2002) consider that these data are sufficiently reliable to enable conservation decisions. However, information provided by specimens can result in inconsistent Red List classifications because of the uncertainty associated with population and distribution parameters that arise from the decision rules of the IUCN Red List (IUCN 1994, 2001).

Information used in Red List assessments is interpreted from locality and habitat information contained on specimen labels to make best estimates, inferences and projections regarding distribution ranges,

⁶⁴ Available at <http://www.iucnredlist.org/technical-documents/categories-and-criteria>

scarcity and declines of species. When limited information is available, data often need to be extrapolated in order to make informed estimates, inferences and projections (Golding 2004). On the other hand, while collections made over the last 50 to 60 years usually provide data about scientific name, locality, habitat, ecology, date of collection, collector name and collector number, the historical specimens (before or early 20th century) may only contain few hand written details of the plant name, collector and locality and therefore may be of limited value to conservation assessments. MacDougall *et al.* (1998) refer to herbarium specimen sheets as a qualitative rather than quantitative data source. Locality coordinate data acquired from herbarium specimen data will often only provide an approximation of species distribution (Willis *et al.* 2003).

Therefore use of specimen passport information from a single population sampling should be regarded as provisional because it can result in an inaccurate assignment of Red List statuses of poorly known species, and consequently, influence conservation recommendations (Golding 2004). But despite the uncertainty these can be a good start in assessing species extinction risk.

Box 39. IUCN Red Listing linked to climate change susceptibility

Red Listing involves the collation of diverse data that may also prove useful for ancillary purposes, such as assessing climate change susceptibility. A methodology has recently been proposed that uses taxon-specific biological traits that are believed to be related to climate change vulnerability. They are: *A. Specialized habitat and/or microhabitat requirements.* Species with generalized and unspecialized habitat requirements are likely to be able to tolerate a greater level of climatic and ecosystem change. *B. Narrow environmental tolerances or thresholds that are likely to be exceeded due to climate change at any stage in the life cycle.* The physiology and ecology of many species is coupled to specific ranges of climatic variables (e.g. temperature, precipitation, pH and carbon dioxide levels) and those with narrow tolerance ranges are more susceptible. *C. Dependence on specific environmental triggers or cues that are likely to be disrupted by climate change.* Many species rely on environmental triggers or cues for seed germination, spring emergence and a range of other essential processes, vulnerability to changes in the magnitude and timing of these cues is associated with greater susceptibility. *D. Dependence on interspecific interactions that are likely to be disrupted by climate change.* Many species interact with symbionts, pollinators, seed dispersers and competitors and the more specific these interactions to more likely the susceptibility. *E. Poor ability to disperse to or to colonise a new or more suitable range.* In general, in response to climate change each species 'bioclimatic envelope' will shift pole-wards and to increasing altitudes, but species with low rates or short distances of dispersal are less able to migrate sufficiently fast to keep apace the shifting climatic conditions. Using expert assessments of these species traits groups of birds, amphibians and warm-water reef-building corals have been assessed – CWR next?
Source: Foden *et al.* (2009)

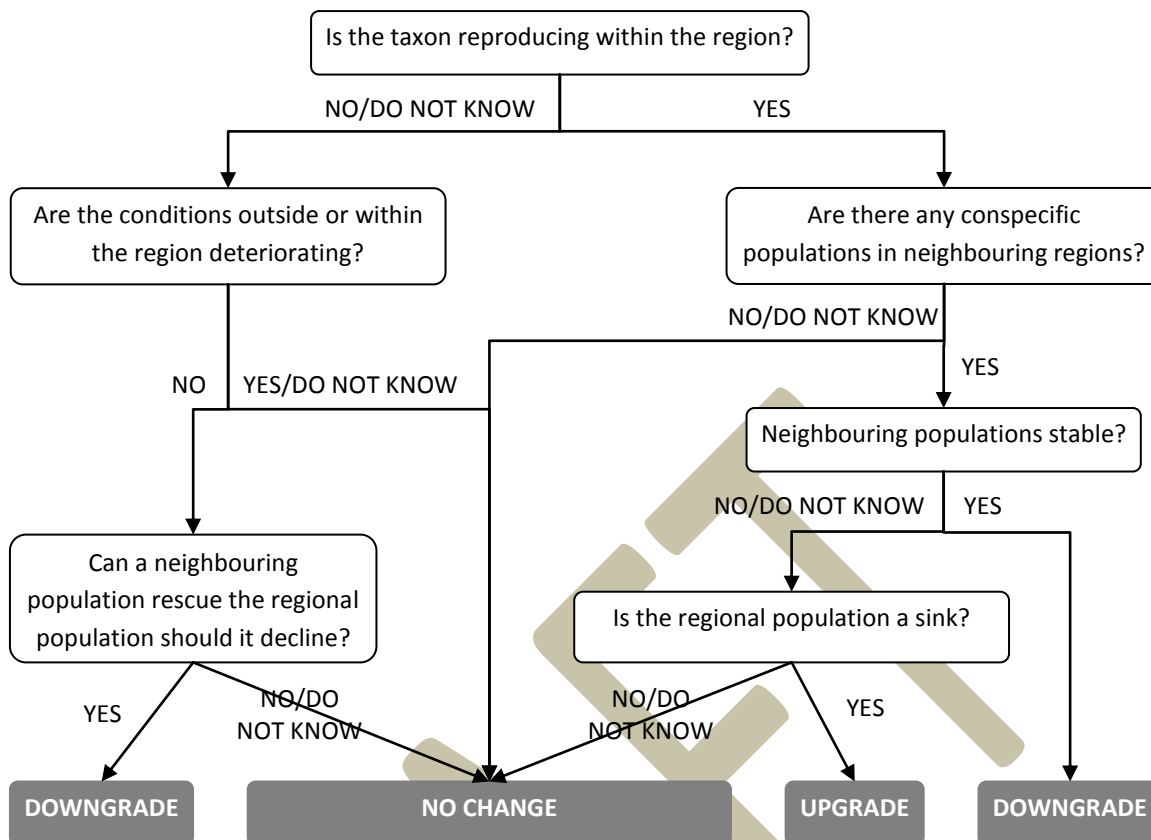


Figure 15. Basic scheme of how to undertake a regional Red List assessment⁶⁵.

A.7.3. Examples and applied use

Box 40. Red List Assessment of *Aegilops* spp. in Armenia

IUCN Red List Categories were obtained for nine *Aegilops* spp. in Armenia using ecogeographic survey data complemented with extensive field surveys. The ecogeographic survey was based on a herbarium survey following the model proposed by Maxted *et al.* (1995) and aimed at drafting the preliminary distribution of the target taxa as well as to plan the timetable and routes for field studies. Data collected during field surveys included: latitude, longitude, altitude, site description (including administrative unit and nearest settlement), conservation status of the area, average density (number of plants per unit of surface), approximate area occupied by each subpopulation, plant community, current and potential threats, growth stage and soil characteristics. The IUCN Red List Categories and Criteria (IUCN 2001) and the IUCN Guidelines for Application of IUCN Red List Criteria at Regional Levels (IUCN 2003). Area of occupancy (AOO) was generally calculated using a grid size of 4 km² except for those species known to have very small populations and limited range distribution in the country where a grid size of 1 km² was used. The result showed four threatened species: *Ae. mutica* Boiss. – CR, *Ae. crassa* Boiss. – CR or Ex(R)?, *Ae. neglecta* Req. ex Bertol. – EN, *Ae. biuncialis* Vis. – EN, *Ae. columnaris* Zhuk. – NT, *Ae. triuncialis* L. – LC, *Ae. cylindrica* Host – LC, *Ae. tauschii* Coss. – LC' and *Ae. umbellulata* Zhuk. – DD
Source: Harutyunyan *et al.* (2010)

⁶⁵ From Magos Brehm *et al.* (2008b) and adapted from IUCN (2003)

Box 41. European Red List of CWR

As part of an initiative to publish the first European Red List, regional assessments of 591 European CWR species in 25 priority crop gene pools/groups were undertaken (see Bilz *et al.* 2011, Kell *et al.* 2012). The assessment process involved the collaboration of more than 70 experts who have good knowledge of the national flora of their country and/or of a particular taxonomic group. A key part in the process was a five day Red List workshop involving 26 experts and a team of facilitators, during which many of the assessments were drafted. The remaining work was undertaken through email correspondence and completion and editing of the assessments was undertaken mainly by three members of staff of the coordinating institutes.

The assessment of a significant sample of European CWR provided a snapshot of the threatened status of these species in the region. At least 11.5% (66) of the species are considered as threatened, with 3.3% (19) of them being Critically Endangered, 4.4% (22) Endangered and 3.8% (25) Vulnerable—a further 4.5% (26) of the species are classified as Near Threatened. More than half of the species were regionally assessed as Least Concern; however, a significant proportion of these are threatened at national level. Regional data are lacking for many species and many are therefore currently regionally assessed as Data Deficient, indicating either a lack of knowledge about these species throughout their range or challenges in accessing the necessary information.

The study found that livestock farming has by far the greatest impact on CWR in Europe, followed by arable farming often associated with the use of herbicides and pesticides. However, it cannot be concluded from these results that all types of farming are threatening CWR diversity; in fact, farmed areas (including arable land and pasture) are one of the primary habitats of CWR species. It is intensive and unsustainable farming practices, such as severe overgrazing, conversion of land to monocultures and the over-use of fertilizers, herbicides and pesticides that are the major threats to CWR that grow in agricultural areas—this includes grazing in semi-natural habitats such as Mediterranean maquis (Kell *et al.* 2011). Development for tourism and recreation are also major threats to CWR in the region, particularly those restricted to coastal and mountainous areas, as well as islands. Other major threats include urban development, invasive alien species, transport infrastructure development, an increase in fire frequency or intensity (or sometimes also fire suppression), severe weather events, such as drought and flooding, and intensive forestry (including pollutants from forestry activities). The significance of climate change as a major threatening factor to European CWR is still to be accurately quantified.

Source: Bilz *et al.* (2011), Kell *et al.* (2012)

A.7.4. List of references used to compile the text

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A.7.5. Additional materials and resources

IUCN Red Listing:



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WWW IUCN Red List of Threatened Species – Assessment Process: <http://www.iucnredlist.org/technical-documents/assessment-process>

WWW IUCN Red List of Threatened Species – Red List Training: <http://www.iucnredlist.org/technical-documents/red-list-training>

WWW IUCN Red List of Threatened Species – References: <http://www.iucnredlist.org/technical-documents/references>

WWW IUCN Red List of Threatened Species – Classification Schemes:

<http://www.iucnredlist.org/technical-documents/classification-schemes>

WWW National Red Lists: Tutorials and case studies:
<http://www.nationalredlist.org/site.aspx?pageid=177>

Technical documents and tools for threat assessment (users should also consult the IUCN Red List website links given above):



Jiménez-Alfaro B, Draper D and Nogués-Bravo D (2012) Modelling the potential area of occupancy at fine resolution may reduce uncertainty in species range estimates. *Biological Conservation* 147: 190-196.



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Analysis Tool for Geospatial Red List Species Assessment (GeoCAT):
<https://sites.google.com/site/rlatkew/>.

The GIS Unit of the Royal Botanic Gardens, Kew has been developing this on-line tool that allows the user to calculate the Extent of Occurrence (EOO) and Area of Occupancy (AOO) needed in the IUCN Red Listing:

- Pick a species to assess or create a new project from scratch,
- Upload your own occurrence data e.g. coordinates of specimens, field observations or plot samples from an existing dataset,
- Manually add/edit occurrence points to the map and edit based on your own knowledge,
- Import occurrence data from on-line sources such as GBIF or Flickr,
- Single-click analysis of Extent of Occurrence (EOO) (using a convex hull) and Area of Occupancy (AOO) (using a grid system),
- Visualise your results on Google Earth,
- Download occurrence data used in the analysis,
- Save your project and add more data later or share with partners in a collaboration,
- View and save all the vital statistics as a mini-report.



NOTE: This tool hasn't been yet recognised by IUCN because there are few improvements needed but they seem to be supportive (Steven Bachman pers. comm.).



GeoCAT demo: http://www.youtube.com/watch?v=eyVHLQy8F_0

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Project Crop Wild Relatives and Climate Change: <http://www.cwrdiversity.org/home/>

A.8. Gap analysis of priority CWR

A.8.1. Overview

What is CWR gap analysis?

Gap analysis is a conservation evaluation technique that assists the prioritization of biodiversity elements for conservation action by identifying ‘gaps’ in the conservation of those elements⁶⁶. Practically, all gap analysis, including that for CWR, involves a comparison between the range of natural diversity and that diversity already effectively represented by current *in situ* conservation actions (*in situ* gap analysis) and all accessions of the target CWR represented in gene bank collections (*ex situ* gap analysis).

There is now an extensive literature associated with gap analysis which essentially identifies areas in which selected elements of biodiversity are under-represented⁶⁷. 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 cited⁶⁸. A systematic gap analysis methodology for identifying gaps in species or genetic diversity conservation has been developed and illustrated with the case study for African *Vigna* wild relatives and LR which aimed at evaluating the effectiveness of current *in situ* and *ex situ* conservation, identifying the ‘gaps’, hence assisting the development of conservation strategies for African *Vigna* genetic resources⁶⁹. More recently, an *ex situ* gap analysis methodology based on GIS tools has been developed for crop gene pools⁷⁰.

The results of genetic diversity and ecogeographic analysis, as well as novel threat assessment (see sections 5, 6 and 7 respectively) provide the information needed to identify gaps in current *in situ* and *ex situ* conservation actions for CWR. Figure 17 summarises how these analyses feed into a gap analysis study.

Conservation gaps (both *in situ* and *ex situ*) can be detected at different levels: (i) Individual CWR taxon level (CWR taxa not conserved *versus* taxa conserved), (ii) Ecogeographic level (for a particular CWR, areas/environmental conditions not covered by *in situ* or *ex situ* conservation activities *versus* those covered), (iii) Trait level (specific CWR populations that present a particular interesting trait that are not conserved *versus* populations with that same trait that are), (iv) Genetic diversity (specific CWR populations that are genetically important that are not conserved *versus* those that are). The level(s) at which gap analysis can be undertaken depends on the types of data available for the study. It should be highlighted that 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’ genetic information, ecogeographic diversity information can be used as a proxy.

The result of an *in situ* gap analysis is the identification of *in situ* conservation priorities, while the result of an *ex situ* gap analysis is the identification of additional CWR germplasm collections required. Figure 17 illustrates the basic *in situ* and *ex situ* gap analysis methodology.

⁶⁶ Noss and Cooperrider (1999), Eken *et al.* (2004), Rodrigues *et al.* (2004), Langhammer *et al.* (2007)

⁶⁷ 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)

⁶⁸ See Ingram and Williams (1993)

⁶⁹ See Maxted *et al.* (2008b)

⁷⁰ Bioversity International *et al.* (2009) and also see R-package GapAnalysis available at: http://r-forge.r-project.org/R/?group_id=645

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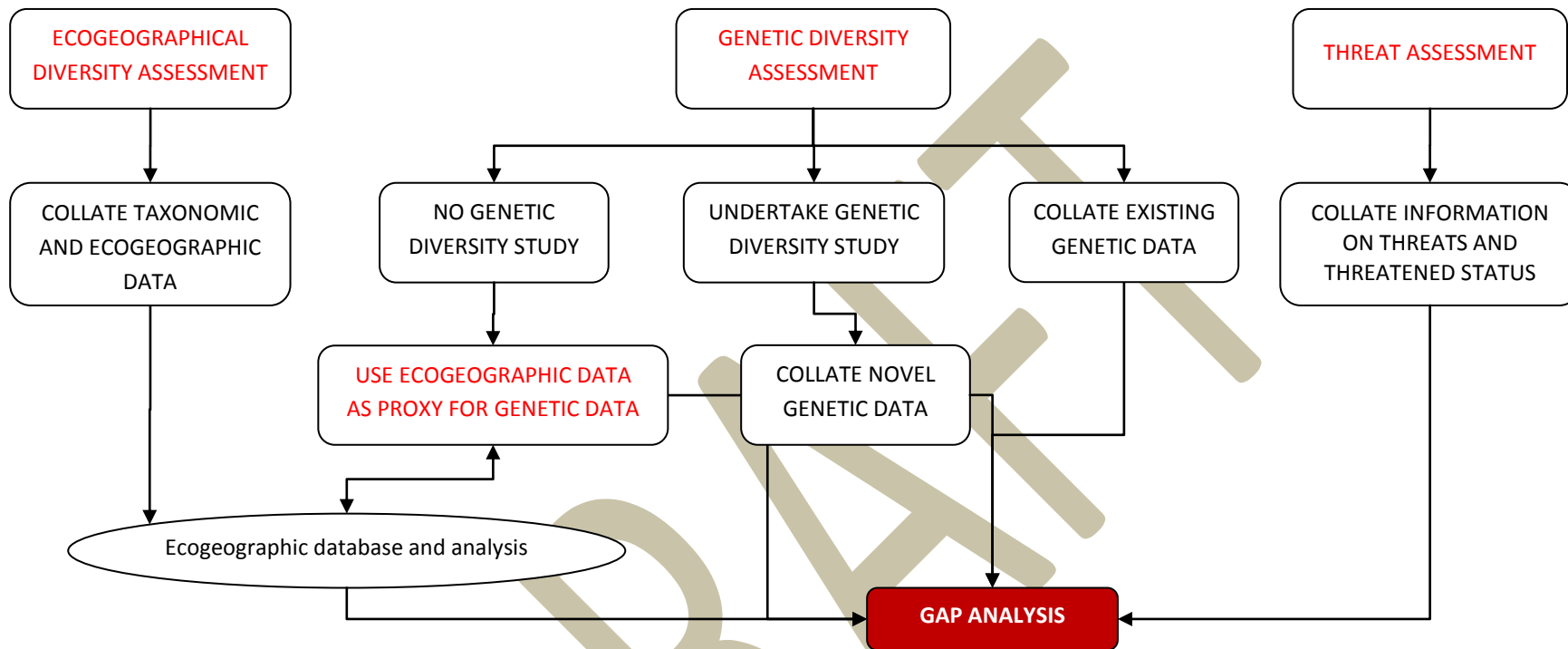


Figure 16. Ecogeographic, genetic and threat assessment aiding gap analysis

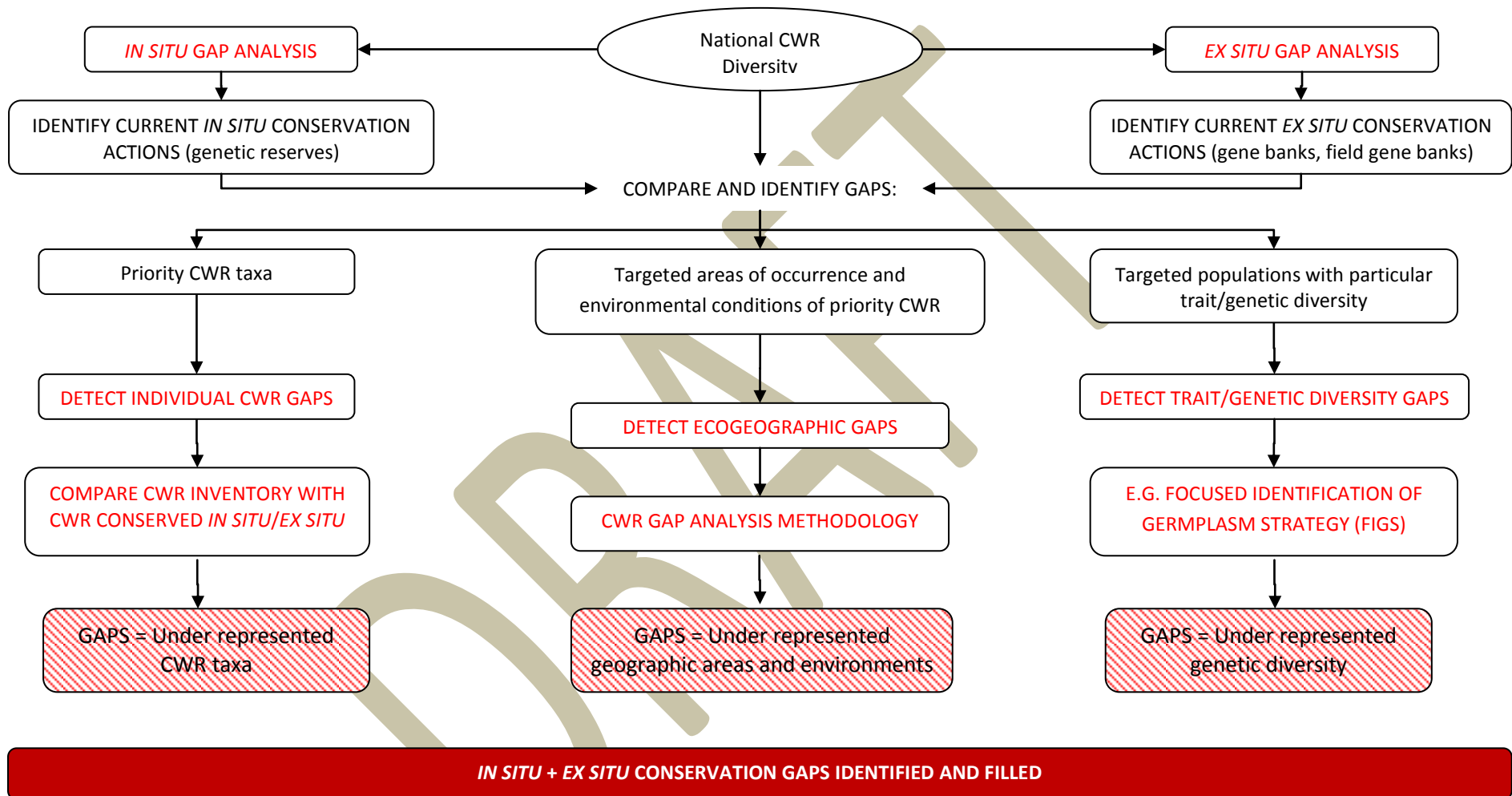


Figure 17. CWR diversity *in situ* and *ex situ* gap analysis methodology

A.8.2. Methodology

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

Individual CWR level: whether the target CWR taxa are adequately represented by *ex situ* accessions or active *in situ* conservation.

- (i) *In situ:* Compare CWR taxon diversity with *in situ* activities to detect priority CWR not actively conserved adequately using *in situ* techniques; GAPS = CWR taxa not actively conserved *in situ* (see Box 41).
- (ii) *Ex situ:* Compare CWR taxon diversity with *ex situ* accessions held in gene banks and field gene banks, via direct contact to gene banks or via on-line databases (e.g. EURISCO, GENESYS, Singer), in order to detect CWR not actively conserved adequately using *ex situ* techniques; GAPS = CWR taxa not conserved *ex situ*.

Ecogeographic level: whether the whole ecogeographic range of the CWR is represented *in situ/ex situ*. Ecogeographic diversity can be used as an indicator of genetic diversity, the assumption being that the conservation of maximum ecogeographic diversity will result in the conservation of maximum genetic diversity. Characterizing populations according to the environmental conditions in which they grow can also help to identify useful abiotic traits such as extreme temperatures, drought, etc.

- (i) *In situ:* Compare ecogeographic CWR diversity and where it is conserved *in situ* will help target new *in situ* activities. GAPS = CWR ecogeographic areas not already covered by *in situ* activities.
- (ii) *Ex situ:* Compare ecogeographic CWR diversity and where diversity has previously been collected will help target further collections. GAPS = CWR ecogeographic areas where collection has not previously been made, See Figure 18⁷¹.

⁷¹ Bioversity International *et al.* (2009)

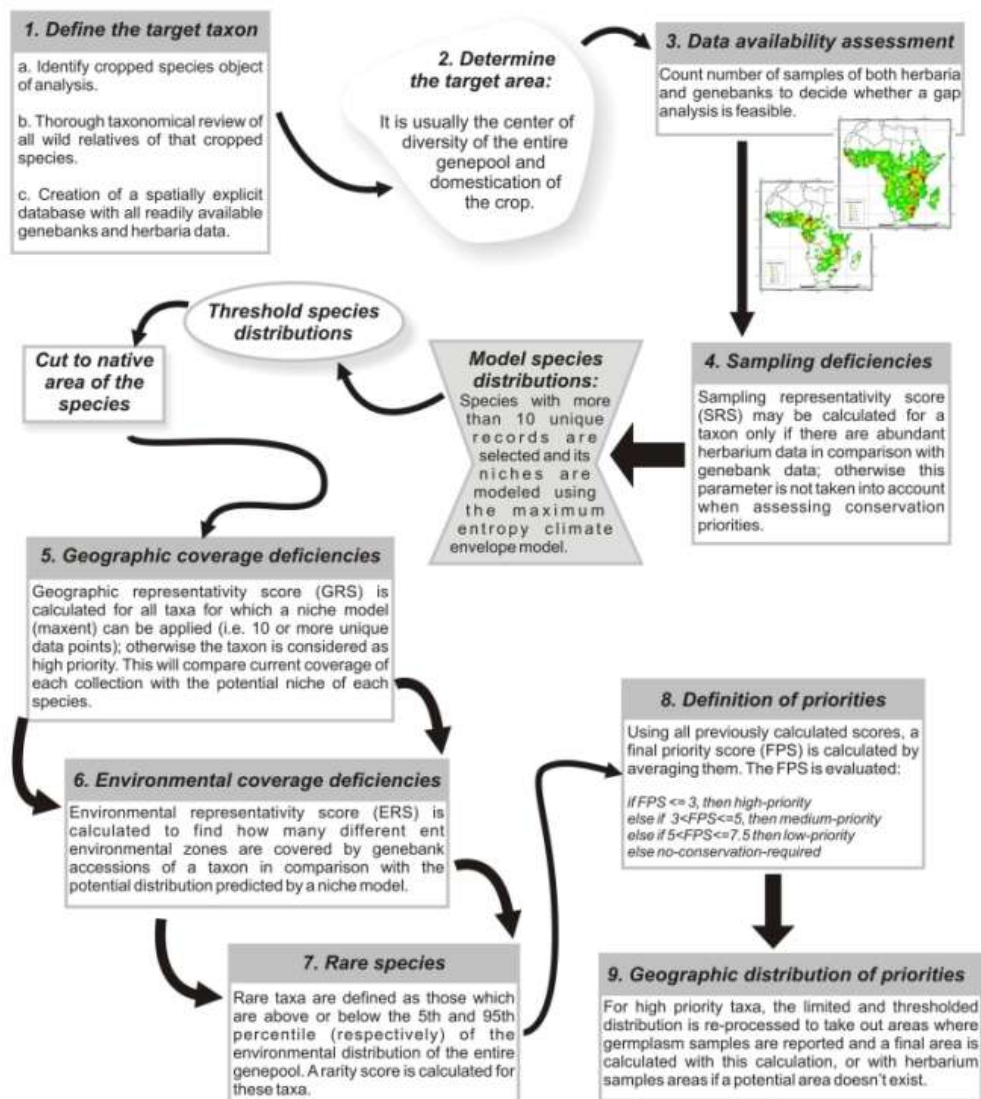


Figure 18. CWR *ex situ* gap analysis methodology at ecogeographic level⁷²

Trait level: whether specific CWR populations that contain a particular interesting trait (e.g. high gluten content, etc.) are conserved *in situ/ex situ* adequately.

- In situ*: Compare CWR natural distribution together with trait diversity data and where it is actively conserved will help target new *in situ* activities. GAPS = specific CWR populations with the trait of interest not conserved *in situ*.
- Ex situ*: Compare CWR natural distribution together with trait information and where it has been previously collected will help target further collections. GAPS = specific CWR populations with the trait 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) (see Box 42). Focused Identification of Germplasm Strategy (FIGS) is a predictive characterisation technique and can be used in this context. The basic FIGS approach is as follows:

⁷² Ramírez-Villegas J. Gap analysis. Available from: <http://www.slideshare.net/laguanegna/castaneda2010-gapanalysis> [Accessed January 2012].

- Compile the geographic distribution of the target CWR;
- Gather the available evaluation data regarding the biotic or abiotic trait of interest and georeference;
- Gather environmental information (e.g. climate, soil, elevation, topography) (see ‘Additional materials and resources’ for sources of data) and extract environmental data for each CWR accession/population using a GIS software (e.g. DIVA-GIS);
- Utilise the existing characterization and evaluation data to identify sites where required variation exists;
- Produce site profiles 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.

An alternative FIGS approach can be used to target abiotic traits which do not make use of existing trait evaluation data but is based on collecting information on the environmental conditions most likely to support the adaptive development of the target traits⁷³. This approach can be used when insufficient trait evaluation data are available for the analysis.

<i>In situ</i>	<i>Ex situ</i>
----------------	----------------

Box 42. GIS-based predictive characterization

Predictive characterization is a means of identifying CWR *in situ* populations/*ex situ* accessions likely to contain desirable traits (e.g. insect pest resistance). Focused Identification of Germplasm Strategy (FIGS) is a technique of predictive characterization that can be used for that purpose. 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 stress (e.g. pest and diseases) for which resistance is being sought, in order to create environmental profiles of the habitats in which a given population (genotype) evolved. The analysis 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 the FIGS methodology can thus aid breeders’ selection in identifying *in situ* populations or *ex situ* accessions of CWR most likely to contain the traits of interest.

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

⁷³ Thormann (2012)

Genetic level: whether specific CWR populations that contain genetic diversity of interest (e.g. high genetic diversity) are not conserved *in situ/ex situ*.

- (i) *In situ*. A comparison between CWR natural distribution together with genetic diversity data and which populations are actively conserved will help target new *in situ* activities. GAPS = specific populations with genetic diversity not conserved *in situ*.
- (ii) *Ex situ*. A comparison between CWR natural distribution together with genetic diversity data and where the taxon has been previously collected will help target further collections. GAPS = specific populations with genetic diversity not conserved *ex situ*.

The following should be noted while *in situ* gap analysis is being carried out:

- If the species distribution locations have different levels of geographic precision, only the most accurate should be used (from Table 2 use the levels of precision from 1 to 3) (Figure 19);
- If there is no digitized information on the distribution of PA or regarding the taxa that occur within them, then species distribution modelling could be performed in order to obtain maps of predicted distribution (Figure 20). See Box 42 for more information on the methods available for modelling species distribution. Field confirmation should be carried out in order to know which taxa occur within PA. It should be noted that field confirmation needs to consider access permission in formal PA, private land and ethnological important areas (e.g. “sacred forests” or Indian reservations).
- Regardless of the level of *in situ* gap analysis (individual CWR, ecogeographic, trait or genetic level), it should also identify the populations that: (i) do not occur within PA (GAPS = specific populations not conserved in situ), and (ii) do occur in PA but that are only passively protected without any specific management (GAPS = specific populations within PA but not actively conserved in situ) (Figure 20).

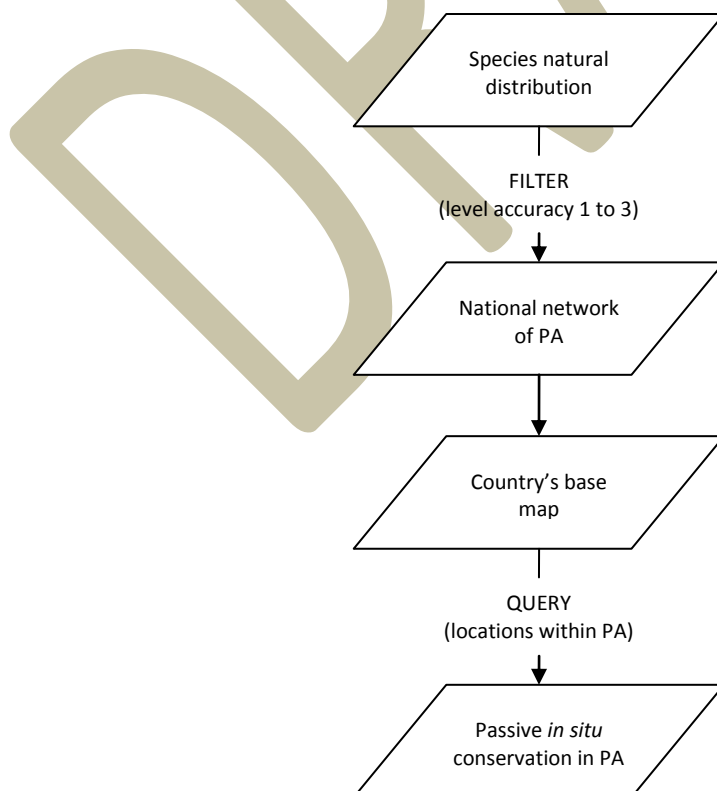


Figure 19. Schematic representation of the *in situ* gap analysis process

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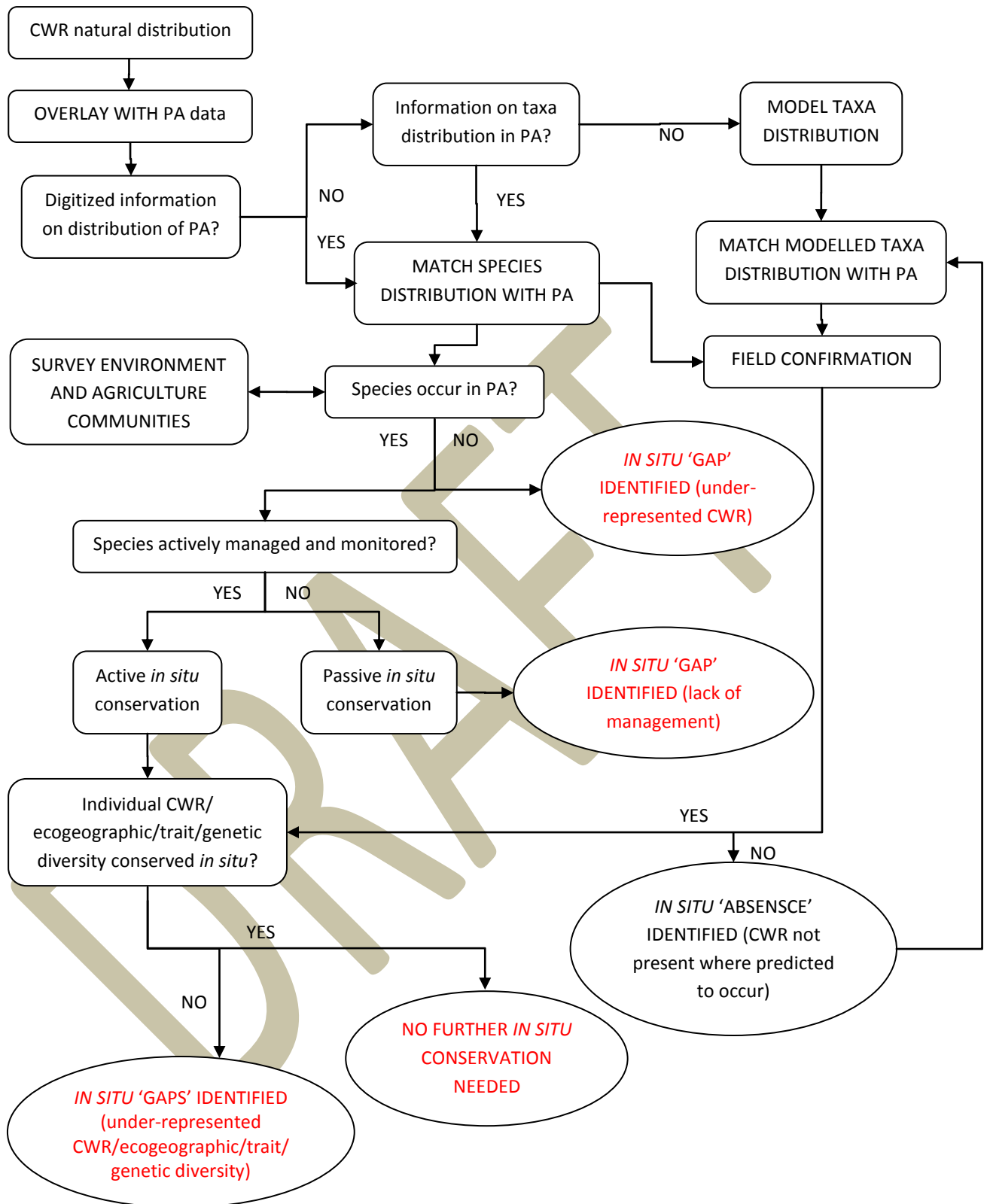


Figure 20. *In situ* gap analysis of CWR diversity

Box 43. Species distribution models

Species distribution models (SDM) are useful tools to predict potential areas of distribution. They have been commonly used to answer questions related to ecology, evolution and conservation (Elith *et al.* 2006). Regarding conservation, SDM have been employed to aid conservation decisions (e.g. Dockerty *et al.* 2003, Midgley *et al.* 2003), to direct field surveys towards locations where taxa are likely to be found (e.g. Engler *et al.* 2004), to establish baseline information for predicting a species' response to landscape alterations and/or climate change (e.g. Huntley *et al.* 1995, Beaumont and Hughes 2002, Thuiller 2003, Thomas *et al.* 2004, Hijmans and Graham 2006), to identify high-priority sites for conservation (e.g. Araújo and Williams 2000, Loiselle *et al.* 2003).

There is a wide range of methods for modelling species' distribution. These include classification and regression trees (CART) (e.g. Breiman *et al.* 1984), generalized linear models (GLM) (McCullagh and Nelder 1989), generalized additive models (GAM) (Hastie and Tibshirani 1990), climatic envelope models (CEM) (e.g. BIOCLIM) (Busby 1991), Gower-similarity models (e.g. DOMAIN) (e.g. Carpenter *et al.* 1993), artificial neural networks (ANN) (e.g. Mastorillo *et al.* 1997), ecological niche factor analysis (ENFA) (e.g. Hirzel *et al.* 2001, freely available from <http://www.unil.ch/biomapper>), generalized dissimilarity models (GDM) (e.g. Ferrier 2002), and maximum entropy models (e.g. MaxEnt by Phillips *et al.* 2006, freely available from <http://www.cs.princeton.edu/~schapire/maxent/>). These models vary in how they model distribution responses, select relevant climatic parameters, define fitted functions for each parameter, weight different parameter contributions, allow for interactions and predict geographic patterns of occurrence (Guisan and Zimmerman 2000, Burgman *et al.* 2005). See Brotons *et al.* (2004), Segurado and Araújo (2004) and Elith *et al.* (2006) for detailed reviews and comparison of existing modelling methods, and Thuiller *et al.* (2005) for discussion on the ecological principles and assumptions of each model as well as their limitations and decisions inherent to the evaluation of these models.

A.8.3. Examples and applied use

Box 44. Individual CWR gap analysis – *Aegilops* spp.

Existing geo-referenced passport data associated with 22 *Aegilops* species were used to identify gaps in current conservation and to develop a global conservation strategy for the genus. Sources of taxonomic, ecological, geographic and conservation information included: ICARDA, EURISCO, GRIN and SINGER datasets. The ecogeographic database contained 9866 unique geo-referenced observations collected between 1932 and 2004. Distribution maps as well as predicted distribution using climatic models were obtained and compared in individual taxon conservation gap analyses using ArcGIS and DIVA-GIS. Species priorities were assigned based on *ex situ* conservation status, highest priority given to *Ae. bicornis*, *Ae. comosa*, *Ae. juvenalis*, *Ae. kotschyi*, *Ae. peregrina*, *Ae. sharonensis*, *Ae. speltoides*, *Ae. uniaristata* and *Ae. vavilovii*. Future *ex situ* collections were recommended, namely in Cyprus, Egypt, Greece, Iran, Israel, Libya, Spain, Syria, Tajikistan, Tunisia, Turkey, Turkmenistan and Uzbekistan.

In addition, patterns of species richness were obtained and five complementary regions of *Aegilops* diversity were identified in west Syria and north Lebanon, central Israel, north-west Turkey, Turkmenistan and south France for *in situ* conservation. Within these areas, 16 IUCN-designated PA were identified as potential sites to establish genetic reserves. However, the most important identified area (on the Syrian/Lebanese border) does not coincide with any existing formal PA, thus, a novel PA needs to be established.

Source: Maxted *et al.* (2008c)

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

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A.8.5. Additional materials and resources

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WWW Examples of CWR gap analyses (*Cajanus*, *Cicer*, *Eleusine*, *Hordeum*, *Lens*, *Pennisetum*, *Phaseolus*, *Sorghum*, *Triticum* and *Aegilops*, *Vicia*, *Vigna*, *Zea* gene pools). Available at: <http://gisweb.ciat.cgiar.org/GapAnalysis/?cat=5>

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



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

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

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

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

Biodiversity occurrence data:

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

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

Environmental data:

WWW Bioclimatic variables: WorldClim – Global Climate Data: <http://www.worldclim.org/>

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

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

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

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WWW BioGeomancer: (<http://www.biogeomancer.org/software.html>)

WWW GeoNames: <http://www.geonames.org/>

WWW Getty Thesaurus of Geographic Names
(http://www.getty.edu/research/conducting_research/vocabularies/tgn/)

WWW Global Gazetteer Version 2.2 (<http://www.fallingrain.com/world/>; Falling Rain Genomics, 2010)



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Ecological niche factor analysis (ENFA): <http://www.unil.ch/biomapper>



MaxEnt (predictive distribution software, tutorials, documentation, discussion forum): <http://www.cs.princeton.edu/~schapire/maxent/> (freely available), <http://homepages.inf.ed.ac.uk/lzhang10/maxent.html> (MaxEnt tutorials and related papers)



Open Modeller (ecological niche modelling library to model species distribution with various algorithms): <http://openmodeller.sourceforge.net/> (freely available)

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A.9. Establishment of *in situ* conservation goals

A.9.1. Overview

What are the in situ conservation goals of a National CWR Conservation Strategy?

A National CWR Conservation Strategy aims in part to establish a national network of *in situ* conservation sites where long-term active conservation (in order to safeguard their genetic diversity) and sustainable use of CWR is carried out as a contribution to national, regional and global food security. Active *in situ* conservation is backed-up with the periodic resampling of CWR populations for *ex situ* collections, which also helps promote sustainable exploitation.

The establishment of *in situ* conservation goals for national CWR diversity involves five main steps (Figure 21): (i) review of *in situ* conservation gaps, (ii) preliminary selection of *in situ* CWR conservation sites, (iii) incorporation of threat data into the preliminary site selection, and (iv) provisional selection of sites for the target CWR.

In situ CWR conservation sites may be set up for individual or multiple CWR taxa. Sites that are established for the conservation of more than one taxon has obvious advantages in terms of the use of limited conservation resources; however, it will not always be possible to establish multi-CWR sites because some priority taxa may only occur in sites where no other priority CWR are found. However, the balance between whether to establish single or multi-CWR *in situ* CWR conservation sites will ultimately depend on the financial and human resources available for and allocated to CWR conservation. The resources dedicated to conservation, and especially to the conservation of PGR, are a crucial limitation to the development of targeted actions and management plans that permit the efficient conservation and utilization of CWR.

Before beginning to plan the national network of CWR *in situ* CWR conservation sites, gaps in current *in situ* conservation of CWR should be identified and taken into consideration (see section A8, 'Gap analysis of priority CWR'). When no *in situ* CWR conservation activities exist at national level, a preliminary selection of genetic reserves should be carried out based solely on the results of the ecogeographic and genetic diversity analysis of priority taxa. When *in situ* conservation activities do exist (they are likely to be passive—in other words, populations of CWR which occur in protected areas but which are not actively managed to maintain their genetic diversity), a preliminary selection of sites should be carried out based on the results of the gap analysis, combined with the ecogeographic and genetic diversity analysis (see Figure 21).

When selecting sites for inclusion in the genetic reserve network, it is critical to take into account potential threats to the sites and/or CWR populations occurring at the sites. Threats may be wide-ranging and can include those that are the direct result of human actions (e.g., changes in land use or site management) to those that are the indirect result of human actions which are largely out of the control of those responsible for the management of the site (e.g., the environmental effects of climate change or catastrophic events such as floods or landslides). Given knowledge of land ownership, use and management, combined if possible with an analysis of potential natural threats affecting the sites (e.g., through climate modelling), a pragmatic approach has to be taken giving priority to those sites whose habitat suitability for the target CWR is predicted not to be altered significantly in the medium to long term.

The establishment of *in situ* CWR conservation sites will often occur within existing protected areas (PA), in which case the PA management plan is amended to facilitate the conservation of the target CWR's genetic diversity. The reasons being: (a) these sites already have an

associated long-term conservation ethos and are less prone to hasty management changes associated with private land or roadside (where conservation value and sustainability is not a consideration), (b) it is relatively easy to amend the existing site management to facilitate genetic conservation of CWR species, and (c) it means creating novel conservation sites can be avoided, so the possibly prohibitive cost of acquiring previously non-conservation managed land is avoided⁷⁴. Therefore often the simplest, most practical way forward in economic and political terms is for countries to locate *in situ* CWR conservation sites in existing protected areas as genetic reserves. It is also thought that the establishment of genetic reserves is likely to provide at least indirect benefit to local people and so is also likely to engender their support.

It is important to note that the vast majority of PAs in any country are likely to contain some CWR populations; however, these PAs have probably been established to target specific landscapes, habitats or fauna, not CWR diversity. Therefore, in most cases the management of CWR within existing PAs is passive (i.e., without any formal management or monitoring plan⁷⁵). Thus, if individual CWR populations decline or disappear entirely, it might pass unnoticed by the PA manager. If, on the other hand, an existing PA is provided with the designation of a 'national CWR genetic reserve', the management plan should be amended to integrate the genetic conservation of CWR populations present so that positive management action is triggered before any deleterious factor could impact on the CWR populations.

However, the common practice of locating genetic reserves within existing PA may be questioned because: (a) CWR are found both within and outside of current PA networks so if the goal is to conserve the full range of CWR genetic diversity then it is unlikely the full range of genetic diversity will be present only within existing PA, (b) CWR are often found in disturbed, pre-climax plant communities, anthropogenic environments and these are rarely designated as PA (PA more commonly being established to conserve pristine habitats or ecosystems, or rare or threatened taxa), (c) countries vary markedly in the representative coverage of PA and coincidentally countries with high levels of priority CWR per unit area (e.g. Lebanon, Israel, Greece, Portugal, Azerbaijan, Bulgaria, Syria and Turkey) also tend to be the countries with poorer representative coverage of PA, and (d) establishing CWR genetic reserves requires close collaboration between agro-biodiversity and PA conservationists but in too many countries the two communities work independently without meaningful collaboration and so there is no administrative route for genetic reserve establishment.

CWR *in situ* conservation outside of existing PA is a possible yet until now largely underexplored alternative to formally establishing genetic reserves. Suitable sites may include roadsides, field margins, orchards and even fields managed using traditional agro-silvicultural practices. In each case of these cases the sites are not managed for biodiversity conservation, and the occurrence of CWR populations is purely incidental. If these sites are to be considered suitable for sustainable conservation, the management they currently receive and that has permitted the existence of a healthy CWR population must be consistent over an extended time frame. Examples of the additional threats faced by non-protected area sites include: the widening of roads, the scrubbing out of hedgerows or orchards, cutting of roadside verges at the wrong time of the year, the introduction of herbicides rather than physical weed control,

⁷⁴ Maxted *et al.* (2008e)

⁷⁵ Passive *versus* active conservation. Passive conservation means that a species and the genetic diversity within it is not being monitored and managed, while active conservation is when a species and the genetic diversity within it is efficiently conserved through long-term monitoring and management of populations. An example of passive conservation is when a particular taxon occurs within a PA but without any formal conservation or management plan.

or even the physical control of weeds earlier in the season. To ensure the long-term survival of the CWR population it would be advisable to reach a management agreement between the CWR conservationists and the non-conventional protected area site owner and / or manager to ensure that current site management is maintained and CWR diversity negatively impacted. As by definition the areas outside PAs are primarily managed for reasons other than conservation, the management interventions at the site are likely to be minimal; it may simply consist of maintaining the current management and agreeing not to make significant changes to the site management without discussion with the conservation agency. The latter will need however to routinely monitor the site in order to ensure efficient management of the target CWR populations. Thus informal *in situ* conservation offers an opportunity to conserve populations or even taxa that may otherwise not be conserved and it obviously is a clear way of integrating agrobiodiversity conservation into normal community activities – the local community however will need to engage with the conservation at an early stage and on a continuing basis.

Therefore, *in situ* conservation of CWR should be planned both inside and outside of PA. There will be added conservation value to genetic reserves and informal CWR management sites if their overall management is coordinated and organised into an *in situ* CWR network. National networks could themselves contribute to regional and global CWR networks that together maximise global, regional and national CWR diversity conservation. In turn the sites and networks should be linked to systematic *ex situ* conservation as a back-up for the *in situ* conservation but also as a means of promoting greater sustainable exploitation of the conserved CWR resource.

A.9.2. Methodology

- (i) Review of *in situ* conservation gaps. *In situ* conservation gaps that resulted from the *in situ* gap analysis should be the foundation of the planning of the national *in situ* CWR network of genetic reserves and informal CWR management sites to conserve priority CWR diversity (see Section 8).
- (ii) Preliminary selection of *in situ* CWR conservation sites.
 - *In situ* CWR conservation sites. A network of genetic reserves and informal CWR management sites can be established based on the minimum number of locations that contain the maximum sample of CWR diversity, either by: (i) identifying CWR ‘hotspots’ (areas with high CWR richness) or (ii) by identifying the minimum number of sites needed to conserve all priority CWR as identified using an iterative process of complementarity analysis^{76,77}. Where the sites overlap with existing PA genetic reserves would usually be established and where sites do not overlap with existing PA then informal CWR management sites could be established or novel PA established.
 - ‘Hotspot’ analysis: identifies one or more locations that have significantly higher levels of CWR diversity than other locations and which together complement each other in terms of maximising CWR diversity inclusion (i.e. two CWR-rich sites could be identified that contain the exact same CWR, therefore it would not be efficient to actively conserve both sites). Having made this point, where genetic diversity within CWR is considered, it may be worth conserving both or multiple sites containing an identical array of CWR taxa if it is known or predicted by ecogeographic and/or genetic diversity analysis that the samples of genetic diversity contained in each site

⁷⁶ Rebelo (1994a, 1994b)

⁷⁷ Rebelo (1992)

complements rather duplicates an individual site's genetic diversity. 'Hotspot' analysis can be carried out using DIVA-GIS (<http://www.diva-gis.org/>).

- *Complementarity analysis*: identifies the minimum number of sites needed to conserve all priority CWR. The analysis is based on the division of the target area into grid squares (the grid square size is set relative to the overall map scale). The first selected grid square is the area that contains the highest concentrations of the target CWR and the second selected grid square is the one with the highest concentrations of CWR not present in the first selected grid square. This selection process is repeated until the selection of further grid squares would only duplicate taxa already included in the previously selected ones^{69, 70}. Note that some grid squares may not include existing protected area so informal CWR management sites may be established outside of the PA network⁷⁸ or novel PA designated. Complementarity analysis can be carried out using DIVA-GIS (<http://www.diva-gis.org/>).

Using both of these approaches, the most common CWR are likely to be duplicated in the selected sites. With the goal of maximising the conservation of genetic diversity, a certain level duplication of CWR taxa is essential to ensure maximum genetic diversity representation, as long as the sites duplicating taxa have complementary genetic diversity. This approach can be used to identify diverse and complementary areas regarding other types of data (e.g. genetic or trait diversity), or used to refine the first complementarity analysis based on geographic data. Two areas may have the same number of CWR (hence both are priorities for conservation), but the CWR in one area may be genetically similar to existing sites while in the second area they may be very different, so the second site would be selected.

Complementarity analysis is recommended over the hotspot approach because it allows the establishment of a network of *in situ* conservation sites that covers most (if not all) target CWR.

- Single-CWR conservation sites. If we look at particular traits/genetic diversity or even ecogeographic diversity, then the multi-CWR conservation site approach is unlikely to broadly represent the diversity for each CWR, meaning that we would need to either look at a single CWR level and choose the sites that are more diverse or use a combination of the single and multi-CWR conservation site approaches. The main objective for setting up an *in situ* conservation site is to ensure that maximum genetic diversity of the target CWR gene pool is captured in the system. Therefore, if financial and human resources are available, a single-CWR site for exceptionally important CWR population could be established based on geographic location or other types of data (e.g. particular traits or genetic diversity, ecogeographic diversity data). It is likely that if an effective informal *in situ* conservation site is established the running costs would be less than a more formal genetic reserve, so increasing the justification for single CWR targeted conservation.

⁷⁸ Maxted et al. (2008e)

In situ conservation

In situ conservation

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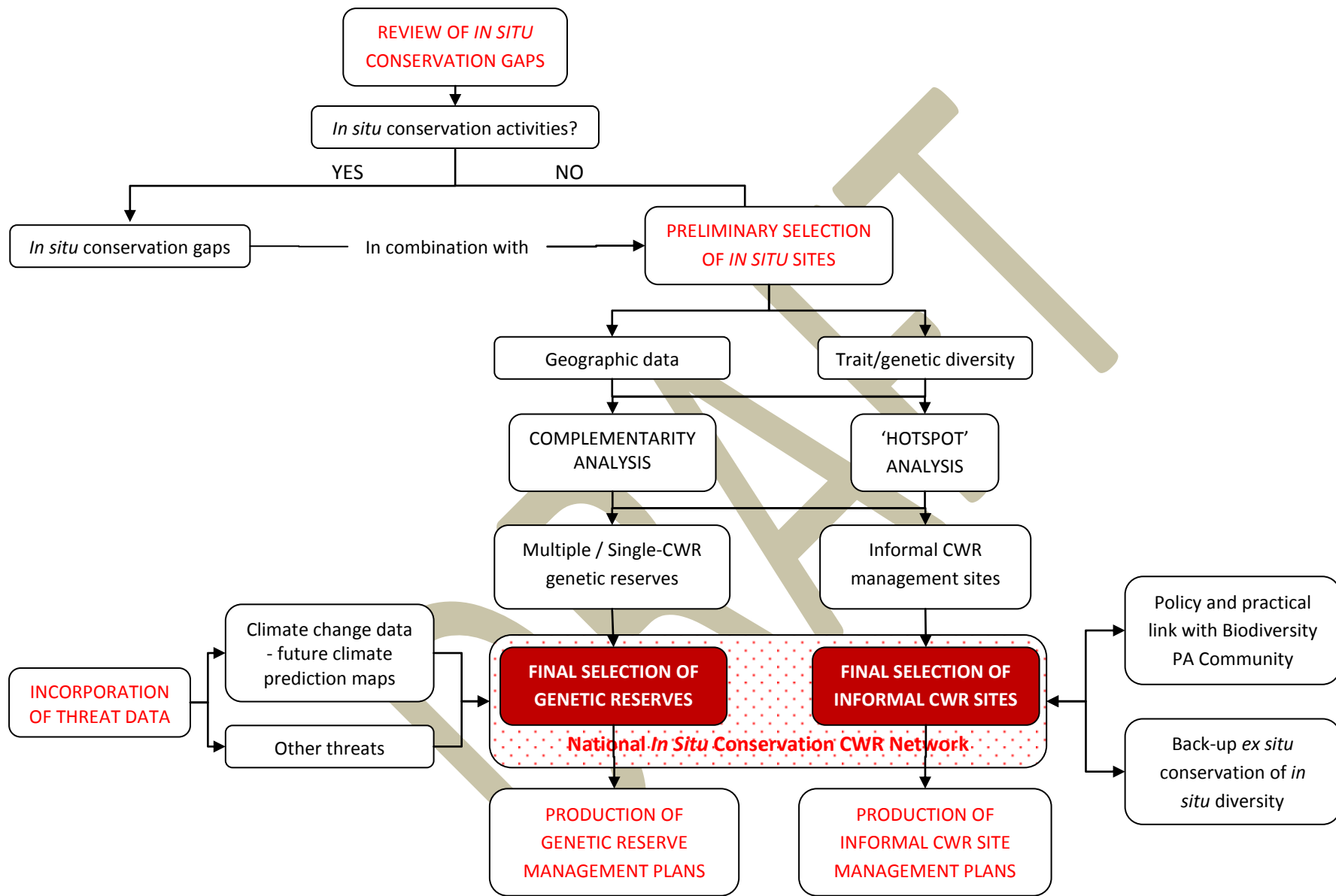


Figure 21. Establishment of *in situ* conservation goals

Complementarity analysis: can be used to identify the minimum number of sites needed to conserve all particular traits/genetic/ecogeographic diversity of a particular CWR within the minimum number of sites. The precise number of *in situ* conservation sites where the CWR is conserved to ensure maximum diversity will vary from species to species and is dependent on the distribution of diversity (trait/genetic/ecogeographic) within the CWR. To establish this number there is a need to review the intra-species pattern of diversity and the relative diversity found within and between CWR populations. However, this does require possible extensive sampling of CWR populations and more in-depth studies. If such studies have not been undertaken or resources are not available to carry out such studies, then it has been recommended that five CWR populations are conserved from the most ecogeographically diverse sites to maximise genetic diversity conservation⁷⁹.

This is not taking account of the fact that some of the exceptionally important CWR may occur in the sites selected on the basis of the taxon level analysis. It is not a case of single v. multi-taxon reserves – a CWR GR network may contain both, or all multi-taxon reserves but with particular emphasis on some taxa that are considered to be more important or possibly more threatened than others.

(iii) Incorporation of threat data on the preliminary site selection. Threat, as outlined above, can in the CWR context be assessed at two levels, the CWR themselves (commonly assessed using Red List criteria) and the potential site where the CWR are to be conserved. CWR threat assessment has already been considered in earlier sections and taken into consideration when establishing conservation priorities, so here when considering the establishment of *in situ* conservation sites, the site itself should be assessed for inherent threats and its long-term suitability for CWR conservation. The threats may be split into known (e.g. plans to develop the area and urbanise the potential PA site) and potential (e.g. predicted climate change impact on potential PA site) threats. The former should be searched for, potential impact estimated and considered when making the decision over whether to proceed with the site. While the latter are more nebulous, are likely to require species distribution modelling research by the conservation team to select those areas less affected, hence ensuring the long-term preservation of CWR. Climate prediction maps, whenever available, can be used, as well as knowledge on existing threats affecting sites, but it must be acknowledged that estimating potential threats to a site is still a relatively new science.

(iv) Provisional selection of *in situ* conservation sites. The provisional selection of *in situ* conservation sites is the result of the screening of the preliminary selection considering information site threat assessment (e.g. climate change), land use, ownership, protection status, local acceptance/involvement and other possible socio-political issues, such as site managers being unwilling to modify site management to facilitate CWR genetic conservation, which might impact the conservation sustainability and practical implementation of CWR conservation at the site. It is recommended that rather than aim for a fixed number of *in situ* conservation sites the potential sites are ranked so that if one site becomes impossible there is an obvious replacement or if further resources become available at a later date the potential additional sites are suggested.

The well balanced set of *in situ* conservation sites will contain a mix of genetic reserves established in existing PA, informal CWR management sites and possibly even novel PA established to contain genetic reserves. Each of these will together form the National

⁷⁹ Lawrence and Marshall (1997).

In Situ Conservation CWR Network that should be managed as a coherent whole with links to non-CWR PA conservation and routine back-up *ex situ* conservation of CWR diversity.

A.9.3. Examples and applied use

Box 45. Examples of CWR genetic reserves

Armenia

Erebuni State Reserve (89 ha) – diversity of wild wheat, including *Triticum urartu*, *T. boeoticum*, *T. araraticum* and *Aegilops* spp.

Australia

Border Ranges National Park (31,683 ha) – Several species of economic importance including macadamia nuts (*Macadamia integrifolia* and *M. tetraphylla*) and finger lime (*Microcitrus australasica* – used as a source of genetic material to improve disease resistance in commercial citrus fruit).

Costa Rica

Corcovado National Park (47,563 ha) – avocado (*Persea americana*), nance (*Byrsonima crassifolia*) and sonzapote (*Licania platypus*).

Germany

Flusslandschaft Elbe Biosphere Reserve (includes the Steckby-Lödderitzer Forest Nature Reserve) (374,432 ha) – wild fruit tree species such as pear (*Pyrus achras* and *P. pyraster*) and apple (*Malus sylvestris*), as well as other important CWR (e.g. *Lolium perenne*).

India

National Citrus Gene Sanctuary, Nokrek Biosphere Reserve, Garo, Meghalayas – conserve great diversity of native citrus varieties including wild oranges (*Citrus indica*, *C. macroptera*).

Iran

Touran protected area (1,102,080 ha) – comprises a national park and a biosphere reserve containing wild relatives of barley (*Hordeum* spp.).

Israel

Amniad reserve (380 ha) – wild emmer wheat (*Triticum dicoccoides*), *Hordeum spontaneum*, *Beta vulgaris* and *Olea europaea* as well as a rich grassland (with > 400 spp.).

Jordan, Lebanon, Palestinian Territories and Syria

Various CWR reserves – cereals, forages and fruit trees.

Kyrgyzstan

Besh-Aral State Nature Reserve (63,200 ha) – with walnut (*Juglans regia*) forests as well as a great diversity of other species such as pear and wild plum (*Prunus sogdiana*).

Mexico

MAB Sierra de Manantlán Biosphere Reserve – wild relative of maize (*Zea diploperennis*).

Palestine

Wadi Sair Genetic Reserve – for legumes and fruit trees.

Source: Hunter and Heywood (2011), Kaplan (2008), Maxted *et al.* (2011), <http://www.cbd.int/lifeweb/ecoservices4.shtml>

Peru

“Parque de la Papa” (Potato Park) (8,661 ha) – the Quechua communities (ca. 8,000 villagers from six surrounding communities) in the Pisac Cusco area of Peru have established this Park to jointly manage their communal land for their collective benefit, thereby conserving their landscape, livelihoods and way of life, and revitalizing their customary laws and institutions.

Syria

Sale-Rsheida Reserve – for *Triticum dicoccoides*, *Hordeum* spp.

Turkey

- Beydaglari Coast National Park (34,425 ha) – contains the rare endemic relative of the faba bean (*Vicia eristalioides*).
- Bolkar Mountains – five genetic reserves for *Pinus brutia*, *P. nigra* subsp. *pallasiana*, *Cedrus libani*, *Abies equi-trojani*, *Juniperus excelsa* and *Castanea sativa*.
- Ceylanpinar State Farm – seven genetic reserves for wild wheat relatives (*Aegilops* spp., *Triticum* spp.)
- Kasdagi National Park – ten genetic reserves for wild plum (*Prunus divaricata*), chestnut (*Castanea sativa*), *Pinus brutia*, *P. nigra* and *Abies equi-trojani*.

United States of America

- Central-Southeast USA – genetic reserve for *Vitis rupestris*, *V. shuttleworthii*, *V. monticola*.
- Organ Pipe Cactus National Monument (133,925 ha) – protects a small populations of wild chilli peppers (*Capsicum annuum*).

Uzbekistan

Nurata State Reserve – for walnut (*Juglans regia*).

Vietnam

Huu Lien Nature Reserve, – for litchi, longan, rice, *Citrus* spp. and rice bean.

Source: Hunter and Heywood (2011), Maxted *et al.* (2011), <http://www.cbd.int/lifeweb/ecoservices4.shtml>

Box 46. Site selection for the conservation of CWR and LR in Vietnam

A GEF project “*In situ* Conservation of Native Landraces and their Wild Relatives in Vietnam” ran from 2002 until 2005 and targeted the conservation of six native LR (rice, taro, tea, mung bean, *Citrus* spp., litchi and longan) and CWR in three areas (the Northern Mountains, Northern Midlands, and Northwest Mountains) in Vietnam and provided technical support to help farmers in effective conservation, development, sustainable management and use of their native LR and CWR. Sites for the conservation of LR and CWR were one of the outputs of this project. The selection of these was carried out in two steps:

1. To identify genetically important areas based on:
 - presence and genetic diversity of target species,
 - presence of endemic species,
 - overall floristic species richness,
 - presence of high numbers of other economic species,
 - presence of natural and/or semi-natural ecosystems,
 - presence of traditional agricultural systems,
 - protection status and/or existence of conservation-oriented farmers or communities that manage a number of species and varieties.
2. To select specific sites and communities within larger genetic reserves where socio-economic conditions indicated good prospects for on-farm agrobiodiversity conservation activities; workshops, stakeholder consultations, and meetings between NGOs, local institutes, and farmer groups aided this process; finally, the community receptivity to sharing traditional knowledge and practices that promote *in situ* conservation was assessed at each site.

The selected sites thus encompass a range of topographic, climatic and socio-economic conditions (e.g., proximity to markets and community-level associations), species and LR.

Eight genetic reserves were selected; two of them include more than one conservation site (in a cultivated ecosystem and an associated site in an adjoining protected area), and the six remaining

reserves consist only of cultivated ecosystems. Most of the targeted sites are both species diverse, maintain more than one crop and are LR diverse within target crops.

Source: <http://www.undp.org.vn/projects/vie01g35/index.htm>

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DRAFT

A.10. Implementation of *in situ* conservation priorities

A.10.1. Overview

Why do *in situ* conserved CWR populations require management?

They don't always require management. When selecting a site for *in situ* CWR conservation the site is unlikely to have been selected unless it has an abundant and viable population of the target CWR taxon or taxa. However, the population may require some form of management intervention to bulk-up the population to ensure it is in excess of the minimum viable population to maintain genetic diversity or the management practice at the site may be imprecise and management experimentation may be required to understand which interventions best promote an abundant and viable population of the target CWR taxon or taxa. Therefore, practically *in situ* CWR populations often require active management.

The establishment of the national CWR *in situ* conservation prioritises results in the identification of sites to form a National *In Situ* Conservation CWR Network. As discussed above, the implementation of CWR genetic reserves within existing PAs is likely to be the widely adopted option for CWR *in situ* conservation given potential financial constraints and the significant additional costs associated with the creation of new PAs for CWR conservation. However, this is not always practical or possible, especially in countries with a limited existing PA network and where priority CWR may not occur in any formal PA. Therefore, the National *In Situ* Conservation CWR Network is likely to include a mix of CWR genetic reserves and informal CWR management sites.

Determination of the actual number and mix of CWR genetic reserves and informal CWR management sites that will be established is pragmatic, directed by science but ultimately dictated by the resources available for *in situ* conservation and the governmental policy context at both the national and local levels. The need for the practical implementation of the National *In Situ* Conservation CWR Network to have a policy context should be stressed, national and local commitment is required to ensure the Networks long-term survival and ensure set-up expenditure is not wasted – *in situ* conservation is a long-term and expensive commitment.

Regardless of whether the priority sites occur within or outside a an existing PA, the implementation of *in situ* conservation priorities may be divided into five steps (see Figure 22): (i) 'Ground truth' potential site to determine whether the site is suitable for *in situ* conservation site implementation, (ii) reformulate the *in situ* conservation goals (if needed), (iii) integrate *in situ* conservation priorities with national/international agri-environmental schemes, (iv) ensure the genetic reserves comply with (at least) the minimum quality standards, (v) ensure local communities value and, where possible, use their local CWR diversity, and (vi) production of action/management plans.

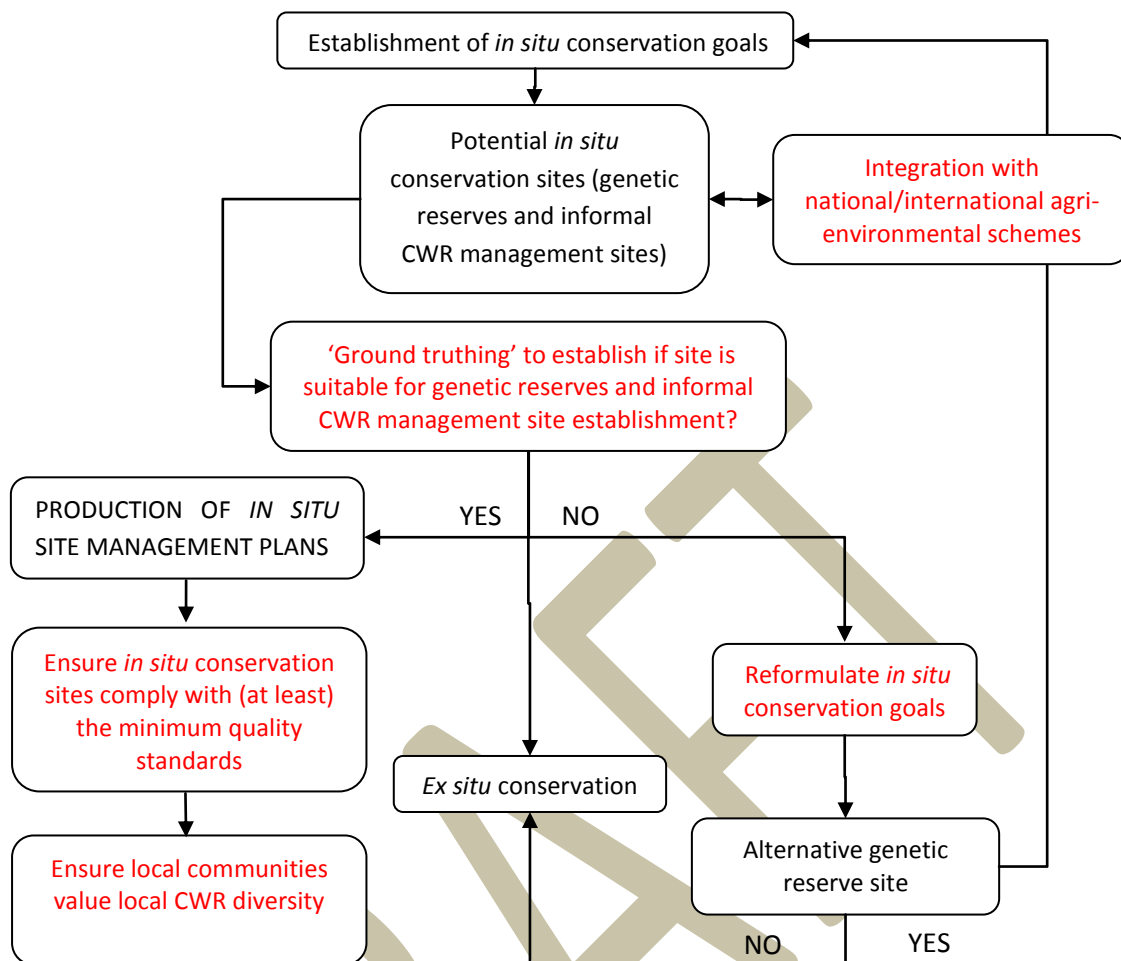
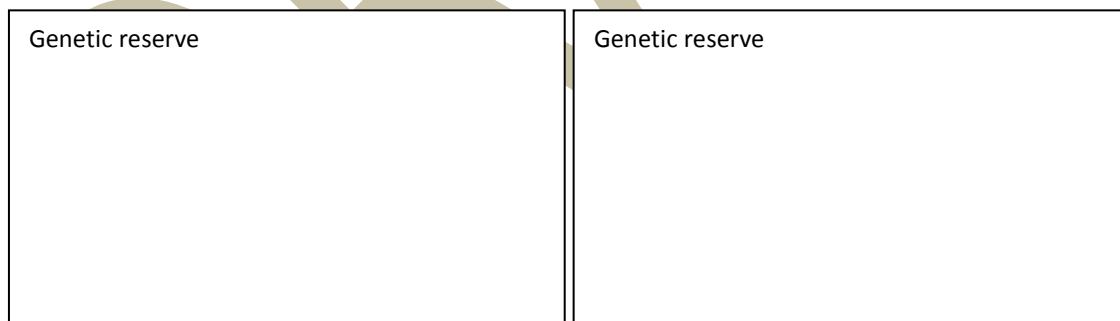


Figure 22. Implementation of *in situ* conservation goals



A.10.2. Methodology

- (i) 'Ground truth' potential *in situ* conservation sites. Having established the *in situ* conservation goals, an ordered list of potential *in situ* conservation sites (genetic reserves and informal CWR management sites) will be available; an effective short-list of potential sites. However, there may be various reasons why even the highest priority potential sites may practically be unsuitable, e.g. CWR population presence, land ownership, current land use and whether inside or outside a PA, PA status, potential threats, local community unresponsive, etc. Establishing the list of potential *in situ* conservation sites is likely to have been achieved remotely from the actual sites, the techniques used may predict that target CWR populations are present but the sites must

be 'ground truthed', checked to see if the prediction matches the reality at the site. If the target CWR population is absent or below the minimum viable population then alternative sites may be preferable. Understanding whether the site is publically or privately owned is likely to be an important consideration because if the site is publically owned it is more likely that the future management of the site can be amended to favour the target CWR population, particularly if the implementation of the *in situ* conservation site fulfils government policy objectives, but if the site is privately owned the owner may be less amenable to making potential management changes to the site. Likewise if the site is already under conservation management it would be easier to amend the site management for genetic CWR conservation than say were the site being managed for more commercial purposes. Even if the site is an existing PA the site would have been established for non-CWR conservation and the objectives of the PA management may not be amenable to adaptation of CWR conservation, e.g. the management of large herbivores or coniferous trees is likely to conflict with herb CWR management. If the CWR conservation is to be successful then local community support is required. To help ensure support the local communities should ideally be involved to some extent in the development and implementation of CWR Action Plans. Agreements with private owners (e.g. tax incentives) could be made. The provision of government incentives, if to be used, must be linked to some form of guarantee from the land owner to ensure CWR diversity thrives, so a management agreement including a conservation prescription is required in order to ensure CWR are properly managed but also to recognise the local communities' role in conserving such a valuable resource.

- (ii) Reformulate the *in situ* conservation goals (if needed). The ordered list of potential *in situ* conservation sites (genetic reserves and informal CWR management sites) produced as part of the *in situ* conservation goals but as mentioned above even the highest priority potential sites may practically be unsuitable and site further down the ordered list would need to be considered. Thus the process of selecting *in situ* sites is pragmatic and iterative until a list of sites can be agreed to implement genetic reserve and informal CWR management site based conservation action.
- (iii) Production of *in situ* conservation site action/management plans. The first step in formulating the revised management plan is to observe the biotic and abiotic dynamics of the site for both CWR and non-CWR species. A survey of the species present in the site should be performed to help understand the ecological interactions within the reserve. A clear conservation goal should be decided and a means of implementation agreed that may involve some compromise between the priorities for CWR and non-CWR species conservation. This then forms the basis of the site action /managements plans, which will contain information on CWR taxonomy, description, image, distribution, ecogeography, current conservation status and action, threat assessment, uses, additional conservation action required, research and monitoring requirements, and incorporation in existing national or local conservation initiatives, but perhaps most importantly it summarises the management interventions recommended for the site and how the CWR are to be monitored to ensure the management is promoting CWR population health⁸⁰. As part of the routine site management there is a need to establish a monitoring regime, to undertake time series surveys of the target population to facilitate a review of project interventions (see Section 11.2).

⁸⁰ Maxted *et al.* (2008)

- (iv) Ensure the *in situ* conservation sites comply with (at least) the minimum quality standards. The quality standards⁸¹ for the conservation of CWR in *in situ* conservation sites are a useful tool both for practitioners involved in the design of *in situ* conservation strategies for CWR and the PA managers interested in their conservation. The standards have two levels—the ‘minimum’ and ‘optimal’ quality standards. ‘Minimum’ quality standards concern those baseline traits required for any genetic reserve to function and fulfil its conservation objectives, whereas ‘optimal’ quality standards include a more rigorous set of requirements. Quality standards are related to (i) the genetic reserves themselves and include traits such as location, spatial structure, target taxa, populations, and management, (ii) the PAs selected for the establishment of genetic reserves, and (iii) informal *in situ* conservation areas outside of formal PAs.
- (v) Integrate *in situ* conservation priorities with national/international agri-environmental schemes. The selected *in situ* sites that now constitute a national network of genetic reserves and informal CWR management sites should be integrated with agro-environmental schemes (e.g. such as those funded by the European Commission or other regional agencies) so that their management is nationally coordinated and the conservation of the target CWR is effective. A growing effort to strengthen the relationship between agriculture and the provision of ecosystem services has been registered⁸². *In situ* and on-farm conservation of PGRFA activities are now being set up as a result of Payment for Environmental Services (PES) schemes in an attempt to encourage and reward local communities for their role in conserving and managing PGRFA for the future; however, the actual implementation of these schemes remains a significant challenge in many countries. The National CWR Conservation Strategy should also be integrated into national programmes for the implementation of the CBD (such as National Biodiversity Strategies and Action Plans (NBSAPs)⁸³, the ITPGRFA, and the Global Strategy for Plant Conservation (GSPC) through the appropriate national focal point(s) and the National Plant Conservation Strategies (which is the basis for national policy), when one exists. Whether CWR are conserved *in situ* within PAs or outside of them, it is advisable that the sites have some form of legal protection to help prevent sudden threats to conserved populations (e.g., through a dramatic change in land use).
- (vi) Ensure local communities value and use their local CWR diversity. Promoting the involvement of local communities in *in situ* conservation and management of CWR is often crucial for conservation to be effective, especially when *in situ* conservation sites are located within (or include as part of) private land. Awareness of the National CWR Conservation Strategy should therefore be raised among the different stakeholders. These can take the form of local community conservation training workshops, etc. See A.10.3 Examples and applied use for some examples on the integration of conservation into local communities and industry.

Finally, it is worth re-stressing that the implementation of specific CWR *in situ* conservation sites will ultimately be pragmatic, dictated by the resources available as well as national and regional level governmental will, and NGO and local community involvement.

A.10.3. Examples and applied use

⁸¹ Iriondo *et al.* (2012)

⁸² FAO (2009)

⁸³ <http://www.cbd.int/nbsap/>

Box 47. Establishment of CWR genetic reserves for cereals, forages and fruit trees

The conservation and sustainable use of dryland agrobiodiversity project was funded by the Global Environment Facility (GEF) through the United Nations Development Programme (UNDP) between 1999 and 2004. The project aimed at promoting the community-based *in situ* conservation and sustainable use of both LR and CWR of cereals, food and feed legumes, *Allium* and fruit tree species originating from Jordan, Lebanon, Palestine and Syria. Ecogeographic surveys of CWR were conducted for the target species across the four countries and 24 key project sites (genetic reserves) were identified for further surveying of agrobiodiversity, potential for long-term *in situ* conservation and site threats. The surveys described the dynamics of site vegetation, collated species data (e.g. growth stage, cover/density, health status, etc.), ecology and land use, as well as identifying which species to monitor for conservation. The species data collated were then entered in a database and time-series data analysed at country and regional levels to facilitate site and species management. The database was installed and used in each country, but maintained by ICARDA, whose staff periodically update with new data sent by national survey teams.

The main results of CWR surveys showed that there is still a wealth cereals, food and feed legumes, *Allium* and fruit tree CWR species in the region but that wealth is being seriously threatened by over-grazing, changes in agro-silvicultural practices, quarrying and urbanization. Local communities see little intrinsic value in CWR maintenance so there is a need for greater awareness raising of the broader value of CWR species among communities but where there is no economic return for farmers and herders from changing their practices national governments need to lead in CWR conservation. Further research is required to demonstrate, if it is the case, which CWR favourable land management would lead to increased income for farmers and to conservation of target CWR species.



a. Informal *in situ* conservation site, Bekaa valley, Lebanon (photo: Nigel Maxted). b. Genetic reserve, Al-haffe, Syria (photo: Nigel Maxted)

Source: ICARDA (2001)

Box 48. Parque De La Papa in Peru

The establishment of potato parks in centres of potato diversity, such as that in the Cusco region of Peru by the indigenous Quechua people working in collaboration with CIP scientists (www.cipotato.org), has focused attention on the *in situ* protection of potato CWR and LR diversity, but the continued practice of traditional agriculture in the region will also favour maintenance of wild potato species. The “Parque de la Papa” (Potato Park) (8,661 ha) was established by the Quechua communities (ca. 8,000 villagers from six surrounding communities) in the Pisac Cusco area of Peru to jointly manage their communal land for their collective benefit, thereby conserving their landscape, livelihoods and way of life, and revitalizing their customary laws and institutions. Similarly highly diverse cultivars of *S. tuberosum* subsp. *andigena*

and related cultivated species are found in the Tiahuanaco region of south of Peru and north of Bolivia and this region may be suitable for establishment of a further potato park.

Box 49. Biodiversity and wine initiative in South Africa

The Cape Floristic Region in South Africa grows nearly 95 % of the country's wine-producing plants. This region is recognised both as a global biodiversity hotspot and a World Heritage Site but it is increasingly threatened by agricultural practices, urban development and invasive alien species.

In 2004, the wine industry developed a pioneering conservation partnership with the Botanical Society of South Africa, Conservation International and The Green Trust to establish the Biodiversity and Wine Initiative (BWI) which puts the country's wine industry and the conservation sector together. This initiative aimed at protecting the Cape Winelands' unique natural heritages of a total of 126,000 ha, but also to encourage wine producers "to farm sustainably and express the advantages of the Cape's abundant diversity in their wines". For every hectare under a vineyard, an additional hectare of natural vegetation is devoted to conservation.

Source: http://www.wwf.org.za/what_we_do/outstanding_places/fynbos/biodiversity_wine_initiative/

Box 50. Development a network of community nature reserves in Benin

The Network of Community Nature Reserves was established by the village community of Papatia, Benin, in response to the rapid depletion of local natural resources. Traditional healers, beekeepers, farmers, women's groups and students from different ethnic groups worked together and created protected community areas (such as the Botanical Garden of Papatia). Key activities undertaken included: conservation of local natural resources, environmental education, documentation and commercialization strategies for traditional knowledge and medicines, socio-economic development of the rural population through the sustainable use of natural resources through eco-tourism, sale of local plants and herbs, apiculture, market gardens etc., and other forms of local and regional development.

Source: http://www.equatorinitiative.org/index.php?option=com_content&view=article&id=614:rederec-ong&catid=175&Itemid=541&lang=en

Box 51. Establishment of a genetic reserve for *Beta patula* in Madeira

Wild *Beta* species are found from Turkey and adjacent countries to the Macaronesian archipelago as well as from Morocco to south Norway, but one rare, annual species *B. patula*, which has value for increasing beet seed production, is an endemic of the Madeira archipelago. An ecogeographic survey showed the species was restricted to the Ponta de São Lourenço peninsular of Madeira, Porto Santo and the uninhabited Desertas Islands, growing on loam-clayey and rocky soils, poor in organic matter, low in moisture content, but with high salinity. *B. patula* is considered one of the 100 most endangered species of Macaronesia and has recently been IUCN Red List assessed as Critically Endangered. Following field survey species population sizes on the two Desertas Islands range between 2,730 and 4,620 individuals. Protection measures undertaken by Natural Park of Madeira have increased population sizes by 10.8 times, but population still suffer strong annual fluctuations and further management is required to reach the minimum viable population size. Although not formally designated as a genetic reserve, the management of the populations of *B. patula* on the Desertas Islands provide a good model for genetic reserve based conservation.



a. *B. patula* habitat (photo: Brian Ford-Lloyd) b. *B. patula* plant with seed head (photo H. Nóbrega).
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NordGen conferences discussing *in situ* conservation and access and benefit sharing of genetic resources in protected areas - "Genetic resources in protected areas": <http://www.nordgen.org/index.php/en/content/view/full/1179>

WWW

CWR Portal resources – presentations on conservation: <http://www.cropwildrelatives.org/resources/presentations.html#c3970>

WWW

Genetic Reserve Information System - GenResIS – AEGRO: <http://www.agrobiodiversidad.org/aegro/>



European Commission project: "An integrated European *in situ* management work plan: implementing genetic reserves and on-farm concepts (AEGRO)": <http://aegro.jki.bund.de/aegro/index.php?id=95>



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A.11. Establishment and implementation of *ex situ* conservation

A.11.1. Overview

What are the ex situ conservation goals of a National CWR Conservation Strategy?

A National CWR Conservation Strategy aims at the development and implementation of a systematic and complementary action plan for the active conservation and sustainable use of CWR within a country. This will include parallel *in situ* and *ex situ* conservation action but it is the *ex situ* collections that primarily facilitate access to these materials for crop improvement and research.

The Convention on Biological Diversity⁸⁴ changed the relative focus of conservation efforts so that following its inception, *ex situ* conservation was seen primarily, at least for the broader biodiversity conservation community, as a safety back-up strategy to provide security for the favoured *in situ* approach. While recognising that it would be foolish to implement a National CWR Conservation Strategy and establish key national conservation areas without a safety back-up to help guarantee long-term conservation of the populations, the policy change fails to recognise the fact that CWR diversity has historically been almost exclusively conserved *ex situ* and it can be argued that *ex situ* collections provide the most practical means of access for the germplasm user community. At least in the short term, how many plant breeders or researchers are likely to approach PA managers for germplasm to use in their breeding programmes? As *ex situ* conservation provides the practical route for germplasm access for the user community; even if populations are adequately conserved *in situ* there is still an imperative to duplicated diversity *ex situ* for the benefit of the user community.

However, *in situ* conservation has unique importance in maintaining the process of adaptation to changing environments which cannot happen with *ex situ* conservation – each *ex situ* accession is a snapshot of that population's diversity at the time of sampling. Therefore both *ex situ* and *in situ* techniques have their advantages and disadvantages, and they should be seen not as alternatives or subservient to one another but as complementary strategies.

There are a range of *ex situ* conservation techniques available (Box 52), but because the vast majority of CWR have orthodox seeds (i.e., they can be effectively dried and stored at -18°C without loss of viability) seed storage in gene banks predominates as the most practical *ex situ* conservation technique applied. The establishment and implementation of *ex situ* conservation priorities includes three steps (Figure 23): (i) review of *ex situ* conservation gaps, (ii) selection of CWR and sites for targeted collecting, (iii) gene bank seed processing, and (iv) post-storage seed care.

Box 52. *Ex situ* conservation techniques

CWR diversity can be stored as seed, explants, living plants and genomic samples using the following *ex situ* techniques:

Seed Storage – The collection of seed samples at one location and their transfer to a gene bank for storage. The samples are usually dried to suitably low moisture content and then kept at sub-zero temperatures;

⁸⁴ CBD (1992)

In Vitro Storage – The collection and maintenance of explants (tissue samples) in a sterile, pathogen-free environment;

Field Gene Bank – The collecting of seed or living material from one location and its transfer and planting at a second site. Large numbers of accessions of a few species are usually conserved;

Botanic Garden / Arboretum – The collecting of seed or living material from one location and its transfer and maintenance at a second location as living plant collections of species in a garden or for tree species an arboretum. Small numbers of accessions of a large number of species are usually conserved.

DNA / Pollen Storage – The collecting of DNA or pollen and storage in appropriate, usually refrigerated, conditions.

Source: Hawkes *et al.* (2000).



CWR seed collecting (photo: Nigel Maxted)



Ex situ seed conservation (photo: ICARDA).

Box 53. *Ex situ* seed conservation

Ex situ conservation is the conservation of biological diversity outside their natural habitats. It involves the location, sampling, transfer and storage of samples of the target taxa away from their native habitat to be conserved at a remote site. Examples of major *ex situ* seed collections include the International Maize and Wheat Improvement Centre (CIMMYT) gene bank with more than 160,000 accessions (i.e., samples collected at a specific location and time), the International Rice Research Institute (IRRI) with 108,925 accessions, the world's largest collection of rice genetic resources, and the Millennium Seed Bank at the Royal Botanic Gardens, Kew, which holds the largest seed collection of 24,000 wild species. Important national/regional collections include: coffee in Côte d'Ivoire, Ethiopia, Cameroon, Kenya, Madagascar and Tanzania; sesame in Kenya; cassava in Malawi, Zambia and Tanzania; and sweet potato in Mauritius, Zambia, Swaziland and Tanzania, as well as China's largest seed bank, the Germplasm Bank of Wild Species (GBWS).

Source: Global Crop Diversity Trust (2007).

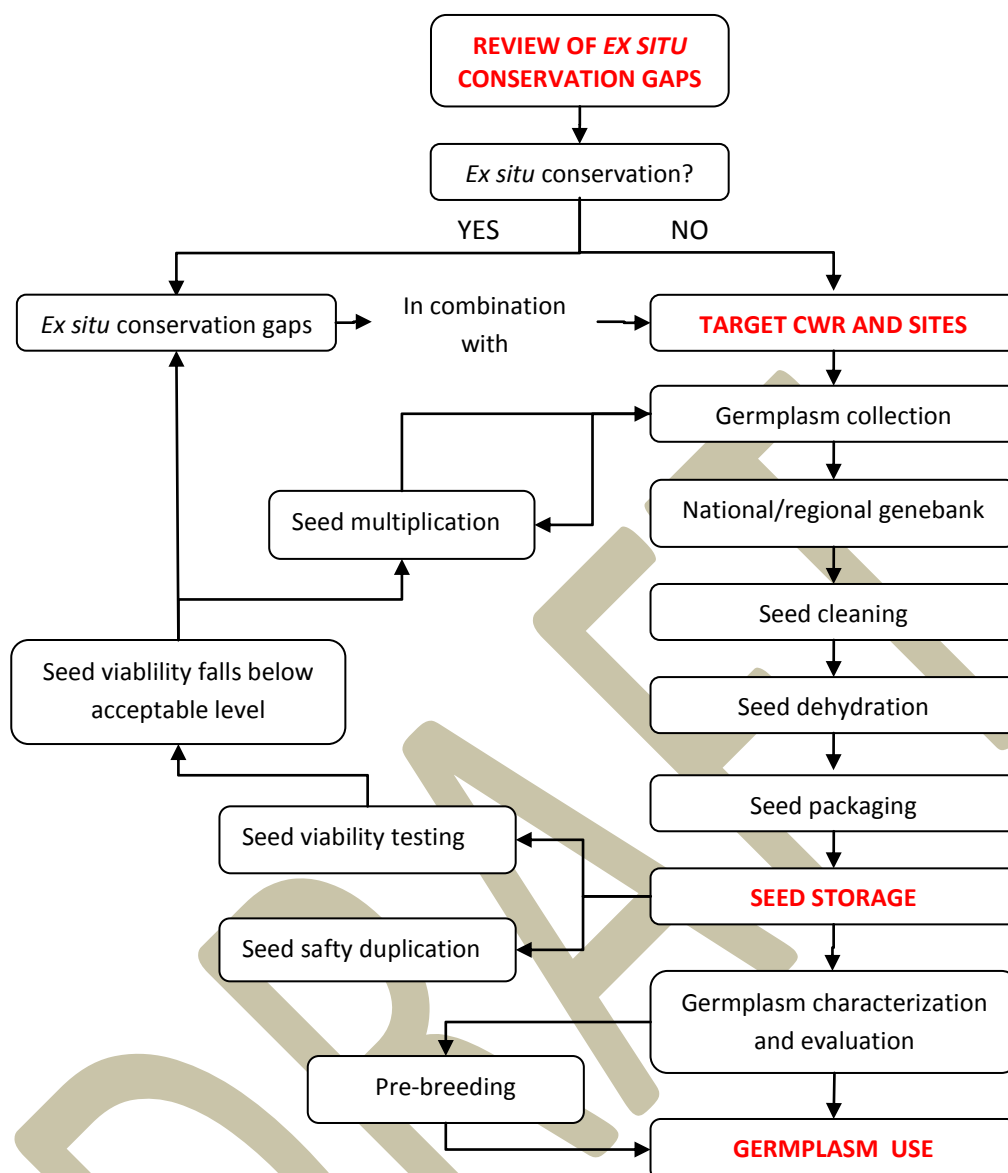


Figure 23. *Ex situ* conservation of CWR

A.11.2. Methodology

- (i) Review of *ex situ* conservation gaps. *Ex situ* conservation gaps that resulted from the gap analysis should be the foundation of the planning of the national *ex situ* collection programme to ensure systematic *ex situ* conservation of priority CWR species (see Section 8). Due to the potentially very large number of CWR species it is unlikely that sufficient resources will be available to conserve all national CWR species. As is mentioned above *ex situ* collections are often the ‘market stall’ through which the germplasm user community access the germplasm they require, therefore another important consideration when formulating the *ex situ* collection programme is meeting the users demands. Further ideally the germplasm curator should anticipate the demand and have germplasm ready to meet that demand whether as directly sampled germplasm or pre-bred lines before the user requests the germplasm.
- (ii) Selection of CWR and collecting sites for targeted collecting. Priority should be given to collecting individual CWR that are not conserved *ex situ* or *in situ*, as well as CWR populations (within the same CWR) (identified by undertaking gap analysis of

ecogeographic, trait or genetic diversity) that are not represented in gene banks (see Figure 17). It may not always be necessary to collect fresh CWR if the necessary gap filling germplasm is held by a sister gene bank then material may be obtained from inter-gene bank exchange or even knowledge that the germplasm is held by a sister gene bank may fill the gap. Note all CWR collection should be undertaken legally with the appropriate national permission and ensuring the collection is not counter to international conventions (e.g. CITES <http://www.cites.org>; International Treaty on Plant Genetic Resources for Food and Agriculture <http://www.planttreaty.org/>). Collectors are also referred to the FAO International Code of Conduct for Plant Germplasm Collecting and Transfer (<http://www.fao.org/ag/agp/agps/PGR/icc/icce.htm>) for further guidance.

CWR will be collected from natural or semi-natural habitats bearing in mind 6 basic field sampling factors:

- Distribution of sites within the target area – using either the cluster (site close together to pick up micro-habitat associated genetic diversity) or transect approach (site along line to pick up diverse ecosystem associated genetic diversity);
- Number of sites sampled – maximum possible with the resources available;
- Delineation of a site – related to the size of the interbreeding unit the edges of the site may also be delineated by dominant habitat changes;
- Distribution of the plants sampled at a site – randomly throughout the site or if there are distinct habitats stratified random that encourages sampling from each habitat type, collecting off-types or interesting material selectively;
- Number of plants sampled per site – 2,500 seeds sampled from 40-50 plants but preferably 5,000 seeds from 100 individuals;
- Indigenous knowledge held by local community – field collectors should note knowledge held by local people on the CWR found in their area, this may relate to population locations, threats, habitat associations and uses.

Each of these factors may vary depending on the nature of the target CWR being sampled and also assumes it is possible to apply the ideal sampling strategy; many CWR are, for instance, found as individual plants or small clumps of plant not dense stands and further ripening is not uniform so all the potential fruit is unlikely to be available during one sampling visit. A further important point to consider is that germplasm is virtually worthless unless it has detailed passport data associated with the collection location, so this data must be collected in the field (including GPS location), placed in a database and made available to the user community. With CWR collections it is also advisable to collect voucher specimens so the accessions identification can be checked post-collection.

- (iii) Gene bank seed processing. Following collection the sample arrives at the gene bank and is processed in the standard manner, which is likely to include: seed cleaning (to separate chaff and fruit debris from seed and ensure the accession is sample of a single species), seed health evaluation (inspection for seed borne diseases and pests), dehydration (normally to around 5-6% relative humidity), packaging (which most often take the form of glass vials, metal cans or laminated aluminium foil packets), registration (entering an associated record in the seed bank management system and making the accession available to the users) and storage (usually in a -18°C cold room). When field collecting CWR species it may not always be possible to obtain a sufficiently

large seed sample to be banked directly so there may need to be a seed multiplication cycle before the seed can be processed and incorporated into the gene bank. See 'Additional materials and resources' for detailed gene bank methodologies.

- (iv) Post-storage seed care. Once the seed is incorporated into the gene bank the seeds viability will gradually decrease over time and there will be a need to extract a sample of seed and test its germination viability at approximately 10 year intervals. Viability is a measure of how many seeds are alive and can develop into normal plants. It is usually expressed as percentage germination and above 75% is an acceptable level of viability. Viability is usually determined before the seeds are packed and placed into storage, and subsequently at regular intervals during storage. When germination falls below 75% the accessions requires regeneration.

The aim of regeneration is to increase the quantity of seed of any accession but while doing so it is very important to ensure that the original genetic characteristics of the accession are retained as far as possible. Each multiplication / regeneration cycle contains hazards to maintenance of the genetic integrity of the accession, such as: (a) contamination from foreign pollen during fertilization, (b) contamination through seed adulteration during harvesting, threshing and packaging, (c) changes due to gene mutation, (d) genetic drift due to random loss of alleles, particularly when regenerating from small numbers of individuals, and (e) genetic shift due to unconscious natural or artificial selection (related to diverse environmental conditions during regeneration)⁸⁵. The risks involved with regeneration will vary considerably according to the crop species, but it is also a costly operation, therefore, the most efficient and cost effective way of maintaining genetic integrity is to keep the frequency of regeneration to an absolute minimum.

A.11.3. Examples and applied use

Box 54. *Lathyrus belinensis*: a CWR discovered and almost lost

In 1987 while collecting legume species near Cavus, Antalya province, Turkey a new species of the genus *Lathyrus* was discovered and described as *Lathyrus belinensis*. The single population was growing alongside a new road that was just then being cut through fields between Kumluca and Tekirova. The population appeared to have its greatest concentration in and around an ungrazed village graveyard in the village of Belin. The new species was most closely related to *L. odoratus* (sweet pea), being just as scented as sweet pea but with more hairy vegetative parts. The most striking and economically interesting distinguishing feature of *L. belinensis* is the flower colour which is yellow with conspicuous red veins, which contrasts with *L. odoratus* flowers which can be purple, blue, pink or cream, but never yellow. Thus the discovery of *L. belinensis* was an opportunity for horticulturalists to breed a yellow sweet pea—a goal of many contemporary sweet pea breeders.

The type population was found over an area of only 2 km² and although the species was published in 1988, no further populations have subsequently been reported. The only known population was threatened the new road construction and the planted of conifers at the time of original collection. On returning to collect more seed in 2010 the original type location had been destroyed by earthworks associated with the building of a new police station. Although a few plants were found in the area and seed is held ex situ, the richest area within the site had been lost. *L. belinensis* has recently been assessed using IUCN Red List Criteria as Critically Endangered—the most highly threatened category, only time will show if field conservation will save this species in the wild!

Maxted (2012)



⁸⁵ Sackville-Hamilton and Chorlton (1997)

Box 55. *Ex situ* conservation of the world's major CWR

The Global Crop Diversity Trust has recently initiated a large scale global project concerned with "Adapting Agriculture to Climate Change: Collecting, Protecting, and Preparing Crop Wild Relatives". Although the bulk of the project will focus on the utilization of CWR diversity, it includes the first systematic attempt to collect and conserve priority CWR diversity at a global scale. This is only feasible now due to 1) the taxonomic and genetic relationships between CWR becoming increasingly clarified, 2) ease of access to large on-line ecogeographic data resources, 3) better knowledge and tools for modelling and mapping the distribution of plant species through geographic information systems (GIS), and 4) a concerted global desire to implement the International Treaty on Plant Genetic Resources for Food and Agriculture (ITPGRFA). The priority CWR species were identified by combining the ITPGRFA Annex 1 and the major and minor food crops listed in Appendix 2 of the *World Atlas of Biodiversity* (Groombridge and Jenkins 2002). This resulted in a list of approximately 10,500 CWR species. To produce a reduced list of priority CWR, only those species present in Gene Pools 1b and 2 or Taxon Group 1b, 2 and 3 were included, as these are the taxa that can most easily be used in plant breeding using conventional techniques. The priority list contains 1,392 CWR species from 109 genera. *Ex situ* gap analysis is being undertaken to identify the locations of genetic diversity un- or under-secured in *ex situ* collections in order to inform planning of germplasm collecting for *ex situ* conservation. The project is currently gathering and geo-referencing species occurrence and conservation data from on-line resources, herbarium and gene bank databases, and following the gap analysis, extensive CWR collection and *ex situ* storage is planned so that for the first time the CWR diversity most important to underpin global food security will be available to the user community. Collected CWR accessions will be stored in relevant national and international gene banks, and will be safely duplicated for long-term security at the Svalbard Global Seed Vault, in Norway. Following collection, traits of value for adaptation to climate change will be transferred into cultivated lines through pre-breeding, and the results will be evaluated in the field. The wild species accessions and the promising lines generated will be collected and made available to the global community for breeding and research under the terms of the ITPGRFA.

Source: Khoury *et al.* (2011)

A.11.4. List of references used to compile the text

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A.11.5. Additional materials and resources

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WWW Bioersity International training modules on plant collecting:
http://www.bioersityinternational.org/training/training_materials.html#c10721

WWW Bioersity International training modules on *ex situ* conservation/genebank management:
http://www.bioersityinternational.org/training/training_materials.html#c10715

WWW European Native Seed Conservation Network (ENSCONET) (with collecting and curation manuals, database, germination recommendations, etc.):
<http://ensconet.maich.gr/>

WWW FAO International Code of Conduct for Plant Germplasm Collecting and Transfer (<http://www.fao.org/ag/agp/agps/PGR/icc/icce.htm>)

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A.12. Monitoring CWR Diversity

A.12.1. Overview

What is monitoring of plant populations and why it is important?

Monitoring of plant populations means the systematic collection of data over time to detect changes, to determine the direction of those changes and to measure their magnitude⁸⁶. The monitoring of CWR populations and habitats in which they occur aims at:

- Providing data for modelling populations trends,
- Assessing trends in population size and structure,
- Assessing trends in population genetic diversity,
- Determining the outcomes of management actions on populations and to guide management decisions.

In terms of CWR monitoring it may occur at three distinct levels (a) monitoring of specific target CWR populations conserved *in situ*, either informally or within formal genetic reserves, (b) monitoring of *ex situ* conserved accessions, and (c) monitoring of higher level indicators of CWR conservation. However, there is a significant literature on CWR monitoring but it nearly all refers to the monitoring of genetic reserves⁸⁰ and that will be the main focus of this section.

Once the *in situ* conservation sites are established, they require regular monitoring to assess any short and longer term changes in CWR diversity, which can help form the basis of assessing the effectiveness of the management regime for maintaining CWR diversity. The monitoring of CWR thus constitutes an important early warning mechanism for detecting species extinction and genetic erosion. The results of regular monitoring are used to inform the management prescriptions of a CWR Action Plan and/or genetic reserve management plan. Therefore, monitoring schemes should be included in CWR Action Plans and/or *in situ* conservation site management plans, and should be initiated immediately after implementation of the *in situ* conservation site (Figure 24). The monitoring of CWR can be measured at two different levels: individual taxa and genetic diversity within taxa. At the individual taxon level, the development of a monitoring plan comprises five phases (Figure 25): (i) Identification and selection of the variables to monitor, (ii) Design of the sampling strategy, (iii) Implementation of a pilot study, (iv) Data analysis, and (v) Adjustment of the monitoring plan. Ideally as we wish to promote the conservation of the genetic diversity with CWR taxa it would be expected that genetic level monitoring would occur sufficiently often to alert the conservationist to deleterious changes but it has also to be recognised that genetic monitoring is costly and therefore there is a need to balance regularity of monitoring against costs⁸⁷.

Just placing seed accessions in a gene bank or other genetic resources collection is the end of the conservation process, the accessions need to be regularly monitored to ensure it has retained its viability so it can be taken out of the collection and used. As seeds viability decrease over time seed germination tested, commonly, at approximately 10 year intervals and if the viability is below 75% the accessions requires regeneration (see Section A11).

⁸⁶ Iriondo *et al.* (2008)

⁸⁷ See Iriondo *et al.* (2008) for recommendations on how, when and why to use genetic monitoring.

The CBD Strategic Plan⁸⁸ includes SMART (Specific, Measurable, Attainable, Relevant and Timely) objectives; meaning that it established desirable outcomes that can be time-series monitored against key performance indicator to evaluate their success in achieving the strategic goal and also help identify potential intermediate actions that will aid goal achievement. Recently, the Second Global Plan of Action for Plant Genetic Resources for Food and Agriculture was agreed by the Commission on Genetic Resources for Food and Agriculture at its 13th Regular Session in November 2011 to “to review existing indicators and identify or develop higher-order indicators, which could be in the form of an index that could enable stakeholders at all levels to effectively monitor the implementation of Second Global Plan of Action for Plant Genetic Resources for Food and Agriculture”⁸⁹. A Technical Consultation was held in Madrid, 2012 and generated a “Revised draft indicators for monitoring the implementation of the Second Global Plan of Action for Plant Genetic Resources for Food and Agriculture”⁹⁰.



Monitoring CWR populations in the West Bank, Palestinian Territories (photo: Nigel Maxted).

Specifically for CWR these were focused on *in situ* conservation:

- Number of Crop Wild Relatives (CWR) surveyed/inventoried
- Number of CWR in situ conservation and management actions with government support
- Number of conservation areas with management plans addressing CWR
- Number CWR actively managed in situ

But some Targets and Higher-order indicators were also identified for CWR as follows:

- Number of threatened crop germplasm

⁸⁸ CBD (2010b)

⁸⁹ CGRFA-13/11/Report, paragraph 98

⁹⁰ FAO (2012)

- Number of Crop Wild Relatives surveyed/inventoried
- Number of accessions resulting from collecting missions in the reporting country
- Percentage/Number of targeted taxa where a collecting gap exist
- Number of taxa conserved ex situ under medium or long term conditions
- Number of accessions [with documentation] conserved ex situ under medium or long term conditions
- Number of accessions safety duplicated
- Number of accessions in need of regeneration
- Percentage of accessions in need of regeneration
- Number of accessions of the collection by number of traits characterized
- Number of accessions distributed from collections

As can be seen these indicators are designed to be specific in the sense of being well defined, easily measurable, where the necessary data would be readily attainable, the data relates clearly the goal and can be periodically assessed to provide a time-series comparison. When implemented by national PGR programmes, the programmes can themselves check their compliance with international conventions / treaties, assess their conservation efficiency and specifically meet the countries obligation on CWR data reporting to the *Global Plan of Action for Plant Genetic Resources for Food and Agriculture*.

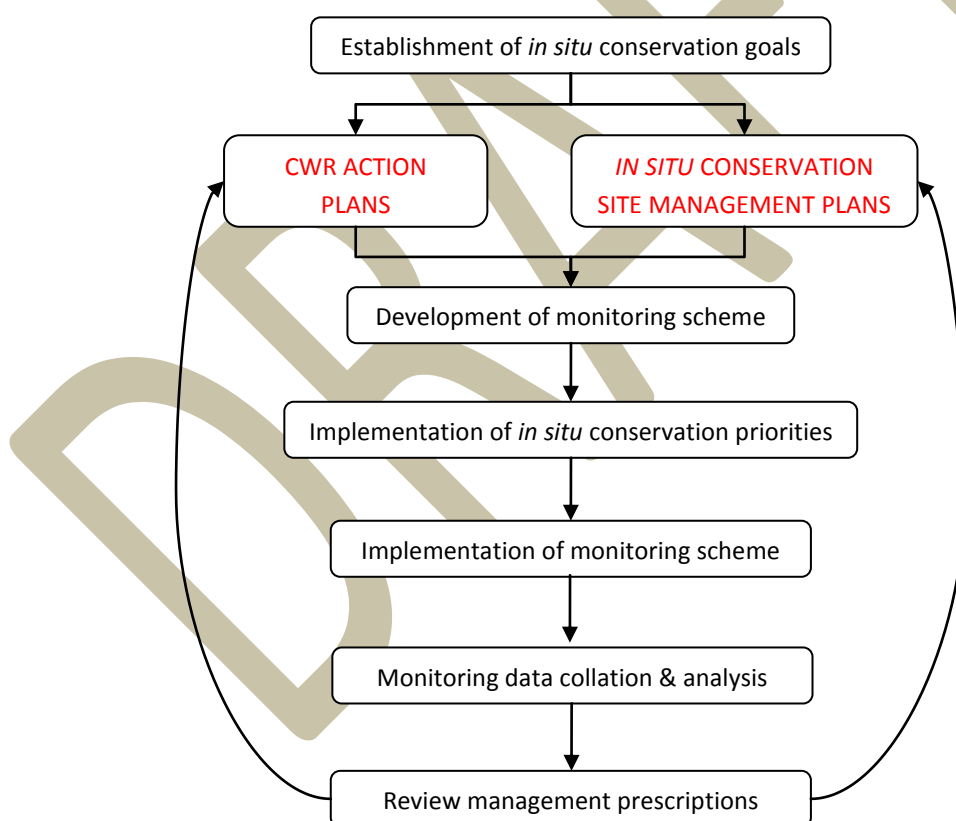


Figure 24. Monitoring of CWR diversity *in situ*

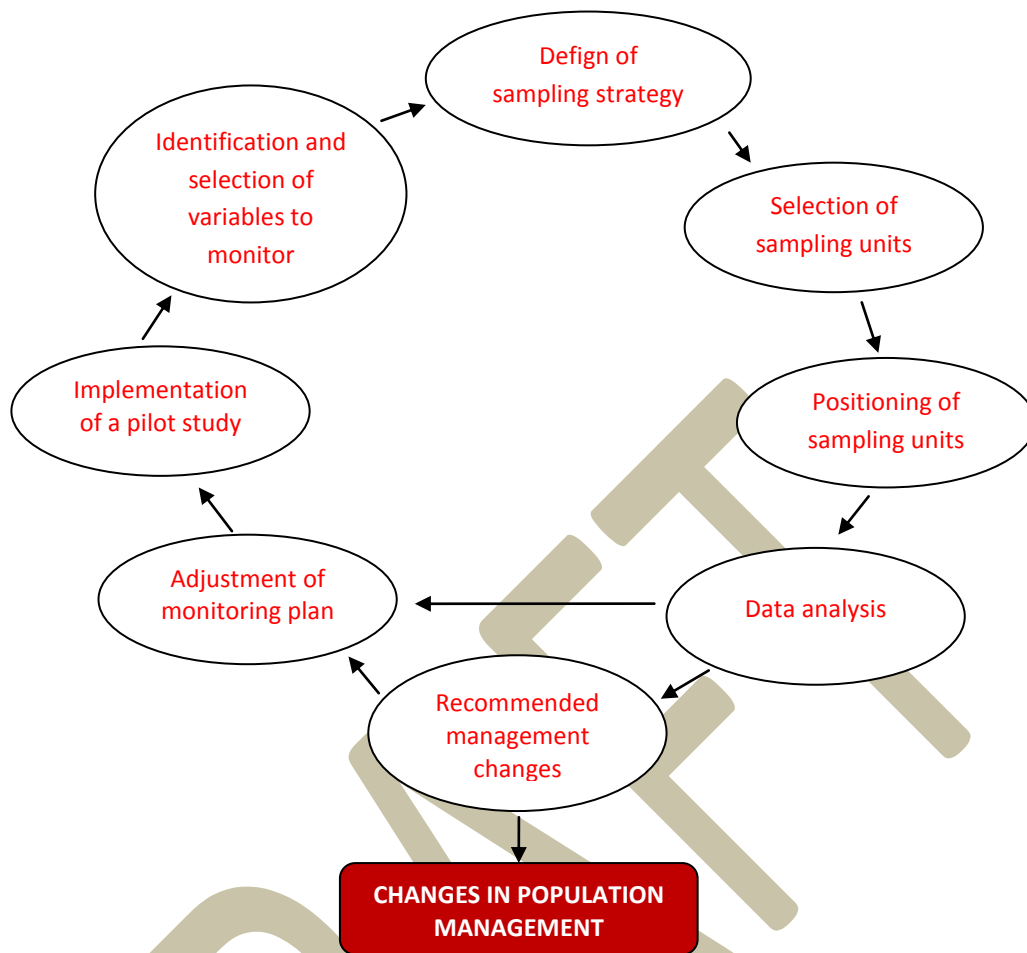


Figure 25. Development of a monitoring plan at the individual CWR level

A.12.2. Methodology

The methodology will focus on monitoring CWR populations conserved *in situ* as the monitoring of *ex situ* conserved accessions is covered in the previous section (see A11) and the monitoring of higher level indicators of CWR conservation is a relatively novel introduction and tried and tested methodologies are yet to be available. Also note that whether the monitoring of CWR populations occurs in formally recognised genetic reserves or an informal *in situ* conservation area, the monitoring will still have the same objectives and is likely to be implemented in a similar manner, as follows:

- (i) Identification and selection of the variables to monitor. These variables may include demographic, ecological and anthropogenic parameters. At this stage, it is important to take into account parameters such as the life form and breeding system of the target taxon, as well as the resources available for monitoring.
- (ii) Design of the sampling strategy. The design of the sampling strategy (which involves making decisions on the type, size, number and positioning of the sampling units and the timing and frequency of sampling⁹¹) should be based on a review of the available literature on the monitoring of taxa with similar life forms and biological traits, as well as through consultation with conservation management experts. The monitoring plan should be designed

⁹¹ Elzinga *et al.* (2001); Iriondo *et al.* (2008)

in a way to detecting changes in the target population but distinguish between significant biological changes in the population that may negatively impact population health and normal seasonal variations that need not trigger changes in management actions.

(iii) Selection and positioning of the sampling units. Sampling can be carried out using various methods: plot (or quadrat within areas of standard size), transect (banded transect or intercept - transects sample diversity within a defined distance either side of a central line, often 1m either side making a 2m wide transect, while the line intercept samples diversity that actually touches the line) methods or even monitoring of individual plants (or plant parts) for particular attributes (e.g. plant height, number of seeds per fruit)⁹². In an *in situ* conservation site, the plot method is most likely to be used with the establishment of permanent quadrats.

(iv) Positioning of sampling units. It should be random and ideally distributed throughout the entire area of distribution of the population. Methods of random sampling include: simple random sampling, systematic sampling and stratified random sampling⁹³.

(v) Determination of the timing and frequency of monitoring. Populations of CWR in genetic reserves should be surveyed regularly in order to detect any changes. Monitoring is commonly most effective when the target species is flowering or fruiting, as often then they can be easily identified. It also can be carried out when leaves are unusually coloured or about to fall, or when the surrounding vegetation does not obscure the target species or other particular character of the target taxon. Either way, it should be scheduled at the same phenological time each year to ensure the data are directly comparable between monitoring events.

The frequency of monitoring (time between surveys) is usually dictated by the perception the researcher has during the first surveys. However, it depends on the life form, the expected rate of change, the rarity and trend of the target species, as well as on the resources available for monitoring. It can be as frequent as every month (e.g. rare or very threatened annuals) during several growing seasons, or annually (e.g. annuals) or less frequently (e.g. perennials). Generally, the monitoring in a newly established reserve is more frequent than in a well-established one. With time and experience, frequency of monitoring can be adjusted.

(vi) Implementation of a pilot study. A pilot study should be carried out once the monitoring scheme has been designed in order to assess how efficient the experimental design is and whether the field techniques are efficient, before the implementation of a long term monitoring strategy.

(vii) Data analysis. The results of the pilot study should be analysed in order to detect possible problems with the monitoring design and field methodologies and if necessary adjust them to ensure that the scheme will detect changes that may indicate a decline in the size and/or genetic diversity of the population.

(viii) Adjustment of monitoring plan. Frequently, refinement of the monitoring plan is needed. Sample size, position of sampling units, etc. may be inadequate to detect meaningful changes in the population so they need to be adjusted. However, changes to the monitoring regime may negatively impact data comparison, so any changes need to be considered, possible with the help of a statistician, before being implemented.

⁹² Iriondo *et al.* (2008).

⁹³ Simple random sampling involves the selection of combination of sampling units that has the same probability of being selected, and that the selection of one sampling unit does not affect the selection of any other. Systematic sampling involves the collection of samples at regular (in time and space) intervals. Stratified random sampling involves dividing the population into two or more groups prior to sampling, where groups within the same group are very similar and simple random samples are taken within each group (Iriondo *et al.* 2008).

Table 4. Monitoring CWR to detect changes in diversity ⁹⁴

LEVEL OF MONITORING	TYPE OF PARAMETERS	PARAMETERS TO MEASURE	EXPLANATION	OBJECTIVES
Individual CWR	Demographic	Population size	Total number of individuals in a population	1. To assess viability of populations – estimate: <ul style="list-style-type: none"> ▪ population trends ▪ extinction risk ▪ population viability analysis (PVA)⁹⁵ 2. To identify demographic factors that are most relevant to population viability
		Population density	Number of individuals per unit area	
		Population frequency	% of plots occupied by the target species within the sampled area	
		Population cover	% of plot area that falls within the vertical projection of the plants of the target species	
		Population structure	Size, stage or age of individuals	
		Survival rate	Proportion of individuals recorded in a first census that are still alive at the second census (usually for each class in structured populations)	
		Growth rate	Probability that a surviving individual moves from one size (or stage) class to any of the others	
		Fertility rate	Average number of offspring that individuals in each class produce from one census to the next	
	Spatial structure	Spatial distribution of each individual		
Ecological	<u>Abiotic components:</u> <ol style="list-style-type: none"> 1. Temperature, precipitation, solar radiation, wind, cloud cover, atmospheric pressure, humidity; 2. Soil moisture, texture, pH, nutrients, 	Environmental conditions of the habitat where the plant occurs	To identify changes in the physical conditions that characterise CWR and their associated communities; it can be used as a surrogate to infer population trends when demographic data are not	

⁹⁴ See Iriondo *et al.* (2008) for more detail.

⁹⁵ Population viability analysis (PVA) uses demographic modelling methods in order to predict the future status of a population, thus helping conservation and management decisions (Iriondo *et al.* 2008).

LEVEL OF MONITORING	TYPE OF PARAMETERS	PARAMETERS TO MEASURE	EXPLANATION	OBJECTIVES
		salinity, redox potential, cation exchange capacity		available
		<u>Biotic components:</u> 1. Density, cover and frequency of all taxa that occur in the community, importance value ⁹⁶ 2. Density and frequency of pollinators, seed dispersers, predators and parasites 3. Identification of pathogens and intensity of pathogen infection	The living organisms that occur in the habitat of the target taxon	
		<u>Disturbance:</u> 1. Natural (fire, flooding, slope movement, wind damage, extreme temperatures, trampling, erosion) 2. Human-induced disturbance (mining, logging, livestock grazing, recreation, road construction or maintenance, weed control)	Threats to the populations of the target species	
		<u>Climate change:</u> 1. Annual recordings of susceptible species and habitats 2. Phenology 3. Changes in composition of communities		

⁹⁶ See Cox (1990) for definition.

LEVEL OF MONITORING	TYPE OF PARAMETERS	PARAMETERS TO MEASURE	EXPLANATION	OBJECTIVES
	Anthropogenic	Social, economic, political and cultural threats and opportunities	-	To account for human influence on the biological status and effectiveness of conservation actions
Genetic		Reproductive fitness	Measure of an individual's ability to produce offspring to the subsequent generation	<ul style="list-style-type: none"> ▪ To evaluate the genetic diversity within populations ▪ To understand the dynamics of populations ▪ To recognise when overall reduction of fitness of a population has occurred ▪ To determine the level of inbreeding/outbreeding of the target species ▪ To determine which populations should be targeted for protection ▪ To determine what to do if a protected population has suffered a severe decline in population size
		Effective population size	The size of a hypothetical population that would lose genetic diversity at the same rate as the population under study	
		Genetic diversity Gene flow Population structure		
		Minimum viable population	The minimum size of a population needed to remain genetically viable and to maintain genetic variation and heterozygosity	

A.12.3. Examples and applied use

Box 56. Assessment and monitoring of agrobiodiversity and its threats in the Fertile Crescent

Biodiversity in the Fertile Crescent is of global significance as it has globally significant populations of LR and CWR of wheat, barley, lentil, chickpea, faba bean and several species of forages, range species and dryland fruit trees. Little is known on the status and trends of the diversity of these species as witnessed by the First and Second reports on the State of the World on Plant Genetic Resources produced by FAO. ICARDA together with national research institutes in Jordan, Lebanon, Palestinian Authority and Syria conducted population surveys in more than 65 monitoring sites between 2000-2005 period as part of a GEF-supported regional project on promoting *in situ* conservation of dryland agrobiodiversity in the four countries. Further surveys were continued in 40 monitoring sites in 2009 and 2011. The CWR demographic data accumulated over 11 years showed that the CWR populations are suffering continued loss due to over-grazing, land reclamation and destruction of natural habitats. However, the CWR demographic data collected in Sweida and Al Haffeh in Syria were less affected compared to all other non-Syrian sites. The sites originally selected for the presence of large, healthy CWR populations in Aarsal in Lebanon and Hebron in the West Bank on re-surveying were found to be complete destroyed due to extensive quarrying. Although eleven of the original 65 sites were recommended for the establishment of protected areas, only one in the Alajjat region of southern Syria was declared in 2008 as natural reserve.

As for LR populations, the farming survey conducted in 2000 and 2004 showed that landraces of barley, lentil, figs and olive still predominant within the farming systems practiced by 26 communities. However, the area of LR cultivation is reduced due to the land management changes and the introduction of exotic plantation of fruit trees (such as cherries, apples and olive). The surveying shows native durum wheat, apple, cherry, almond and apricot LR are being replaced by improved foreign varieties but there are already case where the introduced commercial varieties are failing because of their unsuitability to the local conditions.

Source: Amri, A. (Pers. Comm.)

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http://www.biodiversityinternational.org/training/training_materials.html#c10715

Examples of monitoring plans:



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DRAFT

A.13. Promoting the use of conserved CWR diversity

A.13.1. Overview

Why link conservation with use?

Some conservationists argue that conservation is an end in itself, we do not conserve to benefit humankind, they argue that all species have intrinsic value and therefore have a right to be conserved for their own sake irrespective of their value to humankind. We consider this argument well-meaning, but mistaken because:

- Cost of conservation — conservation does have a real and often significant cost (the annual cost of PGRFA *ex situ* conservation was estimated at US\$ 30.5 million in 2000⁹⁷) those funds might be used to feed the starving, heal the sick or educate the illiterate, so why should humankind meet this cost, politicians and public make such a commitment, unless it is associated with some actual or potential benefit to humankind;
- Investment in PGRFA — although PGRFA conservation has a real cost focusing resources on PGRFA conservation can bring substantial rewards (annual income from using PGRFA in 2000 was US\$ 500-800 billion⁹⁸), so conserving PGRFA is a sound economic investment;
- Conservation sustainability — *in situ* CWR conservation, particularly, requires a relatively high and long-term investment in managing and monitoring of CWR populations, so on-going use of the conserved diversity offers a means of underpinning their value and reinforces conservation sustainability;
- Human altruism — humans are unable to see the world dispassionately, when men, women and children are suffering from malnutrition in many parts of the world, there appears to be no practical alternative than to give those species of most direct use to humankind the highest conservation priority.

Therefore, we consider the conservation of PGRFA and human exploitation as being intimately linked both now or in the future, this linkage forms the basis for enduring human food security and well-being, not to mention the continuing survival of humankind itself.

The conservation of CWR diversity is explicitly linked to utilization, further CWR are in fact defined by their potential contribution for exploitation; the actual or potential donation of CWR traits to crops. The CBD⁸⁴ emphasizes the need to link conservation to use, noting that utilization should be "sustainable" and "meet the needs and aspirations of present and future generations". The use of CWR in crop improvement has recently been reviewed for 29 major crops⁹⁹ and the following points noted:

- For the 29 crop species included there were 234 references that report the identification of useful traits from 183 CWR taxa;
- The degree to which breeders use CWR species varies between crops, it is particularly prominent in barley, cassava, potato, rice, tomato and wheat, but rice and wheat are the crops in which CWR have been most widely used, both in terms of number of CWR taxa used and successful attempts to introgress traits from the CWR to the crop;

⁹⁷ Hawkes *et al.* (2000)

⁹⁸ ten Kate and Laird (1999)

⁹⁹ Maxted and Kell (2009)

- The most widespread CWR use has been and remains in the development of disease and pest resistance, with the references citing disease resistance objectives accounting for 39%, pest and disease resistance 17%, abiotic stress 13%, yield increase 10%, cytoplasmic male sterility and fertility restorers 4%, quality improvers 11% and husbandry improvement 6% of the reported inter-specific trait transfers;
- The number of paper publications detailing use of CWR in breeding has increased gradually over time, presumably as a result of technological developments for trait transfer, with 2% of citations recorded prior to 1970, 13% in the 1970s, 15% in the 1980s, 32% in the 1990s and 38% after 1999.
- It can also be seen that since the year 2000 the number of attempts to improve quality, husbandry and end-product commodities has increased substantially;
- The use of CWR in crop improvement was primarily based upon published journal papers but this is unlikely to reflect closely actual use of CWR in commercial crop breeding because (a) the reporting of useful CWR trait transfer to a crop it does not mean that this exercise resulted in a novel variety, and (b) breeders are unlikely to be forthcoming about their use of CWR due commercially sensitive, so the use of CWR in crop improvement is significant but imprecisely defined;
- The exploitation of the potential diversity contained in CWR species remains *ad hoc* as the approach by breeders to CWR use has not been systematic or comprehensive.

The review concludes that there is a wealth of novel traits available for crop improvement in CWR and thus far the vast majority of CWR diversity is untapped in terms of its potential exploitation value.

Although CWR primarily gain their value from being sources of traits for crop improvement, they have value associated with their use by traditional, general, and professional communities. The work of professional users, the general public and local people can be linked through partnerships with NGOs, which could help by organizing conservation volunteers, and could be involved in sustainable rural development or use of resources in accordance with traditional cultural practices. Raising public and professional awareness of the need to conserve CWR can only help promote specific conservation action, as well as general conservation sustainability. All partners should therefore share the goals of sustainable use of biological resources taking into account social, economic, environmental and scientific factors which form a cornerstone of the nations' proposals to implement Agenda 21.

A.13.2. Methodology

Professional users include various researchers, farmers as well as plant breeders. If associated with trait use the diversity is likely to be characterised, evaluated and screened for the novel traits, and then use of the trait bearing germplasm in crop breeding programmes. Various characterization techniques can be used to identify useful traits. Professional users can utilise CWR germplasm conserved in *in situ* conservation sites but more often they will utilise the samples of these population stored *ex situ* in gene banks. However, the managers of genetic reserves (PA managers together with the support of the relevant conservation authority) should attempt to work with the professional user community to characterise, evaluate and publicise the germplasm found at the site. CWR are wild species and like any other group of wild species may be ecologically and genetically studied and contribute to general ecosystem health.

General users are the public in general who via their taxes fund most CWR conservation and whose support is likely to be essential for the long-term political and financial viability of CWR conservation, particularly *in situ* activities that have higher associated maintenance costs than

germplasm held *ex situ* in gene banks. One way of promoting public awareness of the value of CWR to the general public is to encourage them to visit genetic reserves and during their visit supply them with various formal and informal education material, CWR based cook books, agrobiodiversity ecotourism, art competitions etc., each of which is designed to raise awareness of the value of CWR and their conservation. The PA containing the genetic reserve should have infrastructures that take into account the needs of visitors (e.g. visitor centres, nature trails, lectures, etc.). They are also likely to bring additional income to the PA itself through guided tours and the sale of PA information packs.

Traditional users of CWR are people from local communities who live in the vicinity of CWR populations; they are likely to have an extensive history of local plant collecting and utilization, and possibly of CWR themselves. They often possess extensive knowledge of the ethnobotanical value and direct uses of plants and because of the large proportion of all species that are CWR, a high proportion will be CWR – though their use may be incidental to their value as a CWR (see Box 57).

Within this context it is worth noting that *in situ* CWR conservation sites are not established in an anthropogenic vacuum; in other words whether a genetic reserve is to be established or a particular CWR population sampled for *ex situ* conservation, there are likely to have been traditional or local users of that resource prior to the conservation of that resource. So if the support of the local community for CWR conservation is to be obtained the active CWR conservation should not hinder local resource use, unless in the rare case where it directly conflicts with the long-term viability of the target CWR population. Many studies have shown that conservation cannot succeed without local community support; however, as shown by a recent analysis of the threats to CWR in Europe¹⁰⁰, local communities do not always, or rather are not always permitted, to manage their resources sustainably, even if mismanagement is likely to adversely impact their longer-term interests. For example, the development of tourism or urban expansion is usually governed by the government (at least in terms of planning permission). Local communities may be given a voice and try to resist such development, but in reality have little influence when confronting government policy. Likewise, if a private landowner decides to sell his/her land for development, there is seldom little that the local community can do to stop them. Therefore, the conservationist's role when formulating conservation action may be just as much about resolving conflicts between local community and practical conservation implementation, ensuring continued local community use of their PGR resources while achieving sustainable conservation. Further there is a key role for the conservationist to play in educating both policy-makers and local people about the importance of these critical genetic resources.

In situ CWR conservation sites should not only be seen as a means of conserving CWR diversity, but also as *in situ* research platforms for field experimentation. There is a need for a better understanding of species dynamics within conservation areas to aid the sustainable management of the specific taxa, but also for ecological and genetic studies of *in situ* conserved CWR. Research activities on the material conserved should be encouraged as they provide additional justification for the establishment and long-term management of the conservation area. Monitoring studies (such as of genetic diversity changes), as required by the COP to the CBD adopted Strategic Plan¹⁰¹ can be facilitated by *in situ* site managers, possibly in collaboration with NGOs and local volunteer groups. This way, changes associated with future habitat management scenarios could be detected and actions taken to reduce current rates of diversity loss.

¹⁰⁰ Kell *et al.* (2012)

¹⁰¹ CBD (2010b)



Involving local communities in CWR conservation decision making, Sweida, Syria (photo: Nigel Maxted).

Box 57. Can farmers benefit directly from CWR diversity?

It is interesting to question whether CWR are of any direct value to farmers as CWR. There are a few anecdotal reports in the literature of farmers deliberately growing the crops near CWR to facilitate traits transfer between the CWR and the crop, such as Mexican farmers encouraging teosinte (*Zea mexicana*) to grow alongside the crop maize (*Zea mays*) to permit natural crossing between the CWR and the crop. The corn producers mentioned that in approximately four years they can obtain a new, better adapted maize variety that will out-compete traditional varieties or hybrid maize (Serratos *et al.* 1996).

However this case does seem counter intuitive and contradicts the experience of many plant breeders. Plant breeders often state that the reason that they are reluctant to use CWR in their breeding programmes is because if they cross their elite breeding lines with CWR, not only do they get the possibility of the desired trait but the potentially beneficial traits are greatly outnumbered by the deleterious characters that are also introduced from the CWR. It then takes significant resources to select out the unwanted deleterious characters but retain the desired traits. For any predominantly bred or highly farmer-selected crop, introgression between the CWR and crop is likely to have an overall negative impact on the farmer's crop, potentially reducing yield and crop adaptive characteristics and in the short term reducing farmer's income. The amount of CWR to crop introgression is also likely to vary from crop to crop and be very limited for known inbreeding crops.

So, despite the case made for Mexican farmers directly using CWR, it seems likely that generally farmers do not benefit directly from natural trait transfer between CWR and crops; however it is critical if we are to conserve the full breadth of CWR diversity that farmers understand the role of CWR in under-pinning novel cultivar development. Thus greater effort needs to be placed on raising public and professional awareness of the value of CWR diversity.

A.13.3. Examples and applied use

Box 58. Some examples of CWR use in breeding

To give some idea of the scale of benefits that may accrue from the use of CWR in crop improvement here are some examples for selected crops:

- Desirable traits from wild sunflowers (*Helianthus* spp.) are worth an estimated US\$267 to US\$384 million annually to the sunflower industry in the United States;
- A single wild tomato species (*Lycopersicon peruvianum* (L.) Mill.) has contributed to a 2.4 per cent increase in solids contents worth US\$250 million;
- Three wild peanuts (*Arachis batizocoi* Krapov. & W. C. Gregory, *A. cardenasii* Krapov & W. C. Gregory and *A. diogeni* Hoehne) have provided resistance to the root knot nematode, which costs peanut growers around the world US\$100 million each year;
- In the 1970s the US maize crop was severely attacked by corn blight reducing yield by 50% and economic loss of almost US\$ 1,000 million but was resolved by blight resistant genes from *Tripsacum dactyloides* L.;
- Single gene-controlled traits have been introduced from CWR for virus resistance in rice (*Oryza sativa* L.), blight resistance in potato (*Solanum tuberosum* L.), powdery mildew resistance in wheat (*Triticum aestivum* L.) and Fusarium and nematode resistance in tomato (*Lycopersicon esculentum* Mill.);
- Recently genes from wild *Brassica oleracea* L. have created domestic broccoli with high levels of anti-cancer compounds.
- Overall new genes from wild relatives contribute approximately US\$115 billion worldwide toward increased crop yields per year.

Source: Maxted and Kell (2009); and Hunter and Heywood (2011)



Using wild emmer wheat to increase diversity in cultivated wheat, National Institute of Agricultural Botany field plots (photo: Nigel Maxted).

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A.13.5. Additional materials and resources

See Focused Identification of Germplasm Strategy (FIGS) 'Additional materials and resources' in A.8.

See Genetic studies to search for traits of interest for crop breeding 'Additional materials' in A.5.

Promoting the use of CWR:



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European Commission project: "Novel characterization of crop wild relative and landrace resources as a basis for improved crop breeding" (PGR Secure): <http://pgrsecure.org/>.

WWW

Global Crop Diversity Trust led project 'Adapting agriculture to climate change' has a dominant use component: <http://www.cwrdiversity.org/>

WWW

Bioversity international led project 'UNEP/GEF Crop Wild Relative' project has a use component: <http://www.cropwildrelatives.org/>

A.14. Information system and data management

A.14.1. Overview

Why is data critical to crop wild relative conservation and use?

It is widely accepted within the PGRFA conservation and user community that one major factor hindering effective conservation and use is the lack of easy access to data, as well as obstacles to information exchange due to the many different approaches in managing data. If we are to inventory and build national CWR conservation strategies then consistent data collation and management is required.

To conserve CWR efficiently there is necessarily a significant requirement for data and associated information, that data needs to be sourced, managed and analysed to help ensure the most appropriate conservation actions are implemented. This process is likely to involve taxonomic, ecogeographic occurrences and temporal distribution, threats and conservation status and genetic structure data, as well as the ability to track using time-series data and predicted demographic and genetic changes within a species in relation to land management and environmental factors. The data sources are often not readily available and for CWR are particularly disperse because of the broad taxonomic range of species and the fact that much data are held by those outside of the PGR community. Accessing such information is not only time-consuming, but comparing data sets is often difficult due to the diversity of information management models used. If CWR are to be conserved and sustainably utilized, a means of bringing together this information into an accessible and standard format is required.

To help manage this data both CWR descriptors and information management tools have been developed. The first attempt to produce a set of CWR descriptors was made by the EC funded PGR Forum project¹⁰² and these were developed further within the GEF funded 'In situ conservation of crop wild relatives through enhanced information management and field application'¹⁰³ and are now being further developed with the EC funded PGR Secure project¹⁰⁴; the current version of the CWR descriptors is available at PGR Secure helpdesk (<http://pgrsecure.org/>). Within PGR Forum a stand-alone information systems was developed to help make available CWR data for Europe and the Mediterranean to the user community, the Crop Wild Relative Information System (CWRIS) (see Box 59) and this was extended in the EC funded AEGRO project¹⁰⁵ (see Box 60). Although there are currently no plans to develop CWRIS further, it is functional and can be used in the creation of national checklists for Europe and the Mediterranean countries, CWRIS users gain access to the checklist data by selecting the country or geographical units of interest and then downloading the dataset. These data can then be cross-checked against local floras, databases and other documentation, verified and edited as necessary to ensure it meets the national requirement.

Box 59. CWRIS

The Crop Wild Relative Information System (CWRIS - <http://www.pgrforum.org/cwris.htm>) was the first information management system specifically designed to facilitate CWR conservation and use. CWRIS has two main dimensions: taxon information breadth is provided by the *PGR Forum CWR Catalogue for Europe and the Mediterranean*, while the CWR descriptors for conservation and use for individual CWR

¹⁰² See Moore *et al.* (2006) and <http://www.pgrforum.org/cwris/cwris.asp>

¹⁰³ See <http://www.cropwildrelatives.org/>

¹⁰⁴ See <http://pgrsecure.org/>

¹⁰⁵ See <http://aegro.jki.bund.de/aegro/index.php?id=95>

taxa provide taxon information depth. The CWR descriptors provide a comprehensive set of data standards that can be used to effectively manage genetic conservation of CWR taxa and their component populations. The descriptors provide the structure within which existing data can be accessed or mapped onto the data model, and novel data can be provided. CWRIS was designed to facilitate access to CWR data for a diverse range of user communities, including plant breeders, protected area managers, policy-makers, conservationists, taxonomists and the wider public. CWRIS also provides access to ancillary information on the taxa contained in the Catalogue via links to external online resources, such as Mansfeld's World Database of Agricultural and Horticultural Crops, GRIN Taxonomy, European Nature Information System (EUNIS), the IUCN Red List, Electronic Plant Information Centre (EPIC) and key publication search engines. CWRIS comprises:

- A searchable database of crop species and their associated wild relatives that occur in Europe and the Mediterranean region. The taxonomic back-bone to CWRIS was provided by Euro+Med PlantBase (<http://www.emplantbase.org/home.html>) version August 2005. CWRIS provides occurrence records according to geographic boundaries, not political boundaries.
- Information on the taxa contained in the database via external web links.
- A data model for the management of CWR information, with an emphasis on site and population data, which is required for the effective genetic conservation of *in situ* CWR populations. The data model is illustrated with a number of CWR case studies.

Source: Kell *et al.* (2008)

Box 60. CWRIS PLIS

The Crop Wild Relative Information System (CWRIS - <http://www.pgrforum.org/cwr.htm>) was also extended to provide information at the species level within the EC funded AEGRO project, using four independent modules collectively called "Population Level Information System" for *Avena*, *Beta*, *Brassica* and *Prunus* European species population level occurrence data. The population level information system was designed to facilitate CWR conservation management and monitoring via:

- a. Data exploration
 - Search for occurrences by taxonomic criteria (hierarchical search through taxonomic ranks including synonyms according to different taxonomic views)
 - Search for occurrences by geographic information (hierarchical search through levels of administrative units or within protected areas)
 - Combined search by taxonomic and geographic criteria
- b. Data acquisition
 - Downloading results and displaying them on a map
- c. Data contribution
 - Editing taxonomic and geographic data for atomization, harmonization and geo-referencing
 - Acquisition of population data in the field with portable data assistants and uploading these data to a central database.

The data exploration and data acquisition use cases have been fully implemented in CWRIS-PLIS (<http://aegro.jki.bund.de/index.php?id=168>), while the data contribution use cases have been only partly implemented.

Germeier *et al.* (2012)

A.14.2. Methodology

Information on CWR is available from wide range of sources, but retrieving it presents a number of challenges. Firstly, in existing databases, such as those managed by plant gene

banks, CWR accessions are not identified as CWR; this issue is not helped by the fact that in the current FAO/IPGRI Multi-crop Passport Descriptors V. 2¹⁰⁶ the SAMPSTAT descriptor allows for designation of wild species samples but does not make a distinction between CWR and non-CWR wild species. Secondly, although information on CWR per se is possible only of specific interest to the PGR conservation and use community because CWR are 'normal' wild species they are also collected, conserved and studied by a broad community of taxonomist, ecologists, geneticists, physiologists, etc. and so when collating CWR information these other communities need to be consulted. Further these non-PGR communities often have significantly larger data sets than the PGR community itself. These challenges are not insurmountable but they do demand a carefully considered and tested approach (particularly with regard to obtaining information from non-PGR communities) and a considerable amount of time. However, like all data mining activities the more background data available the more predictive the analysis results in formulating effective conservation plans.

Information at the CWR at the taxon level is primarily gathered from the relevant literature: monographs, revisions, field guides, floras, gazetteers, articles, papers, soil, vegetation and climatic maps, atlases, etc., while at the accession level it is gathered from herbarium and germplasm collections of the target taxon from the target area, and the latter will often involve visiting the herbarium or gene bank to collect the data. However in recent years there has been exponential growth of web-enabled ecogeographic datasets, most notably the Global Biodiversity Information Facility (GBIF) established in 2001 (<http://data.gbif.org>), which provides extensive access to global taxon nomenclature, taxon and accession distribution, conservation and environmental data.

Table 5. Internet resources for CWR¹⁰⁷

DATA SET	DESCRIPTION	URL
Botanical Garden Conservation International	Botanic garden holdings information	http://www.rbgekew.org.uk/BGCI/http://www.biodiv.org/
Crop Wild Relative Information System (CWRIS)	PGR Forum CWR Catalogue for Europe and the Mediterranean	http://www.pgrforum.org/cwrism.htm
European Native Seed Conservation (ENSCOBASE)	European database of major <i>ex situ</i> botanic garden gene bank holdings	http://enscobase.maich.gr/
European Plant Genetic Resources Search Catalogue (EURISCO)	European database of major <i>ex situ</i> agrobiodiversity gene bank holdings	http://eurisco.ecpgr.org/nc/home_page.html
FAOSTAT	Agricultural statistics and data	http://www.faostat.fao.org/
Gap Analysis Project	<i>Ex situ</i> gap analysis results of 13 crop gene pools	gisweb.ciat.cgiar.org/gapanalysis/
GBIF	Global Biodiversity data	http://data.gbif.org/
GENESYS	Global database of major <i>ex situ</i> gene bank holdings	http://www.genesys-pgr.org/
Glob cover	European Space Agency Global Land Cover map, latest version	http://ionia1.esrin.esa.int/

¹⁰⁶ http://eurisco.ecpgr.org/fileadmin/www.eurisco.org/documents/MCPD_V2_2012_Final_PDFversion.pdf

¹⁰⁷ Castañeda Álvarez *et al.* (2011)

	= 2009	
Harlan and de Wet Global Priority Checklist of CWR Taxa	Global checklist and database of priority CWR taxa in 173 crop gene pools	http://www.cwrdiversity.org
IUCN Red List	Database of red list (extinction threat) assessments	http://www.iucnredlist.org/
JSTOR herbaria	Herbaria resources	http://plants.jstor.org/
Plant list	Working list of all known plant species	http://www.theplantlist.org/
Tropicos (Missouri Botanical Gardens, USA)	Herbaria resources	http://www.tropicos.org
UNEP WCMC World Database of Protected Areas	World Database on Protected Areas (polygons)	http://www.protectedplanet.net/
US Genetic Resources Information Network (GRIN)	Database of USDA <i>ex situ</i> gene bank holdings	http://www.ars-grin.gov/npgs/acc/acc_queries.html
National program accession datasets		
Russia	AgroAtlas	www.agroatlas.ru
Brazil	CRIA	www.cria.org.br
Japan	NIAS	www.gene.affrc.go.jp/databases_en.php
Mexico		www.biodiversidad.gob.mx/genes/proyectoMaices.html
Other accession datasets		
CWRIS PLIS		http://aegro.jki.bund.de/index.php?id=168
Harold and Adele Lieberman Germplasm Bank (cereals)		www.tau.ac.il/lifesci/units/ICCI/genebank1.html
Manchester Museum		http://emu.man.ac.uk/mmcustom/BotQuery.php
Millennium Seed Bank, Kew		www.kew.org/science-conservation/save-seed-prosper/millennium-seed-bank/index.htm
Natural History Museum, UK		www.nhm.ac.uk/research-curation/collections/departmental-collections/botany-collections/search/index.php
Royal Botanic Gardens Kew		http://apps.kew.org/herbcat/navigator.do
Royal Botanical Garden of Edinburgh		www.rbge.org.uk/databases
SolanaceaeSource		www.nhm.ac.uk/research-curation/research/projects/solanaceaesource
United States Virtual Herbarium		http://usvirtualherbarium.org
Virtual Australian Herbarium		http://plantnet.rbg Syd.nsw.gov.au/HISCOM/Virtualherb/virtualherbarium.html#Virtual

The types of data managed will fall into four basic types, which may be subdivided:

- Ecogeographic data (taxonomic, ecological, geographic and genetic);

- Taxonomy and nomenclature,
- Degree of relationship between crop and CWR,
- CWR uses: historic, current and potential,
- Other uses: other than as a trait donor,
- Current, historical and potential distribution, including:
 - o Country occurrence/extent of occurrence,
 - o Number of populations,
 - o Record of extinctions,
 - o Mapping function/GIS layers,
- Genetic diversity and biology,
- Ecology and habitat,
- Threat status,
- Conservation measures, including:
 - o Occurrence in named protected areas and genetic reserves,
 - o Conservation management techniques,
 - o *Ex situ* holdings in gene banks,
- References to specific research projects,
- Contacts,
- Field population data (passport);
 - Precise population location (distributional polygon),
 - Land management regime (protected area, private ownership, common land),
 - Population characteristics,
 - o Size,
 - o Cover
 - o Genetic characterization,
 - o Age structure,
 - o Obligate associated species (associated keystones, pollinators, seed dispersers)
- Conservation management data (curatorial);
 - *In situ* criteria
 - o Management regime and interventions
 - o Monitoring regime
 - o Place in national, regional and global CWR networks
 - o Place in non-CWR specific conservation networks
 - o Local community participation
 - *Ex situ* criteria
 - o Gene bank holding collection,
 - o Location of seed in gene bank,
 - o Germination and regeneration testing,
 - o Access and benefit sharing policy,
- Characterization and evaluation data (descriptive);
 - Taxonomic morphological description

- Genetic description,
- Agronomic description
- Breeder desired characteristic evaluation (disease, pest, drought resistance, etc.)

Although this list of CWR data types is extensive it is not exhaustive, it is indicative of the types of data involved in CWR conservation and use.

Each of these data types are collated using some type of standard descriptor. A descriptor may be defined as “any attribute referring to a population, accession or taxon which the conservationist uses for the purpose of describing, conserving and using this material”. Descriptors are abstract in a general sense, and it is the descriptor states that conservationists actually record and utilise. Standard descriptors for ecogeographic, field and conservation management data are included in the Descriptors for CWR¹⁰⁸, while formal characterization and evaluation descriptors are associated with various standardized ‘Crop descriptor lists’ published by FAO, Bioversity, UPOV (see <http://www.bioversityinternational.org/publications.html>) – these may or may not be suitable for describing the crop’s associated CWR. It is important to stress that standard lists of descriptors should be used when they are available. The use of well-defined, tested and rigorously implemented descriptor lists for scoring descriptors considerably simplifies all operations concerned with data recording, such as updating and modifying data, information retrieval, exchange, data analysis and transformation. When data are recorded, they should be classified and interpreted with a pre-defined list of descriptors and descriptor states to consult. This clearly saves a considerable amount of time and effort associated with data entry. The use of lists ensures uniformity, while reducing errors and problems associated with text synonyms.

A.14.3. Examples and applied use

There are a growing number of National CWR Conservation Strategies that have been completed in recent years and each involves significant data collation and analysis, and its application to practically conserve the priority CWR taxa. In terms of data management each step in creation and updating the National CWR Conservation Strategy (see Figure 26) involves:

a. *CWR National Checklist* – The common first step in production of a National CWR Conservation Strategy is to produce a national CWR checklist; this is normally a simple table of the Latin names of the CWR taxa present in the country, as follows for the national CWR checklist of Saudi Arabia:

Genus	Species	Species Author	Subspecific Rank	Subspecific Author
<i>Aegilops</i>	<i>kotschyi</i>	Boiss.		
<i>Aegilops</i>	<i>peregrina</i>	(Hack.) Maire & Weiller		
<i>Aegilops</i>	<i>vavilovii</i>	(Zhuk.) Chennav.		
<i>Aerva</i>	<i>javanica</i>	(Burm.f.) Juss. ex Schult.		
<i>Aerva</i>	<i>lanata</i>	(L.) Juss.		
<i>Agathophora</i>	<i>alopecuroides</i>	(Moq.) Bunge		

¹⁰⁸ <http://www.cropwildrelatives.org/>

Agathophora alopecuroides (Moq.) Bunge

var. papillosa (Maire) Boulos

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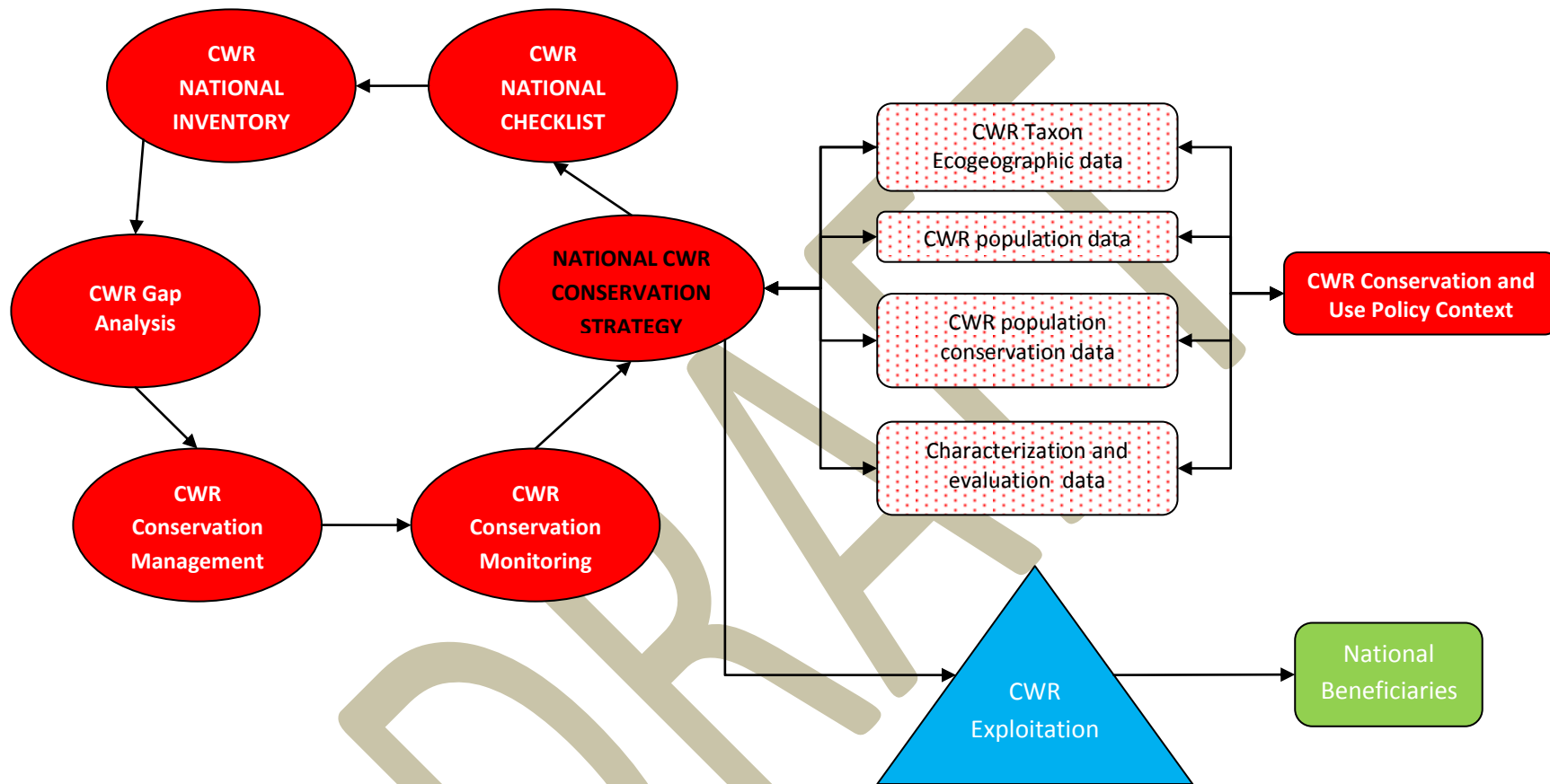


Figure 26. Summary of data flow in CWR conservation

b. *CWR National Inventory* – The difference between the checklist and the inventory is that in an inventory the checklist is annotated; in that it each taxon has a range of ancillary information associated with each CWR taxon. As a result the data structure is now more complex and usually involves a multiple file structure such as Figure 27.

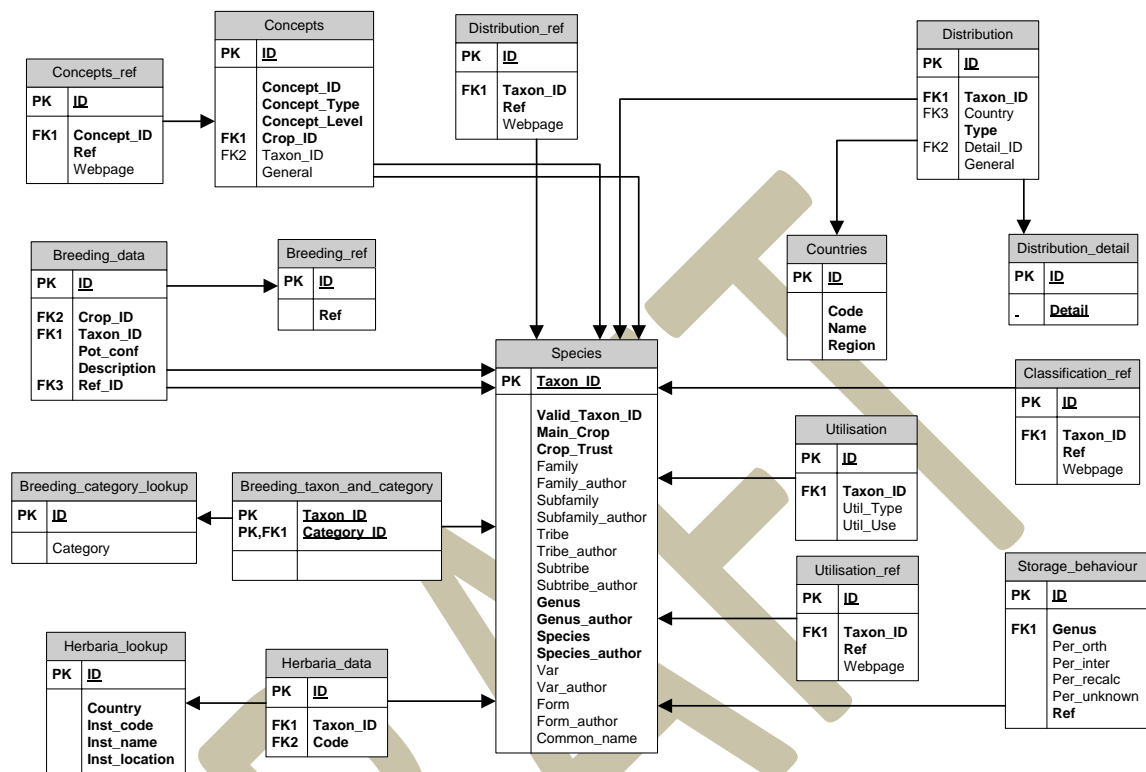


Figure 27. Entity relationship model for the CWR database ¹⁰⁹

c. *CWR Gap analysis* – The CWR checklist and inventory are primarily taxon based but the gap analysis based largely on data associated with individual accessions that represent those taxa. Normally significant resources will be invested in the collation of large herbarium specimen and gene bank accession data sets. There is no standard format for the database that contains this data, but Annex 5 contains an extended list of data descriptors ¹¹⁰ that will include those used as a basis for gap analysis.

d. *CWR conservation* – The data associated with CWR management will vary depending on whether it is associated with *in situ* or *ex situ* conservation, but falls into three basic categories (ecogeographic, field population, conservation management and monitoring) as detailed with examples above.

e. *Promotion of use* – As stated throughout the Toolkit, CWR conservation should be directly linked to utilization, so once the CWR diversity is conserved it needs to be characterized and evaluated so that the potential users have some basis on which to select the accessions they

¹⁰⁹ Vincent (Pers. Comm.)

¹¹⁰ Castañeda Álvarez *et al.* (2011)

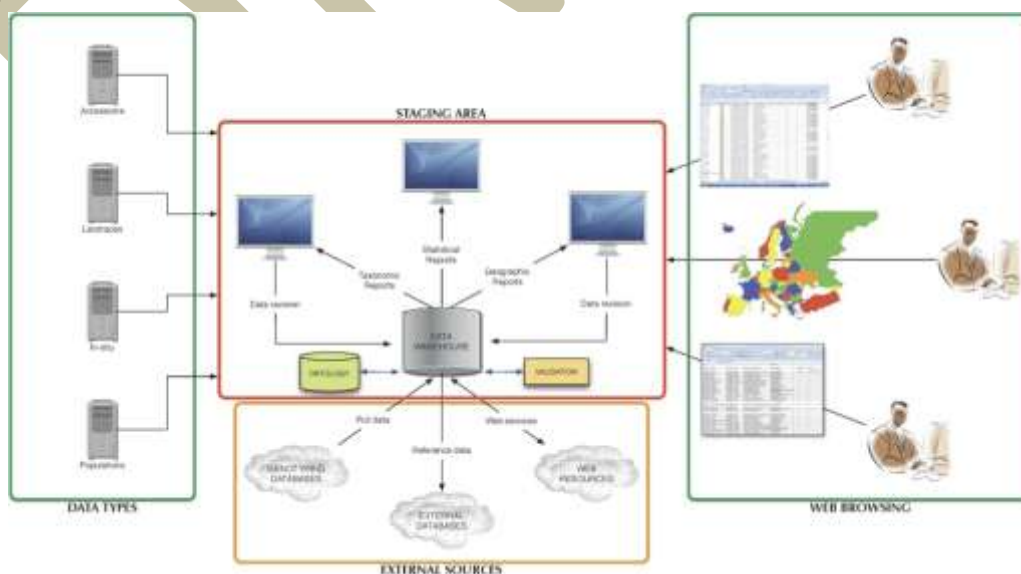
wish to utilise. The data associated with characterization and evaluation is, as noted in the previous section, often lacking and seldom available to the user community. However, within the context of the European Cooperative Programme for Plant Genetic Resources (ECPGR) several Central Crop Databases were established that hold accession passport data and, to varying degrees, characterization and primary evaluation data of the major crop related collections in Europe, these database are web-enabled. The next conceptual advance in making characterization and evaluation data easily available to the user community has been to develop an internet portal that facilitates access to the existing data. This is currently being developed as the Trait Information Portal (TIP), which is envisaged will provide a unique entry point for access trait-specific information to help direct their research and allow them to effectively exploit CWR diversity.

Box 61. Trait Information Portal

The TIP is planned to have a simple platform architecture accommodating input and output data types, including the following elements: (a) Use a document store database system; (b) Have an upload system with flexible template driven options for data being sent by providers; (c) Include and use the Generation Challenge Programme (GCP) data annotation and trait ontology curation tools developed by the Bioversity team; (d) Be searchable through ontology-driven views; (e) Include information on traits, locations, trial sites, georeference, geographical information; (f) Use web scraping (gather related information/data) to include external data sources, molecular data, bibliography, characterization and evaluation data, images, etc.; (g) Link with external information sources; and (h) Provide data analysis outputs. Additionally, the TIP will include three different entry points (trait information, CWR and LR inventories), allowing users to choose their entry/access point to the information they require, while maintaining the capacity to link or tap into existing online sources of information such as GENESYS, EURISCO and ECCDBs.

This concept has been planned to create a system that primarily serves the data provider so that it can efficiently serve the users. To make the most of this idea the rationale for the TIP framework conceptualization was to use existing developments and resources, focusing the development team's efforts towards using and further enhancing existing and evolving resources being developed in other communities of practice. The TIP is being developed in the context of the PGR Secure project (<http://pgrsecure.org/>) and is expected to be available as a beta test version in 2013.

TIP platform architecture



Source: Dias (2012)

A.14.4. List of references used to compile the text

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A.14.5. Additional resources and materials



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Dulloo ME, Thormann, I and Engels J (2011) Standards and best practices for gene bank management. European Plant Genetic Resources Conference 2011 “To Serve and Conserve”. 5-7 April. Wageningen, The Netherlands. Available from <http://www.slideshare.net/BioversityInternational/standards-and-best-practices-for-genebank-management> [Accessed January 2012].

WWW European Cooperative Programme for Plant Genetic Resources (ECPGR) Documentation and Information Network. Available at http://www.ecpgr.cgiar.org/networks/documentation_information.html

WWW FAO/IPGRI Multi-crop Passport Descriptors (MCPD) version 2 published in June 2012 ([http://www.bioversityinternational.org/index.php?id=19&user_bioversitypublications_pi1\[showUid\]=6901](http://www.bioversityinternational.org/index.php?id=19&user_bioversitypublications_pi1[showUid]=6901)) [Accessed June 2012].

WWW Crop wild relatives in national inventories available via the CWR Portal. http://www.cropwildrelatives.org/national_inventories.html [Accessed June 2012].

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WWW Crop Genebank Knowledge Base. Available from: <http://croptgenebank.sgrp.cgiar.org/> [Accessed June 2012].

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SECTION B. LANDRACES

B.1. Introduction

What is a 'landrace'?

Is definition of landraces possible?

There has been extensive discussion on what constitutes a landrace (LR), and even whether it is possible to define them¹¹¹, however although it may be difficult to precisely define LR, practically they are widely recognised by farmers and scientists alike and are key components of PGRFA. As such they exist and if we wish to study them practically we need a working definition, two such definitions are:

“Dynamic population(s) of a cultivated plant that has historical origin, distinct identity and lacks formal crop improvement, as well as often being genetically diverse, locally adapted and associated with traditional farming systems”.¹¹²

“A landrace of a seed-propagated crop can be defined as a variable population, which is identifiable and usually has a local name. It lacks “formal” crop improvement, is characterized by a specific adaptation to the environmental conditions of the area of cultivation (tolerant to the biotic and abiotic stresses of that area) and is closely associated with the traditional uses, knowledge, habits, dialects, and celebrations of the people who developed and continue to grow it”.¹¹³

Within LR two types are distinguished¹¹⁴:

- **Primary landrace:** a crop that has developed its unique characteristics through repeated *in situ* grower selection and that has never been subjected to formal plant breeding (as opposed to selection / breeding undertaken by independent LR maintainers). These can be divided into **autochthonous** (a crop that is grown in the original location where it developed its unique characteristics through grower selection; its genetic and socio-economic characteristics are associated specifically with this location) and **allochthonous** (an introduced crop that is locally adapted but that has developed its unique characteristics through grower selection in another region)¹¹⁵.
- **Secondary landrace:** a crop that has been developed in the formal plant breeding sector but which is now maintained through repeated *in situ* grower selection and seed saving, which is likely to be genetically distinct from the original bred material.

Some authors question whether locally adapted '*allochthonous landraces*' fit within the above definitions of LR because they lack a historical origin among farmers (see Box 62). However, these LR do have local economic importance, are likely to contribute increase crop diversity availability to farmers and breeders, and many were introduced a significant time ago so that

¹¹¹ Zeven (1998)

¹¹² Camacho Villa *et al.* (2005)

¹¹³ Negri (2007) who took into account the discussions presented by Anderson and Cutler (1942), Harlan (1975), Brush (1992, 1995), Papa (1996, 1999), Zeven (1998), Asfaw (2000), Friis-Hansen and Sthapit (2000), Negri (2003, 2005a), Camacho Villa *et al.* (2005), Saxena and Singh (2006).

¹¹⁴ Kell *et al.* (2009)

¹¹⁵ Zeven (1998) after Mayr (1937)

they have passed through numerous sowing, cultivation, harvesting cycles since introduction so may not be regarded as distinct from the original introduction.

Example of a primary autochthonous landrace

Example of a primary allochthonous landrace

Example of a secondary landrace

Box 62. Farmers, growers, gardeners or maintainers

The literature on LR and on-farm conservation almost always assumes that the person planting, cultivating and harvesting LR are farmers, but a farmer may be defined as “a person cultivates a tract of land cultivated for the purpose of agricultural production” and this would exclude cultivation associated with home-consumption. As such there is a distinction between farmers and gardeners growing crops for sale and home-consumption on the basis of scale of production, cultivation techniques used, crops grown, economic valuation, marketing and end-consumer. So farmers and gardeners (and growers) are not synonyms, they each maintain distinct LR diversity that should form part of the national LR checklist / inventory; it would be more accurate to refer to them as maintainers. But given the wide use of farmers in the literature it is taken in the Toolkit that the term farmer is used to include, unless otherwise stated, anyone cultivating LR diversity.

***Genetic erosion is the main threat to landraces. What is genetic erosion?*¹¹⁶**

Genetic erosion is the main threat to LR and has been referred to in the literature as:

- the loss of a crop, variety or allele diversity^{117,118,119,120};
- the reduction in richness (in the total number of crops, varieties or alleles)^{121,122,123,124};

¹¹⁶ See Maxted and Guarino (2006) and Van de Wouw *et al.* (2009) for reviews on the concept of genetic erosion in crops.

¹¹⁷ Peroni and Hanazaki (2002)

¹¹⁸ Gao (2003)

¹¹⁹ Tsegaye and Berg (2007)

¹²⁰ Willemen *et al.* (2007)

¹²¹ Hammer *et al.* (1996)

¹²² Hammer and Laghetti (2005)

¹²³ Ford-Lloyd (2006)

- the reduction in evenness (i.e. of genetic diversity)^{125,126}.

Why are landraces threatened?

There are numerous factors that negatively impact plant species and their populations which will result in taxonomic (species, subspecies, and varietal) and genetic diversity erosion, and eventually extinction.

The main factors that contribute to the genetic erosion of LR diversity include:

- changes in agricultural practices and land use;
- use of pesticides and herbicides;
- replacement of traditional varieties with modern, uniform cultivars which lead to a genetic bottleneck; once LR have been replaced by modern cultivars, unless the LR is conserved *ex situ*, the unique combination of genetic diversity is unavailable to breeders; as a consequence, the total number of different varieties grown is reduced and/or cultivars grown by farmers become increasingly similar to each other;
- type of variety and seed certification system associated with the enforcement of plant breeders' rights, which limits the sale of crop seed unless the variety is included in the national or regional varietal list; LR growers do not usually register their varieties since this process is relatively expensive and generally returns limited value to individual farmers; therefore, as it is illegal to grow non-registered varieties in many countries, farmers are inadvertently encouraged to switch to registered varieties and their LR material is lost;
- simplification of silvi-agriculture productive processes due to high manpower costs;
- subsidy schemes that promote the use of uniform varieties;
- perverse incentives given by, for instance, government agricultural advisory services, such as the free distribution of modern cultivars;
- constant decrease of rural populations due to migration and emigration;
- research programmes that ignore LR and their associated knowledge and uses;
- ageing of farmers and the unsuccessful passage of LR and associated knowledge from one generation to the next;
- lack of education of the unique value of LR as a local, national and global resource;
- changes in consumption habits;
- food standards that limit entry of LR and products into markets;
- political system such as in the ex-Soviet Union where agriculture was structured into a system of state (*sovkhoses*) and very large collective farms (*kolkhozes*) with centralized planning (what to cultivate and where) and relatively high mechanization, which have favoured the cultivation of introduced varieties rather than of local LR;
- war and political instability, as in Cambodia where nearly all traditional varieties were lost during civil unrest, though subsequently some Cambodian LR were repatriated from the International Rice Research Institute collection¹²⁷;

¹²⁴ Nabhan (2007)

¹²⁵ Khlestkina *et al.* (2004)

¹²⁶ Ford-Lloyd (2006)

¹²⁷ Hawkes *et al.* (2000)

- climate change – changes in climate are expected to directly affect the cropping patterns and result in extinction of traditional varieties, particularly in drier regions where certain LR are already marginally being grown near their limits of minimum rainfall requirement.

Many of these threats are associated with external changes in fragile traditional agro-ecosystem, the introduction of various alien factors stressing the agro-ecosystem dynamic and results in change from traditional LR to modern cultivars. Like oceanic island vulnerable to alien species introduction, traditional agro-ecosystem have ‘evolved’ in isolation and demonstrate ‘evolutionary innocence’ often being out-competed by the more aggressive introductions, ultimately resulting in the loss of native diversity.

Example of threat	Example of threat
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What are the practical consequences of LR genetic erosion?

- A decrease in genetic diversity availability means genes and alleles will not be available for breeders to develop improved varieties and meet:
 - changing consumer demands;
 - changing environmental conditions;
 - exploit new markets or environments;
 - provide food security
- Cultivars grown by farmers become increasingly genetically homogenous.
- Agro-ecosystem functioning and its provision of services (e.g., pest and disease control, pollination, soil processes, biomass cover, carbon sequestration, prevention of soil erosion, etc.), as well as potential innovation in sustainable agriculture are each likely to be seriously impacted.

What is landrace on-farm conservation?

Landrace on-farm conservation is the active management of LR diversity within the traditional agricultural systems where they have developed their unique characteristics. It implies that conservationists work closely together with farmers in order to manage and monitor their LR populations aiming at the long-term preservation of the dynamic of the agricultural systems while maintaining genetic richness and evenness of the included diversity.

Why do landraces need a National Conservation Strategy?

Landraces are unique resources for food security but are becoming more threatened and suffering from genetic erosion. The systematic, coordinated and integrated *in situ* and *ex situ* conservation of LR diversity is thus fundamental and best implemented via a national conservation strategy.

What are the general goals of a National Landrace Conservation Strategy?

A National LR Conservation Strategy aims at the long-term active conservation of the country's LR diversity, while at the same time promoting its use.



Cucurbitaceae diversity in *Baccealia* village (Căușeni district, Moldova) (photo: Anatol Ganea).



Farmers showing their sorghum and cowpea LR in Zingnyama, Phalombe, Malawi (photo by Edwin A Chiwona).



LR Diversity from a home garden in Griblje, Bela Krajina, Slovenia (photo: Pavol Hauptvogel).

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Padulosi S, Bergamini N and Lawrence T (eds) (2012) *On-farm conservation of neglected and underutilized species: status, trends and novel approaches to cope with climate change*. Proceedings of the International Conference, Frankfurt, 14-16 June 2011. Bioversity International. Available from: http://www.bioversityinternational.org/fileadmin/bioversity/publications/pdfs/1512_On_farm_conservation_of_neglected_and_underutilized_species_status_trends_and_novel_approaches_to_cope_with.pdf [Accessed June 2012].



Diverseeds Documentary Film. Plant Genetic Resources for Food and Agriculture: <http://www.diverseeds.eu/index.php?page=video> (shows the importance of agricultural biodiversity for food and agriculture, with astonishing pictures from Europe and Asia)

WWW Agricultural Biodiversity Weblog: <http://agro.biodiver.se/>

DRAFT

B.2. National LR Conservation Strategy planning – overview

What is a National LR Conservation Strategy?

A National LR Conservation Strategy is a document that outlines the national approach to LR conservation and use, it is likely to incorporate a list of LR, their distribution, cultivation and use practices, threat assessment, conservation status and priorities, and maintainer, breeder and other user information.

Given the numerous LR management scenarios across the world, the available data, the financial and human resources allocated to conservation, as well as the different levels of commitment by national agencies and governments, the formulation and implementation of a National LR Conservation Strategy will undoubtedly differ markedly from country to country. Nevertheless, there are likely to be common elements in the development of a National Strategy of this kind that comprises a series of steps aiming at successful LR diversity conservation and promotion of its use. These steps are:

- (i) Preparation of a national LR checklist: to prepare a national list of the country's LR diversity (floristic approach), or alternatively, a list of LR of selected crops (monographic approach).
- (ii) Preparation of a national LR inventory: to collate ecogeographic, agricultural cultivation, farmer and commodity exploitation data for each LR that enhances the checklist.
- (iii) Identification of threats to LR diversity and threat assessment: to identify threats that affect LR diversity as well as to undertake threat assessment.
- (iv) Prioritization of national LR: to prioritize the LR grown in the country, only if the number exceeds the number that can be conserved using the available resources.
- (v) Genetic analysis of priority LR: to collate genetic data for priority LR or, if unavailable, to carry out genetic analysis.
- (vi) Gap analysis: to identify *in situ* (on-farm) and *ex situ* conservation gaps to help establish *in situ* and *ex situ* conservation goals and priorities.
- (vii) Formulation of the National LR Conservation Strategy: to establish *in situ* and *ex situ* conservation goals and priorities.

The conclusion of this process is the National LR Conservation Strategy which identifies key on-farm sites for *in situ* conservation of LR diversity and LR under-represented in *ex situ* collections. The National Strategy should be closely linked to the utilization of LR diversity conserved on-farm and in *ex situ* accessions by farmers, breeders and other potential users.

Figure 28 summarizes the model for the development of national LR conservation strategies as well as the link with international legislation and strategies and the utilization of LR diversity by promoting cultivation, niche development, and development of market chains, cultural heritage activities, research and education, and breeding activities.

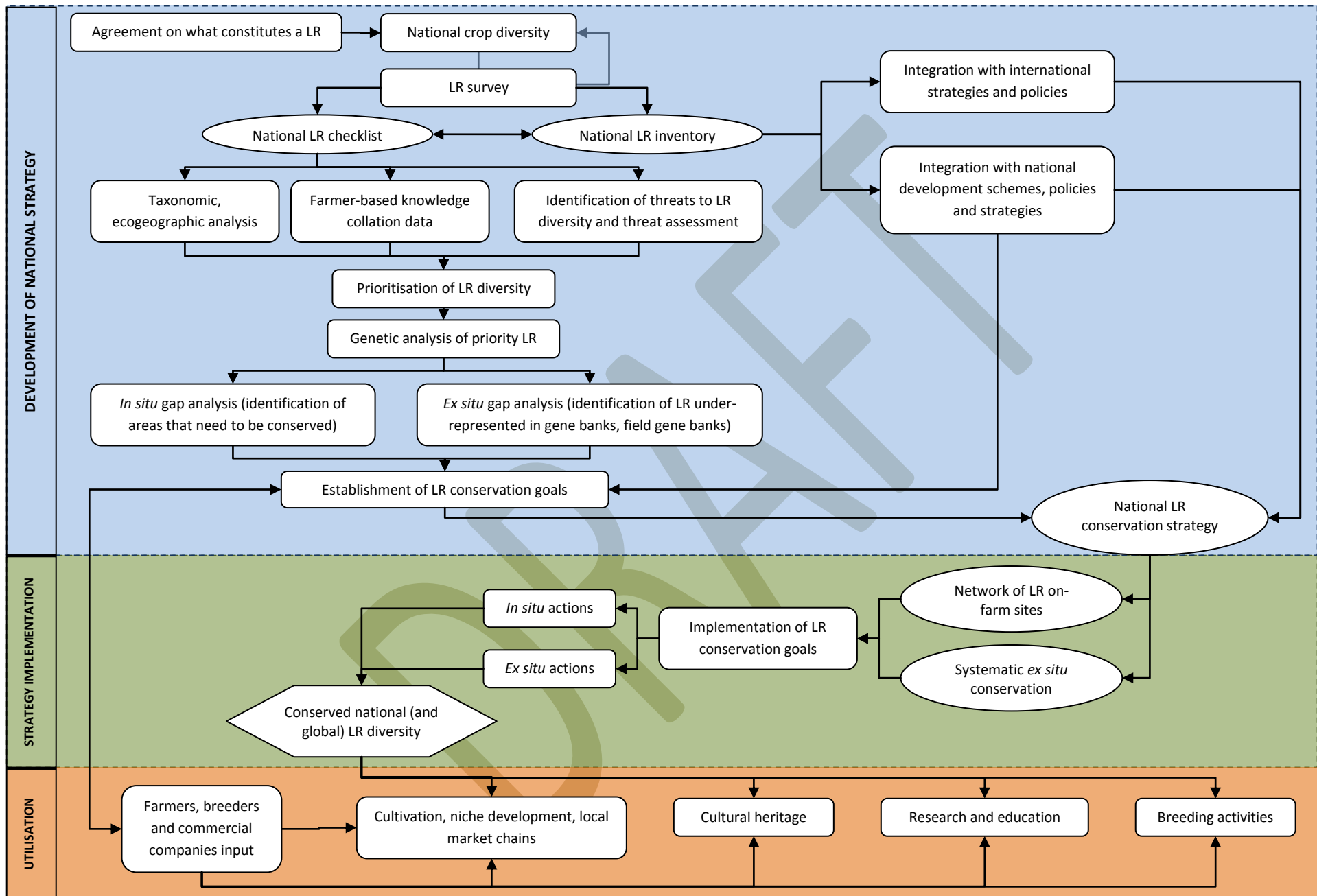


Figure 28. Model for the development of national LR conservation strategies

B.2.1. Additional materials and resources

General references:



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National biodiversity strategies that refer to LR conservation:



Saving Nature for People. National Strategy and Action Plan for the Conservation and Sustainable Use of Biodiversity in Finland 2006-2016. Available from: <http://www.syke.fi/download.asp?contentid=75624&lan=en> [Accessed on December 2011].



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WWW

Ireland's National Strategy for Plant Conservation. Specific actions regarding agrobiodiversity: <http://www.botanicgardens.ie/gspc/targets/inspc9.htm>

National on-farm conservation projects:



"On-farm conservation in Finland" (2006-2008) by MTT Agrifood Research Finland

Other references:



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B.3. National checklist of landraces

B.3.1. Overview

What is a checklist of landraces?

A LR checklist is a list of names of LR cultivated in a geographically defined area (for instance in a community, a region or a country). This is distinct from an inventory which is a checklist that has associated management, cultivation and use information added.

We need to know what exists, and where, to determine how we can conserve and use it effectively. Checklists of crops and their varieties is therefore a fundamental tool for supporting, facilitating and monitoring the conservation and sustainable use of agro-biodiversity. This was addressed in the Global Strategy for Plant Conservation (GSPC) which recognized a checklist as a means of organizing information in a logical and retrievable way, preventing duplication of effort when planning conservation actions and enabling the planning of the sustainable use of plants—essential resources for food, medicines and ecosystem services.

The knowledge we obtain from checklists of LR will:

- i. help characterising the LR diversity existing in a particular geographic unit hence assist authorities in planning and implementing policies and strategies for conservation and use of agro-biodiversity, which is essential in underpinning national food security,
- ii. help future germplasm surveys and collections to be more efficient,
- iii. allow the accessibility and exchange of information within existing PGR networks, as well as other researchers and research stations.

There are several publications on inter-crop diversity (i.e., diversity between crops) both at a global and national level, but intra-crop diversity (i.e., diversity within crops) information at global and national levels for LR is generally lacking. The Second Report on the State of the World's Plant Genetic Resources for Food and Agriculture noted a substantial increase in the number of inventories, both with regards to single crops, groups of species, or within geographically defined areas, but they remain far from systematic. There is to date no standardized methodology for generation of a LR checklist which may explain why the creation of national LR checklists has received little research attention or practical application.



Farmer showing panicle of Nunkho (scented) sorghum landrace in Waruma, Phalombe, Malawi (photo by Edwin A Chiwona).



"Uzgen" rice LR in Sorobasat, Os Province, Kyrgyzstan (photo: Pavol Hauptvogel).

The preparation of a national checklist of LR can be seen as a five stage process: (i) determine the geographical and crop category scope, (ii) produce a list of included crop diversity (regionally or nationally), (iii) agree on what constitutes a LR, (iv) survey stakeholders to produce the checklist, and (v) Make the checklist available to users. These steps constitute the general methodology, which is illustrated in Figure 29 and described further below.

If there is no prior information of the presence of LR then the compilation of a list of national crop may provide an introduction the national crop networks and experts that can help identify LR diversity. As noted above we have distinguished between a LR checklist (list of LR names from a geographically defined area) and LR inventory (checklist annotated with management, cultivation and use information). This distinction is pragmatic, in that it often easier to rapidly collate a list of names and then subsequently collate the additional data. However, in practice, when there are little or no pre-existing data on the LR that exist in a certain area, the compilation of the LR checklist and inventory may proceed in parallel. Yet the checklist and inventory are likely to serve different uses, the checklist being used for governmental statistics and the inventory being necessary if the LR are to be fully exploited by the various stakeholder communities. Therefore, both LR checklists and inventories have a distinct role in LR conservation and use.

B.3.2. Methodology for creating a LR checklist

(i) Determine the geographic scope and the target crops.

Discuss and agree the scale of the checklist, whether to cover the whole country or a subunit, whether to cover all crops, a crop category or a subset of priority crops. Two alternative approaches are often referred to in the development of an inventory of LR:

- **A floristic approach** is used to produce inventories of all LR grown in a geographically defined area, either region or country. LR inventories of different regions in a country can eventually be compiled to create a national inventory of LR.
- **A monographic approach** is used to produce an inventory of LR of one or several selected crops. The main difference from the floristic approach is therefore the focused selection of particular target crops for which the inventory is being developed. The selection of crops can also be made at the prioritization level when a national inventory of LR already exists and the National LR Conservation Strategy is aimed at solely those crops. LR inventories of specific crops can eventually be compiled to create a national inventory of LR.

Which approach to use, depends on the particular study, as well as financial resources and human capacities. The assumption being the more inclusive the inventory, the greater its use and the likelihood of multiple studies is avoided, therefore a broad geographic and crop scope is recommended where possible.

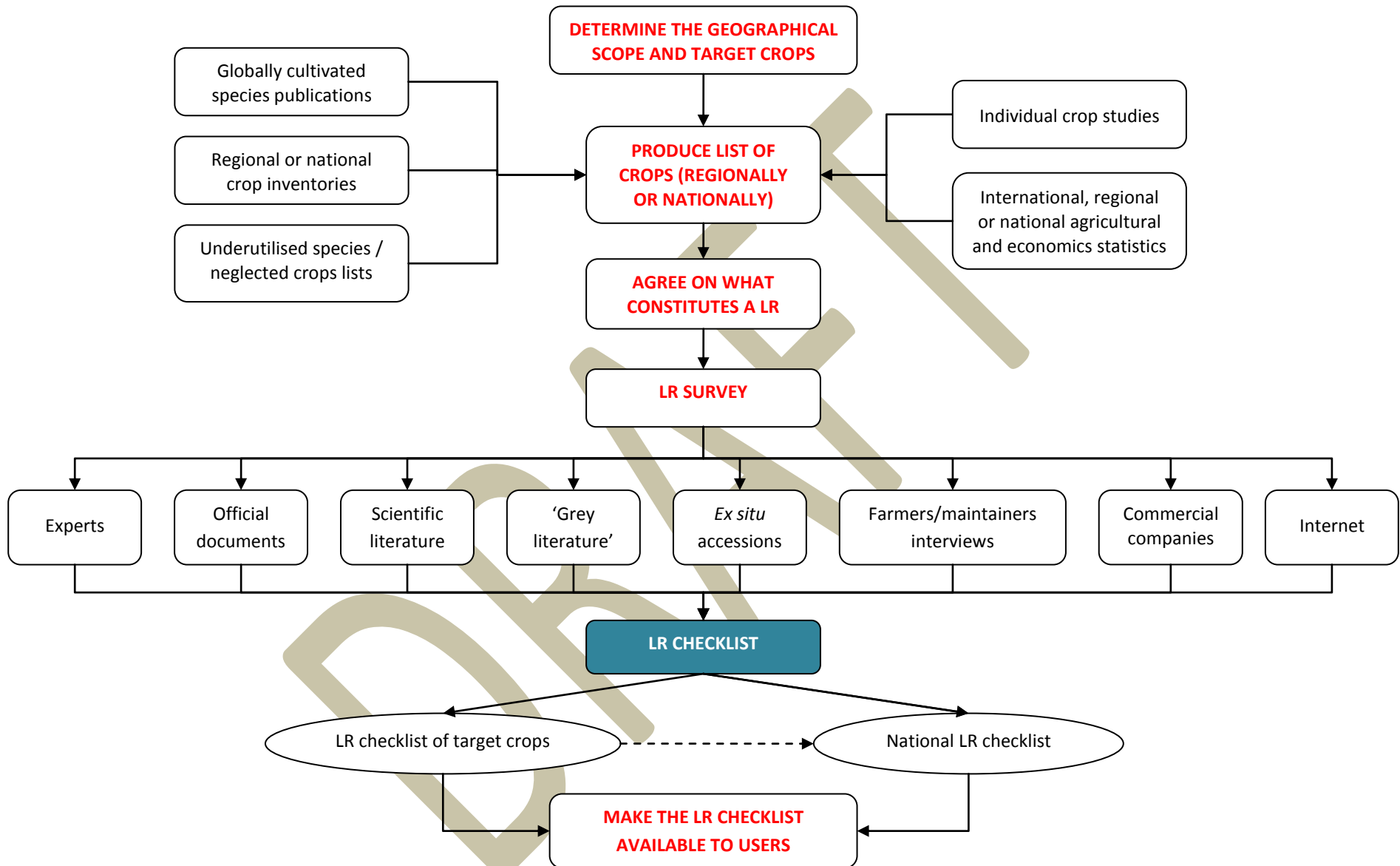


Figure 29 Overview of the creating a national (or regional) checklist of LR

(ii) Produce a list of crop diversity (regionally or nationally).

Several sources have to be consulted when compiling a list of crops grown in a particular country or area. Key sources are:

- Globally cultivated species publications
- Regional or national crop checklists,
- Underutilised species/neglected crops lists,
- Individual crop studies,
- National, regional or international agricultural and economics statistics.

See the 'Additional materials and resources' for concrete references under each key source.

(iii) Agree on what constitutes a LR.

Discuss and agree the working definition to be applied. The definition of what constitutes a LR is of crucial importance and the starting point when formulating a National LR Conservation Strategy. The definition of LR to be applied is likely to vary between projects, the resources available, the crop scope of the inventory and the reasons of the agency commissioning the inventory. There is unlikely to be one universally accepted definition for all situations and for all crops but common elements of a working definition of a LR are:

- recognisable, distinct crop variety,
- dynamic population character,
- historical origin,
- lacks formal crop improvement,
- genetically diverse,
- locally adapted,
- associated with local cultural, historic or religious values,
- associated with traditional farming systems.

LR can be crops that have developed unique characteristics through repeated farmer selection and never been subjected to formal plant breeding, as well as crops that have been developed in the formal plant breeding sector but which have later been maintained through repeated farmer selection and seed saving schemes. Examples of LR that do not conform to each of the criteria listed above can be found, so a pragmatic decision needs to be taken by each project on what components will be included in the working definition.

Once the definition is agreed, the researchers need to decide whether to recognise LR based on their nomenclature (two LR with different names are assumed to be distinct) or whether a stricter recognition is required that is based on genetic distinction. The former is likely to be pragmatically adopted but with the rapid development of more efficient molecular techniques this situation is likely to change in forthcoming years. Nevertheless, the use of the nomenclature definition is problematic because it does rely on the assumption that actual genetic distinction is related to LR names, which might not always be the case (see Box 63). The definition of LR used as the basis for the national inventory will ultimately depend on the national scenario and will vary from one country to another.

It should also be recognised that the goal of LR conservation is to maximise the LR diversity conserved and it is by definition assumed that LR will be locally adapted and this adaptation will be reflected in its genetic composition, therefore even if two or more LR have the same name if they are grown in different environments they will be genetically distinct. This of course assumes there is no exchange of seed between local maintainers. However, given this general point it could be argued that should be LR + maintainer not just individual LR, this is a research question that has yet to be investigated and in the interim it seems valid to assume LR with the same name are more closely linked to each other than to other LR, therefore the individual LR, identified on the basis of its name, will remain the focus of the national checklist.



Emmer wheat (*Triticum turgidum* ssp. *dicoccum*) LR grown in Monteleone di Spoleto, Umbria, Italy and Renato Cicchetti, the farmer who ensured the survival of this LR (photo: Renzo Torricelli).



LR of cabbage (*Brassica oleracea*) in Orava, Slovakia (photo: Pavol Hauptvogel).

Box 63. Nomenclatural versus genetic definition of landraces in Malawi

To test the hypothesis that there exist correlation between local nomenclature and genetic diversity in sorghum and cowpea, Amplified Fragment Length Polymorphism (AFLP) and morphological characterization was undertaken on farmer identified LR of sorghum and cowpea found in three regions of Malawi. The sorghum landraces results found significant intra-LR genetic diversity but individual LR were differentiated within the same agroecological region. Also sorghum LR that shared the same local name but were sampled from different environmental conditions were genetically diverse, which implies that when assessing LR genetic diversity it is important to consider differences in the prevailing physical (soils, topography, climate), biological (flora and fauna) and socio-economic (main economic activities, land ownership, gender, age, farming practices, cultural practices, etc.). Further, higher genetic relatedness exists among sorghum LR within agroecological region of origin than between regions, so sorghum LR cultivated in relative close proximity with different names were genetically more closely related than those with the same name at other locations. For cowpea LR, the results showed only partially correlation between local nomenclatural and genetic diversity, even for those LR with the same name grown relatively closely to each other. Though in the case of cowpea LR are generally recognised by the farmer on the basis of seed size and relative days to maturing and other characteristics may vary. Therefore, the indication is that the local names used by farmers to distinguish LR cannot for cowpea be relied on as a consistent proxy for genetic similarity. In conclusion and in the absence of alternatives we may be forced to use LR names in preparing LR checklists but the relationship between local nomenclature and genetic diversity should be considered when studying diversity.

(iv) Survey and produce a checklist of LR. A number of methods can be used to seek out LR information, including media releases (television, radio, press and internet), advertisements, questionnaires, internet searches, email correspondence, telephone calls and face to face meetings. These are likely to be followed-up by:

- **Farmer interviews.** Farmers themselves can be approached indirectly through advertisements, articles in farmers' magazines and local newspapers, radio or other

non-print media, and directly via personal contacts. See examples of LR diversity information collecting form and data descriptors for management data associated with each LR surveyed with the farmers in the 'Additional materials and resources'.

- **Expert consultations.** From gene banks, national testing centres, statutory collections associated with national cultivar listing, research institutes, agricultural extension divisions, farmers' organizations, agricultural statisticians, other professionals and NGOs.
- **Commercial companies** involved in seed production, brewing, milling, distilling, etc.
- **Scientific literature**, including historical literature, research reports, papers and articles.
- **'Grey literature'** associated with gene banks, research institutes, seed companies, NGO newsletters, local farmers' society publications, and farm records.
- **Official documents**, for instance agricultural statistics or national varietal lists.

Also it should not be assumed that all LR must be identified by novel investigations, some may exist and even be conserved but are not recognised as LR. For example, in gene banks LR may not be distinguished from modern varieties or other types of PRGFA. Therefore an initial stage in the survey maybe to clarify whether any LR are present in existing collections but simply not designated as LR accessions.



Gene bank scientists facilitating cowpea and sorghum LR discussion with traditional farmers, Mateyu, Chikwawa, Malawi (photo: Edwin A Chiwona).



Gene bank team interviewing farmer about sorghum LR in Hungary (photo: Vojtech Holubec).

- (iv) Make the LR checklist available to users. It is essential that the checklist that is created is made available to users, both locally, nationally and globally. To facilitate the widest use, the inventory should ideally be created as a digital database which should be made available to users, ideally via a web-enabled database. Some of the databases currently available are found in the list of 'Additional materials and resources'.

B.3.3. Examples and applied use of LR checklists

There are no examples of complete national checklists of LR. On the other hand, partial national checklists of LR have been prepared in some countries, including Libya^{128,129} (Box 64) and Ethiopia¹³⁰ (Box 65). Most examples are based on organized expeditions to collect specimens and *ex situ* accessions for conservation and evaluation, as well as to collect information on the cultivation method, history and traditional knowledge and use of LR.

Box 64. Checklist of landraces in Ghat Oases (Libya)

A checklist of the cultivated plants occurring in the Ghat oases in Libya was obtained following a collecting mission in 1983. A total of 57 accessions of landraces were collected. The results obtained during this mission, together with observations from all over the Fezzan and from a literature review allowed the preparation of a checklist of the cultivated plants of the Ghat oases.

Source: Hammer and Perrino (1985)

¹²⁸ Hammer and Perrino (1985)

¹²⁹ Hammer *et al.* (1988)

¹³⁰ Yemane *et al.* (2009)

Box 65. Checklist of Sorghum LR in South and Central Tigray region (Ethiopia)

A checklist and inventory of varieties of *Sorghum* LR existing in the South and Central Tigray region in Ethiopia was obtained through a farmer survey. 93 selected farmers were interviewed using a structured questionnaire regarding various socio-economic aspects, as well as landrace characteristics and seed selection and management. A total of 165 collections from 31 locally named *Sorghum* varieties were retrieved and stored at the Mekelle University. The socio-economic factors that affect varietal diversity as well as conservation and incentives strategies were discussed.

Source: Yemane *et al.* (2009)

LR in Ghat oases	<i>Sorghum</i> LR in Ethiopia
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B.3.5. Additional materials and resources

Lists of global or regional crop diversity:



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WWW

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WWW

Freedman B (2011) Famine foods database. Available from: http://www.hort.purdue.edu/newcrop/faminefoods/ff_home.html [Accessed January 2012] (list of plants that are not normally considered as crops but that are consumed in times of famine)

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Albania:

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Libya:



Hammer K and Perrino P (1985) A check-list of the cultivated plants of the Ghat oases. Kulturpflanze, 33: 269-286.

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Smekalova T (2009) "Cultivated plants inventory of Russia". In: Veteläinen M, Negri V and Maxted N (eds) *European Landraces: On-Farm Conservation, Management and Use*. Bioersity Technical Bulletin, No 15. pp.143-154.

South Italy and Sicily:

Hammer K, Knüpffer H and Perrino P (1990). A checklist of the South Italian cultivated plants. *Kulturpflanze*, 38: 191–310



Hammer K, Knüpffer H, Laghetti G and Perrino P (1992) *Seeds form the past. A catalogue of crop germplasm in south Italy and Sicily*. Instituto del Germoplasma del Consiglio Nazionale delle Ricerche, Bari. 173 p.

Central and north Italy:

Hammer K, Knüpffer H, Laghetti G and Perrino P (1999) *Seeds form the past. A catalogue of crop germplasm in central and north Italy*. Instituto del Germoplasma del Consiglio Nazionale delle Ricerche, Bari. 253 p.

Monographs of crops:



Promoting the Conservation and Use of Underutilized and Neglected Crops Series which have monographic inventories available from <http://www.biodiversityinternational.org/>

International agricultural statistics:

WWW FAOSTAT: <http://faostat.fao.org/> (data on global production and value for crops that may be queried at a national level)

WWW EUROSTAT: <http://epp.eurostat.ec.europa.eu> (provides information for European Union countries)

Nomenclatural versus genetic definition of landraces:



de Haan S, Bonierbale M, Ghislain M, Núñez J and Trujillo G (2007) *Indigenous biosystematics of Andean potatoes: folk taxonomy, descriptors and nomenclature*. *ISHS Acta Horticulturae* 745: 89-134.



Huamán Z and Spooner DM (2002) *Reclassification of landrace populations of cultivated potatoes (Solanum sect. Petota)*. *American Journal of Botany* 89: 947-965.



Majaju C and Chakuya E (2008) *Morphological variation of sorghum landrace accessions on-farm in semi-arid areas of Zimbabwe*. *International Journal of Botany*, 4(4): 376-382.

B.4. National inventory of landraces and analysis

B.4.1. Overview

What is a national inventory of landraces?

The national LR inventory is the checklist plus associated information for priority individual LR maintained by each farmer in the country. So, for instance, a national inventory of LR may include 200 LR, but each of these LR may be cultivated by more than one farmer (a LR grown by a farmer is considered a different LR population), therefore each LR population will have unique associated data, regarding its maintenance, in that particular farm by that particular farmer.

What is the difference between the LR national checklist and the LR national inventory?

Whereas the national checklist is the list of the different LR that occur in the country, is the checklist plus associated information (ecogeographic, cultivation, characterization, evaluation and farmer-based knowledge data) for priority individual LR maintained by each farmer in the country. In practice, there is only one entry for each LR name in the national LR checklist, whereas in the inventory each LR can have multiple accessions as different farmers/maintainers can grow the same LR.

Nevertheless, when preparing a National LR Conservation Strategy and pre-existing knowledge on nationally grown LR is limited or non-existent, a LR survey is needed so practically the creation of the national LR checklist and inventory may run, at least in part, in parallel.

A national inventory of LR results from the collation of taxonomic, ecogeographic, characterization and evaluation data as well as farmer knowledge on management and conservation of each LR grown. The knowledge we obtain from inventories of LR will:

- i. help to characterise and evaluate the LR diversity present in a country;
- ii. assist authorities in planning and implementing policies and strategies for conservation and use of agro-biodiversity, which is essential in underpinning national food security; and
- iii. allow the accessibility and exchange of information within existing PGR networks, as well as other researchers and research stations.

The process of collating geographic, agroecological, taxonomic and genetic data and using it to help plan conservation is called an 'ecogeographic survey'. It is formally defined as "an ecological, geographical, taxonomic and genetic information gathering and synthesis process, where the results are predictive and can be used to assist in the formulation of collection and conservation priorities"¹³¹. The ecogeographic model was originally developed for wild plants^{132,133} but can be equally well used for crop LR conservation^{51, 134}. The LR characterization and evaluation data along with farmer knowledge on management complements that normally collated as part of an ecogeographic survey and should be integrated with it when undertaking an ecogeographic survey of LR diversity.

Figure 30 illustrates the ecogeographic survey methodology. It comprises three main phases: project design, data collection and analysis, and the ecogeographic products. The project design includes: (i) Identification of taxon or crop expert, (ii) Selection of target taxon/crop

¹³¹ Castañeda Álvarez *et al.* 2011

¹³² For *Trifolium* spp. by Bennett and Bullitta (2003)

¹³³ For African *Vigna* spp. by Maxted *et al.* (2004)

¹³⁴ Guarino *et al.* (2005)

taxonomy, and (iii) Design and creation of the database structure. The data collection and analysis include: (iv) Survey of passport, management, site and environment, and existing characterization and evaluation data, (v) Collation of data into database, (vi) Data verification, and (vii) Data analysis. The ecogeographic products include: (viii) LR inventory (which contains raw data on existing LR grown by each farmer together with the ecogeographic, characterization, evaluation and farmer knowledge on its management and conservation), (ix) Conspectus (that summarizes all data for each LR), and (x) Report (which interprets the data obtained).

B.4.2. Methodology for the LR ecogeographic survey

- (i) Identification of taxon/crop expertise.
 - Farmers (often female): generally play a key role in the management of many crops, should also be identified and contacted
 - Crop experts or botanists: can give advice on the location of important plant collections and suggest relevant grey literature, monographs, crop databases and other works;
 - Breeders, agronomists with experience in the crop gene pool, and other users of PGR working in national agricultural research centres: they are usually familiarised with documenting, interpreting, and using genetic diversity at the infra-specific level, as well as identifying gaps in existing collections, regions known or suspected to harbour interesting LR germplasm, and what traits to look for and pay particular attention to when in the field;
 - Global and regional crop-specific networks, NGOs, governmental or international agencies working in rural development projects in the target region (Guarino *et al.* 2005);
 - Social scientists working in the target region: can provide information on farming systems and crops.
- (ii) Selection of target taxon/crop taxonomy. The generally accepted taxonomic classification can be determined with the help of:
 - Target taxon experts;
 - National or global Floras;
 - Crop monographs;
 - Recent crop studies;
 - Crop databases, etc.
- (iii) Design and creation of the ecogeographic, characterization, evaluation and farmer-based knowledge database structure.
 - A careful reflection on the types of data to be included in the database should precede its creation. The collecting form (when surveying farmers for LR information) should be strongly linked to this database meaning that all fields in the collecting form are included in the database structure. See 'Additional materials and resources' for an example of a questionnaire used in interviewing farmers and of Passport Descriptors.

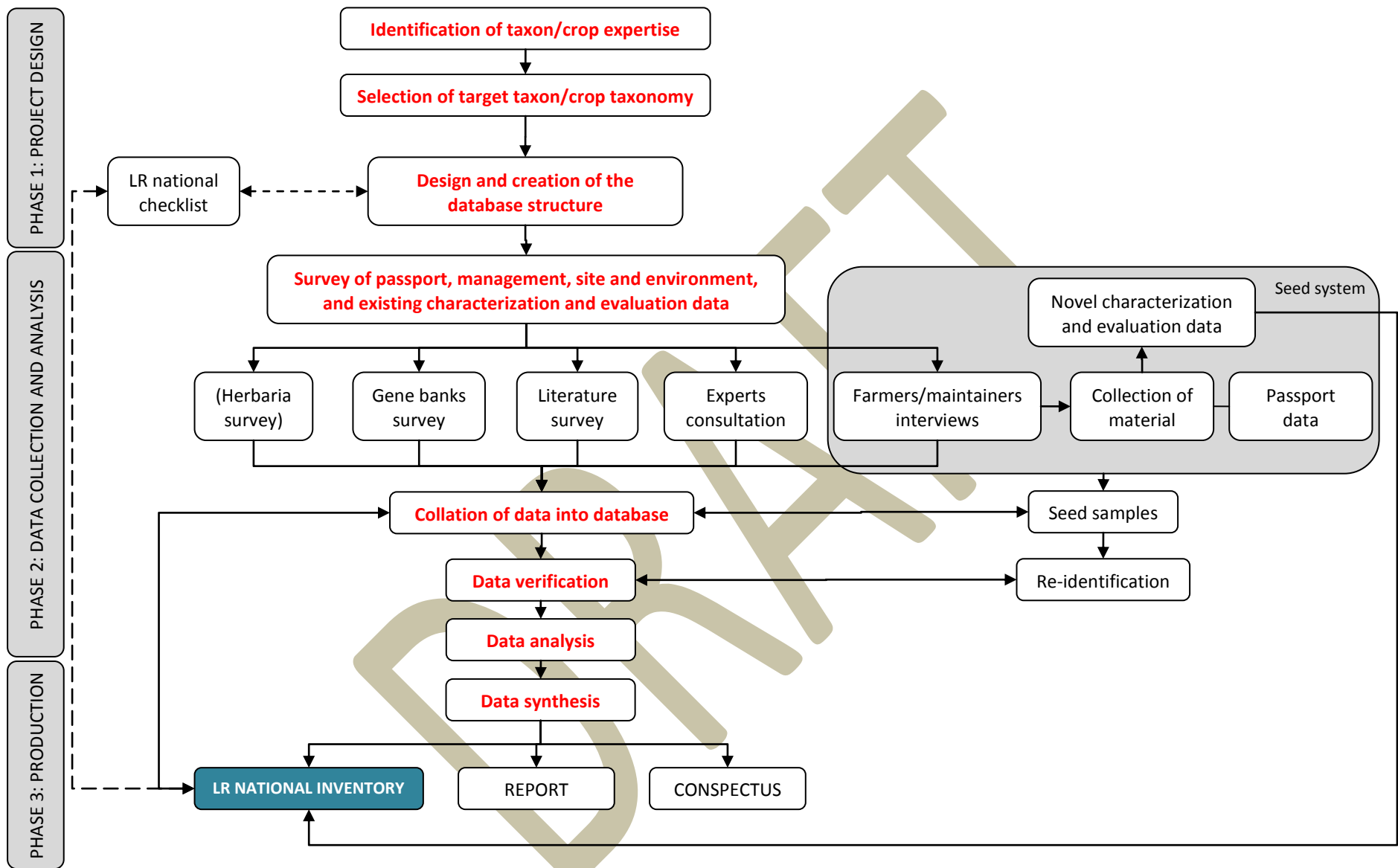


Figure 30. Ecogeographic study / survey model.

- Types of data include: passport data (generally include accession descriptors, collecting descriptors, nomenclatural data, socio-economic data, and farmer-based knowledge descriptors), site and environment data (describe environmental and site-specific parameters which can be associated with characterization and evaluation trials, characterization data (related to the highly heritable traits that are expressed in all environments), and evaluation data (associated with the traits that are susceptible to environmental differences). See Box 66 for different data types to include in the database.
 - Data descriptors and data standards should be determined.
 - The database software package should be both user-friendly and able to accommodate the complexity of a database of this kind. Several database software packages are available (Microsoft Access, MySQL, etc.).
 - The data format should be standardised.
 - The ecogeographic, characterization, evaluation and farmer-based knowledge database may be directly linked to the LR national inventory through a unique identifier number (LR name or LR ID); alternatively, they can be two independent products.
- (iv) Survey and collation of passport, management, site and environment, and existing characterization and evaluation data into the database. Sources of data are likely to include:
- Gene banks: e.g., SINGER, IPGRI's Germplasm Holdings Database, etc. See Box 67 for issues to take into consideration when using *ex situ* data.
 - Scientific and 'grey' literature: crop monographs, recent crop studies, crop databases, gazetteers, scientific papers, soil, vegetation and climate maps, atlases, etc., available both in conventional printed paper and in digital files.
 - Crop experts.
 - Herbaria: not so important for LR and only a limited number of herbaria accept vouchers of cultivated species (e.g. the Vavilov Institute of St. Petersburg, Russia).
 - Farmers and maintainers of LR: engaging farmers/LR maintainers in conservation, even before starting the inventory, is important to facilitate the exchange of information; while collecting farmers' knowledge on the management of LR, material can be collected (e.g. whole plants or seeds) together with passport and other relevant associated data (see Box 66).

It should be noted that each LR there may be several LR populations or *ex situ* accessions as different farmers/maintainers can grow the same LR. It is thus important to link LR populations to sites or farmers/maintainers to ensure any local intra-LR diversity is potentially recognisable. The passport, site and environmental data should be available for every accession of every LR. The characterization and evaluation data are usually not available and may require specific trials. However, when available, characterization and evaluation data will help contribute to the identification of the LR.

ID	CROPNAME	GENUS	SPECIES	SUBTAXA	SPAU/THCI	ACCESSNAME	UK_USE	LOCATION	NO. FARMERS	EST. AREA
35	Barley	Hordeum	vulgare		L	Bere	feed	Orkney	5	4.06
28	Barley	Hordeum	vulgare		L	Bere	feed	North Uist	1	1
31	Barley	Hordeum	vulgare		L	Bere Barley	feed	North Uist	1	0.81
34	Barley	Hordeum	vulgare		L	Bere	brewmeal	Orkney	2	4.06
38	Barley	Hordeum	vulgare		L	Bere barley	research into malting q	Orkney	n/a	n/a
40	Barley	Hordeum	vulgare		L	Bere	birds (RSPB)	Ormsay	1	4
43	Barley	Hordeum	vulgare		L	Bere	feed	Shetland	1	0.20
33	Barley	Hordeum	vulgare		L	Bere	brewmeal	Orkney	1	1.21
41	Oat	Avena	sativa		L	Dandy (Oat)	feed	Pembrokeshire	1	2.02
39	Oat	Avena	stiposa		Schreb	Small Oat	birds (RSPB)	Ormsay	1	4
53	Oat	Avena	sativa		L	Black Oat	green manure	Yorkshire	2-5	80.94
37	Oat	Avena	sativa		L	Muckle Oat	multiplication	Orkney	n/a	n/a
36	Oat	Avena	sativa		L	Black Potate	research	Orkney	n/a	n/a
32	Oat	Avena	stiposa		Schreb	Small Oat	feed	North Uist	1	10
42	Oat	Avena	stiposa		Schreb	Shetland Oats	feed	Shetland	1	0.20
30	Oat	Avena	stiposa		Schreb	Small Oat	feed	North Uist	1	1.21
65	Oat	Avena	sativa		L	Sliver (Oat)	feed	Kent	1	80.94
25	Oat	Avena	sativa		L	Sun-2	feed	Northfolk	1	unknown
23	Oat	Avena	stiposa		Schreb	Small Oat	feed	Lewis	1	0.40
21	Oat	Avena	stiposa		Schreb	Grey Oat	feed	Islay	1	unknown
18	Oat	Avena	sativa		L	Black oat	feed	Hampshire	1	0.10
14	Oat	Avena	sativa		L	Black oat	feed	Devon	1	3
2	Oat	Avena	sativa		L	Forwards	feed	Aberdeenshire	1	4.06
60	Oat	Avena	stiposa		Schreb	Wild Whiskers Oats	feed	Wales	1	unknown
52	Oat	Avena	sativa		L	Sun-2	feed	Suffolk	1	2.02
44	Oat	Avena	stiposa		Schreb	Shetland oats	feed, baskets, furniture	Shetland (North)	1	1 field (last year)
59	Oat	Avena	stiposa		Schreb	Small Oat	stopped	Wales	2	n/a
46	Oat	Avena	stiposa		Schreb	Small Oat	food/feed	South Uist	1	1.52
57	Oat	Avena	sativa		L	Black Potate Oat	feed	Suffolk	1	2.02
29	Oat	Avena	stiposa		Schreb	Small Oat	feed	North Uist	1	10
61	Oat	Avena	stiposa		Schreb	Small Black Oat/Bye mixture	feed	Berberuta	1	6.07
58	Oat	Avena	stiposa		Schreb	Small Oat	forage	Tiree	9	15
62	Rye	Secale	cereale		L	Huffman Rye	green manure	Wiltshire	1	unknown
19	Rye	Secale	cereale		L	Schmidt	feed	Hampshire	1	0.10
17	Wheat	Triticum	aestivum		L	Hotblast wheat	feed	Hampshire	1	0.10
16	Wheat	Triticum	aestivum		L	Mixture	thatch + flour	Essex	n/a	unknown
15	Wheat	Triticum	aestivum		L	Mixed 5 turch wheats	feed	Devon	1	3
13	Wheat	Triticum	aestivum		L	Red Standard	thatch	Devon	1	4.06
12	Wheat	Triticum	aestivum		L	Squareheads Master	thatch	Devon	1	4.06
11	Wheat	Triticum	aestivum		L	NEB	thatch	Devon	1	40.47
9	Wheat	Triticum	aestivum		L	Red Standard	thatch	Devon	1	2.43
55	Wheat	Triticum	aestivum		L	NEB	thatch	Suffolk	1	3.64
8	Wheat	Triticum	turgidum	ssp. Dicoecon	(Schrank) T	Emmer	milling thatch	Buckinghamshire	2	6.09
7	Wheat	Triticum	aestivum		L	Apri Bearded	thatch	Buckinghamshire	1	6.09
6	Wheat	Triticum	turgidum		L	Rampton Rivet	thatch	Buckinghamshire	1	6.09
5	Wheat	Triticum	turgidum		L	Rivet	thatch	Buckinghamshire	1	6.09
4	Wheat	Triticum	turgidum		L	Blue Cone, Blue Ball, Blue Poll	thatch	Buckinghamshire	1	6.09
3	Wheat	Triticum	aestivum		L	Squareheads Master	thatch	Buckinghamshire	1	6.09
10	Wheat	Triticum	aestivum		L	Squareheads Master	thatch	Devon	1	40.47
1	Wheat	Triticum	aestivum		L	Squareheads Master	thatch	Suffolk	1	2.77

Screenshot of UK national LR inventory database (photo: Shelagh Kell).

Box 66. Types of data to include in a national inventory of landraces

- **Crop maintainer details:** name, address, contact details, year of birth, gender, family structure, education, main source of income, owned or rented land, etc.
- **Crop maintainer data:** how long maintainer will continue cultivation/conservation, whether someone (from younger generations, other relatives, neighbour, etc.) will continue to cultivate the LR.
- **Site geographic data:** location, coordinates, size of farm, site environmental data: cropping site type, altitude, landform, aspect, slope, soil texture, soil drainage, soil pH, temperature, rainfall.
- **Crop nomenclature data:** genus, species, authority, infra-specific epithet, infra-specific epithet authority, taxonomic rank, crop cultivar name, synonyms, vernacular names.
- **Socio-economic data:** crop purpose and the contribution it makes to income and nutrition, usage (e.g., description of main usage, secondary usage, home consumption or marketed, marketing, current and past values, member of grower or marketing cooperative), maintainer-perceived value, type, source, country of origin, history of cultivation, crop qualities, local or national maintainer incentives.
- **Crop cultivation and management data:** area currently sown, history of area sown, sowing date, crop system (arable or mixed farming system), harvesting date, irrigation, fertiliser, fungicide and pesticide types, organic status, crop resistance as noted by maintainer, propagation method, selection criteria for propagation, variation displayed by the LR with regard to characterization and evaluation traits, major agronomic problems faced by the crop (pest, diseases, drought, etc.), relationship to other landraces.
- **Relative uniqueness of LR** (i.e. grown on single farm or more widespread, genetic distinctness).

- Crop conservation status: whether the crop is stored *ex situ*, method of selection of seed saved method of seed storage, maintainer exchange frequency, whether it is adequately managed *in situ*, threat of genetic erosion (e.g. perverse incentives, lack of sustainability of farming system, lack of market), length of seed saving, etc.
- Characterization data: e.g. leaf shape, flower colour, plant habit, seed colour, chromosome number, etc.
- Evaluation data: plant height, days to maturity, protein percentage, disease resistance yield, maintainer's comparison with modern varieties, product processing details etc.
- Photographs.

Some of this information may have implications for data protection and so may not be included in an on-line version of the database to protect the privacy of the data providers, but it should not be anonymised so that individual collections may be traced if desirable traits are located.

Note: The data types listed above are extensive it is not necessary to have a complete set to constitute a national inventory, a pragmatic approach should be taken when collating the data, however, the more complete the dataset, the more sophisticated the analysis and the more detailed the conservation to be implemented. An absolute minimum for the data types to be included would be LR name, site and crop maintainer.



Interviewing a farmer about “Broa 29” LR of maize (*Zea mays*) on how seeds are selected for the next season, in S. Pedro do Sul (Portugal) (photo: Pedro Mendes-Moreira).



Collection of seeds of cowpea (*Vigna* spp.) LR, near Harmanli (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").

Box 67. Considerations when using *ex situ* data

Care must be taken when interpreting information on current germplasm conserved. In many cases the coordinates are (wholly or partly) missing, imprecise or wrong. Moreover, the material held might be incorrectly identified (though this is less likely to be the case of crop species), it might not be representative of the genetic diversity of the sampled population and it might be duplicated in several institutions giving a false idea of the actual genetic diversity being conserved. Further it may for various reasons be unavailable to potential users, some collections might not be efficiently managed and therefore records may contain errors and the germplasm might not be effectively conserved.

Source: Maxted *et al.* (1995), Hijmans *et al.* (1999)

(v) Ecogeographic data verification (Figure 31).

- Check for duplicates. Namely regarding the gene bank and herbaria survey, those records with the exact same data should be highlighted as duplicates so to avoid a false impression of the intensity of LR collection.
- Check for spelling errors and standardise the data format.
- Georeference all the entries, if possible. While undertaking the farmers' survey, LR populations should be georeferenced *in situ*; data from other sources should also be georeferenced by using (on-line) gazetteers, maps, Google Earth, etc.
- Assign a level of geographic precision; different levels of precision should be assigned to each record (see Table 6 as an example of geographic precision for LR).
- Check for outlier locations. Distribution maps should be created (with a GIS, if possible) to look for outlier collection sites. All individual records should then be corrected for these mistakes or deleted if correction is not possible.

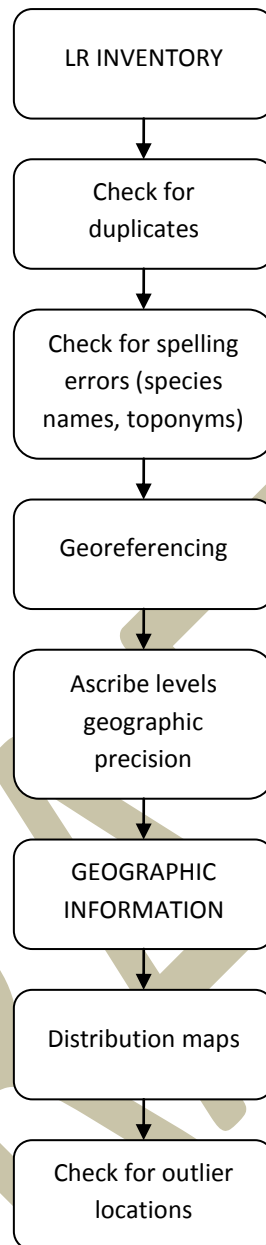


Figure 31 Schematic representation of ecogeographic data verification

(vi) Analysis of collated data. It may include:

- The distribution of LR;
- The distribution of specific character states within LR;
- The variation displayed by the LR with regard to characterization and evaluation traits;
- Analysis of major agronomic problems faced by the crop (pest, diseases, drought, etc.);
- The mapping and detection of ecogeographic patterns (e.g. phenology of the crop in different areas, whether a particular LR occurs on a particular soil type, or whether the frequency of a character state changes along an environmental gradient);
- The identification of sites for on-farm conservation;

- Target LR with traits of interest for plant breeders or to complement existing *ex situ* conservation.

See B.8. Gap analysis of priority landraces for methodologies and corresponding ‘Additional materials and resources’ on ecogeographic analyses and resources.

- (vii) Data synthesis. The products that synthesise the data collated include the LR national inventory (which contains raw data), the conspectus (that summarizes all data collated for each LR) and the report (which interprets the data obtained).

Table 6. Examples of types of data and the corresponding level of geographic precision for LR¹³⁵

LEVEL OF PRECISION	TYPE OF DATA
1	Exact places (e.g., farms)
2	Within an area of 1 km ²
3	Within an area of 10 km ²
4	Within an area of 20 km ²
5	Within an area of 100 km ² or more

B.4.3. Examples and applied use

There are no examples of complete national inventories of LR. On the other hand, partial national inventories have been prepared in several countries, including Bulgaria¹³⁶, Hungary¹³⁷, Italy, Portugal¹³⁸, Sweden¹³⁹ (Box 68) and United Kingdom¹⁴⁰, but none are systematic or comprehensive. Most examples are based on organized expeditions to collect specimens and *ex situ* accessions for conservation and evaluation, as well as to collect information on the cultivation method, history and traditional knowledge and use of LR. This is the case for example for Denmark¹⁴¹, Japan and Lao People’s Democratic Republic¹⁴².

Box 68. Inventory of landraces in Sweden

Potential LR growers were reached through several different channels: media (TV, radio broadcasting, local and national newspapers, garden magazines), exhibitions, seed growers, farmers, retirees’ organizations, regional organizations for agricultural outreach, amongst others. Crop demonstration trials were also set up by various organizations.

The growers of LR were asked to contact the Swedish programme for the diversity of cultivated plants (POM) and provide as much documentation as possible about their plant material. The growers were asked to answer the following questions:

¹³⁵ Adapted from Magos Brehm (2009)

¹³⁶ Krasteva *et al.* (2009)

¹³⁷ Holly *et al.* (2009)

¹³⁸ Mendes Moreira and Veloso (2009)

¹³⁹ Weibull *et al.* (2009)

¹⁴⁰ Scholten *et al.* (2004, 2009)

¹⁴¹ Poulsen (2009)

¹⁴² FAO Country Reports (2009)

- Where, by whom and how long had it been grown?
- Was something known of its origin?
- Was it still being grown?

- The name of the cultivar, if available.
- The age of the seed.
- The information on the seed bag.
- Some particular traits or characteristics of the cultivar.

The LR growers then sent their seeds for evaluation together with the above information; the seeds were submitted to germination tests and/or seed multiplication and finally stored at NordGen in Alnarp, southern Sweden and safety-duplicated at Svalbard. The inventory of Swedish LR was then compiled.

Source: Weibull *et al.* (2009)

LR in Sweden?

Advert in national/regional newspapers/
garden magazines

Monographic LR inventories have been compiled for particular crop groups and/or in particular geographic areas, for instance in three strategic areas in Romania¹⁴³ (Box 69), rice in three major rice agro-ecozones in Nepal¹⁴⁴ (Box 70), coastal agroecosystems in Luong Vien Commune, Vietnam¹⁴⁵, fruits in the Czech Republic¹⁴⁶, forage LR in Central Italy¹⁴⁷, vegetables in England and Wales¹⁴⁸, barley (*Hordeum vulgare*), oat (*Avena strigosa*), rye (*Secale cereal*), cabbage (*Brassica oleracea*) and Timothy grass (*Phleum pratense*) in Scotland¹⁴⁹, and maize (*Zea Mays*) in Chiapas, Mexico¹⁵⁰.

The data compiled in the LR inventories can also be analysed in several ways. Box 72, Box 73 and Box 74 show some examples of how data analysis can be carried out.

Box 69. Inventory of landraces in Romania

The initial source of data for the LR inventory was a database (BIOGEN database) designed and managed by the Suceava Gene bank (<http://www.svgenebank.ro/>) holding information gathered during 20 years of systematic survey and collecting missions. Three strategic areas with great genetic diversity of major crops such as wheat, maize, bean, potato and faba bean, were surveyed (Suceava, Maramures and

¹⁴³ Strajeru *et al.* (2009)

¹⁴⁴ Bajracharya *et al.* (2010)

¹⁴⁵ Son *et al.* (2003)

¹⁴⁶ Paprštejn and Kloutvor (2001)

¹⁴⁷ Negri (2005b)

¹⁴⁸ Kell *et al.* (2009)

¹⁴⁹ Wright *et al.* (2002) and http://www.scottishlandraces.org.uk/scotlandrace_index.htm

¹⁵⁰ Bellon and Brush (1994)

Apuseni Mountains). Based on the importance in rural people's diet, the high number of LR, and the wide distribution in Romania, LR of *Phaseolus vulgaris* L. were given priority. Agricultural extension services, local authorities, biology and agronomy teachers, as well as local priests, who selected farmers recognized as 'conservationists', were interviewed and an inventory of LR was compiled. The information collected was revalidated with farming communities during collecting trips in 2007 and 2008.

Source: Strajeru *et al.* (2009)

Box 70. Rice landraces in three rice agro-ecozones in Nepal

A survey of rice LR was undertaken in three sites representing three agro-ecosystems (Bara: 100-150m, Kaski: 700-1206m, Jumla: 2200-3000m). A total of nine villages were surveyed for rice diversity through a Participatory Rural Appraisal (PRA) methodology (direct observations and group interviews) where socio-economic and cultural diversity that influences agrobiodiversity were assessed. This way, an inventory of LR representative of these three agro-ecosystems was carried out.

Source: Bajracharya *et al.* (2010)

LR in Romania	Rice LR in Nepal

Box 71. Inventory of maize in Mexico

The project "Proyecto Global de Maíces Nativos" [Global Project of Native Maize] was carried out by CONABIO, the Instituto Nacional de Investigaciones Forestales, Agrícolas y Pecuarias (INIFAP) and the Instituto Nacional de Ecología (INE) in Mexico, between 2006 and 2010. This global project included 12 smaller projects with specific objectives:

- Collation and analysis of bibliographic information about the origin and diversification of maize;
- The digitizing of the information obtained from the main national *ex situ* collection of maize and teosinte in Mexico (at the Unidad de Recursos Genéticos del Banco de Germoplasma of the CEVAMEX - Campo Experimental del Valle de México - of the INIFAP);
- Ten projects aiming to collect seeds in most of the agricultural areas where native maize is still cultivated.

The main products obtained with this global project were: (i) a document on the centres of origin and genetic diversity of maize in Mexico (see Kato *et al.* 2009), (ii) a database of all known maize LR and wild relatives (available from http://www.biodiversidad.gob.mx/genes/pdf/proyecto/Anexo13_Base%20de%20datos/BaseMaicesNativos.xlsx) which comprise the collection of the main national gene bank and the new collections resulted from the smaller ten projects. By October 2010, the database included a total of 24,057 records (22,931 native maize, 599 teosinte and 527 *Tripsacum* wild relatives of maize).

The global project gathered about 235 researchers from 70 academic and research institutes who participated in the collecting missions, characterization of samples, systematization and collation of information on maize and teosinte.

Source: <http://www.biodiversidad.gob.mx/genes/proyectoMaices.html>

Box 72. Conservation and sustainable use of dryland agrobiodiversity

The conservation and sustainable use of dryland agrobiodiversity project was funded by the Global Environment Facility (GEF) through the United Nations Development Programme (UNDP) between 1999 and 2004. The project aimed at promoting the community-based *in situ* conservation and sustainable use of both LR and CWR of cereals, food and feed legumes, *Allium* and fruit tree species originating from Jordan, Lebanon, Palestine and Syria. The project was coordinated by the International Centre for Agricultural Research in the Dry Areas (ICARDA) in cooperation with IPGRI-CWANA and ACSAD. Its activities were carried out mainly by National Research Institutions or the Ministry of Agriculture in two target areas in each country. Universities and NGOs also helped implement some of the project activities.

Among other tasks, socioeconomic and ecogeographic (agrobiodiversity) surveys were conducted periodically in 63 monitoring areas over 24 project sites in order to evaluate the conservation status of agrobiodiversity and its main threats. Comprehensive ecogeographic data were compiled in order to describe the dynamics of vegetation and monitor key plant populations. Ecogeographic data included species data (e.g. growth stage, cover/density, health status, etc.), ecology and land use. Data were then collated in a database to facilitate its management and use as well as the analysis of time-series data at country and regional levels. The database was installed and used in each country, but maintained by ICARDA, whose staff periodically update with new data sent by national survey teams.

The main results of LR surveys showed that LR of wheat, barley, lentils, olives, figs, and almonds are still widely used by farmers (despite a decrease in area of cultivation), whereas improved varieties are mainly used in the case of apples, apricots, and plums. On average, local communities reported to cultivate about six LR of wheat and barley and more than 10 of olives, grapes and figs. The socioeconomic studies revealed that local communities prefer LR of barley, wheat, chickpea, lentil, olives, figs, grapes and apricots due to their adaptation to extreme environments, and because they provide good food and processing qualities in comparison to the improved varieties of those crops. Lack of marketing opportunities was highlighted as the major constraint to the more widespread cultivation of LR.

Source: ICARDA (2001)

Maize LR in Mexico

Maize LR in Mexico



Wheat landrace growing near Tel Kalakh, Syria (photo: Nigel Maxted)

Box 73. Use of agroecological and characterization data to establish a core collection

A core collection of *Phaseolus vulgaris* was established using ecogeographic analysis methodologies. Based on the history of the crop, regions of collection were prioritized. GIS surfaces layers for four parameters (length of growing season, photoperiod, soil type, moisture regime) were interpolated and used to define 54 distinct ecogeographic areas. To each 10-minute grid cell, one of those areas was assigned. Passport data were used to match each LR accession to an ecogeographic class. Accessions in each ecogeographic area were stratified according to characterization data (growth habit, grain colour, grain size). Finally, accessions were selected randomly from within each stratum within each environmental class.

Source: Tohme *et al.* (1995)

Box 74. On-farm conservation of legume landraces in Turkey

A project on the *in situ* and on-farm conservation of legume LR in Turkey was initiated in 1993 and funded by the Turkish Scientific and Technical Board together with AARI. It focused on the on-farm conservation of LR of lentil, chickpea and bean grown in NW transitional zones. Its main objectives were to collect and conserve LR and to analyse agromorphologic, ecogeographic and socioeconomic data in order to understand farmers' preferences and cultivation methods and study the possibility of on-farm conservation of LR. Socioeconomic and ecogeographic surveys were conducted in the north western transitional zone adjacent to the north western Black Sea, northeaster Aegean and Central Anatolian regions. LR distribution maps were produced and the socioeconomic status of LR cultivation was evaluated. LR of hulled wheat, bean, chickpea and lentil were selected as the priorities for on-farm conservation in the transitional zone in Turkey.

Source: Tan and Açıkgöz (2002)

Legume LR in Turkey	Legume LR in Turkey
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WWW Italian LR from which typical Italian products were obtained: <http://biotec.casaccia.it>

WWW Lazio and Marche Regions (Italy) LR inventory: <http://www.arsial.regione.lazio.it/portalearsial/RegistroVolontarioRegionale/>

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WWW Bioversity International training modules on ecogeographic surveys and spatial analysis:
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WWW For crop specific characterisation and evaluation descriptors search at: <http://www.biodiversityinternational.org/publications/search.html>

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DRAFT

B.5. Threats and threat assessment of landrace diversity

B.5.1. Overview

Why do we need to assess threat to landraces?

Relative threat is one of the most obvious criteria used in establishing conservation priorities: the more threatened (i.e. increased likelihood of genetic erosion or actual extinction of the species) the greater the conservation priority. Therefore, threat assessment will allow us to use that information when prioritising landraces for conservation but, perhaps more important, will give us an indication of the extinction risk and help to identify which landraces are threatened, to detect its degree of threat as well as to act upon it in order to avoid its genetic erosion and/or landrace extinction.

Here the distinction is made between identification of threats and threat assessment, identification of threats is the documentation of adverse factors that may impact on the LR diversity (e.g. changes in land management, introduction of modern cultivars, urbanization, lack of niche market for LR production), while threat assessment is the process of formally assessing each LR and providing a relative indication of the degree threatened appropriate for that LR.

The loss of LR diversity can be seen in two different but complementary perspectives: genetic erosion, and 'local cultural erosion'.

Genetic erosion¹¹⁶ of LR has been referred to in literature as: (i) the loss of a crop, variety or allele diversity^{117,118,119,120}, (ii) as a reduction in richness (in the total number of crops, varieties or alleles)^{121,122,123,124}, and (iii) as a reduction in evenness, i.e. genetic diversity^{125,126}. Numerous factors currently negatively impact plant species and their populations (see *Why are landraces threatened?* in B.1. Introduction, for a comprehensive list of threats) resulting in genetic erosion, and eventually extinction. This will bring serious consequences to food security (see *What are the practical consequences of LR genetic erosion?* in B.1. Introduction).

'Local cultural erosion' relates to the crop-related cultural activities which underpin local selection and breeding activities, are likely to be lost once the LR are lost and halt further cultural development within the community^{151,152}.

Threat assessment of LR diversity is crucial as an early warning system to detect and prevent genetic erosion and extinction. It can be assessed at two levels: (i) individual LR (i.e. the extinction of individual LR), and (ii) genetic diversity within LR (allelic loss within a LR). LR threat assessment using the IUCN Red List Categories and Criteria¹⁵³, as successfully applied to CWR and other elements of biodiversity, is not an option as the criteria cannot be applied at the within species level (Negri *et al.* 2009). LR are variable populations of a crop taxon and the goal of LR conservation is to conserve the full range of genetic diversity within the LR and not just the LR itself (Negri *et al.* 2009). Alternative methods based on several different categories and criteria have been suggested by some authors^{154,155,156}; however, to date there is no standardised methodology for threat assessment of erosion or extinction for LR even though

¹⁵¹ See e.g. Negri (2003)

¹⁵² See e.g. Torricelli *et al.* (2009)

¹⁵³ IUCN (2001)

¹⁵⁴ Joshi *et al.* (2004)

¹⁵⁵ Porfiri *et al.* (2009)

¹⁵⁶ Antofie *et al.* (2010)

the need for such a methodology is widely accepted. Meanwhile, the simple methodology described here can be applied (Figure 32). It is a three stage process that can be run at the same time as the LR survey is being carried out and the LR inventory prepared: (i) Definition of indicators of threat, (ii) Identification of threats to LR diversity, and (iii) Evaluation of the relative degree of threat.



Norwegian farmer, Johan Swärd, in a field where the rye LR 'Svedjerug' is grown; this LR has been used by immigrating Finns in the eastern part of Norway in their shifting and burning cultivation system (*svedje*) and is especially adapted to the alkaline soil that arise from burning the vegetation. This LR was saved when seeds were found in an old farmhouse and only 11 seeds germinated; Johan and a group of farmer colleagues have started to grow the LR and have now a significant market for flour of this particular LR; Johan Swärd received the "Plante Heritage Prize" from The Norwegian Genetic Resource Centre in 2011 for his valuable work in saving this LR from extinction (photo: Åsmund Asdal).



Angelica archangelica subsp. *archangelica* is a native plant to the mountain areas of Norway (and other countries); it has a long tradition as a vegetable and spice plant, and it has historically been the most

important plant for export from Norwegian agriculture to the continental Europe. Farmers from Voss area (western part of Norway), through centuries, have developed the LR “Vossakvann” which possess stems with more flesh than wild growing specimens. Farms had their own fields with “Vossakvann” and it was also mentioned in ancient law that intruding and stealing from *Angelica* gardens caused severe penalties. The art of growing “Vossakvann” was forgotten, but some fields of Vossakvann have survived. The farmer in the picture Knut Arvid Olde (left) did not know what kind of plant/treasure he had on his farm before he was told about it by the agricultural advisor Jorunn Ringheim. In recent years the production of “Vossakvann” for several purposes and products has increased. The LR was named a specific scientific name: *Angelica archangelica* subsp. *archangelica* var. *majorum* (photos: Åsmund Asdal)

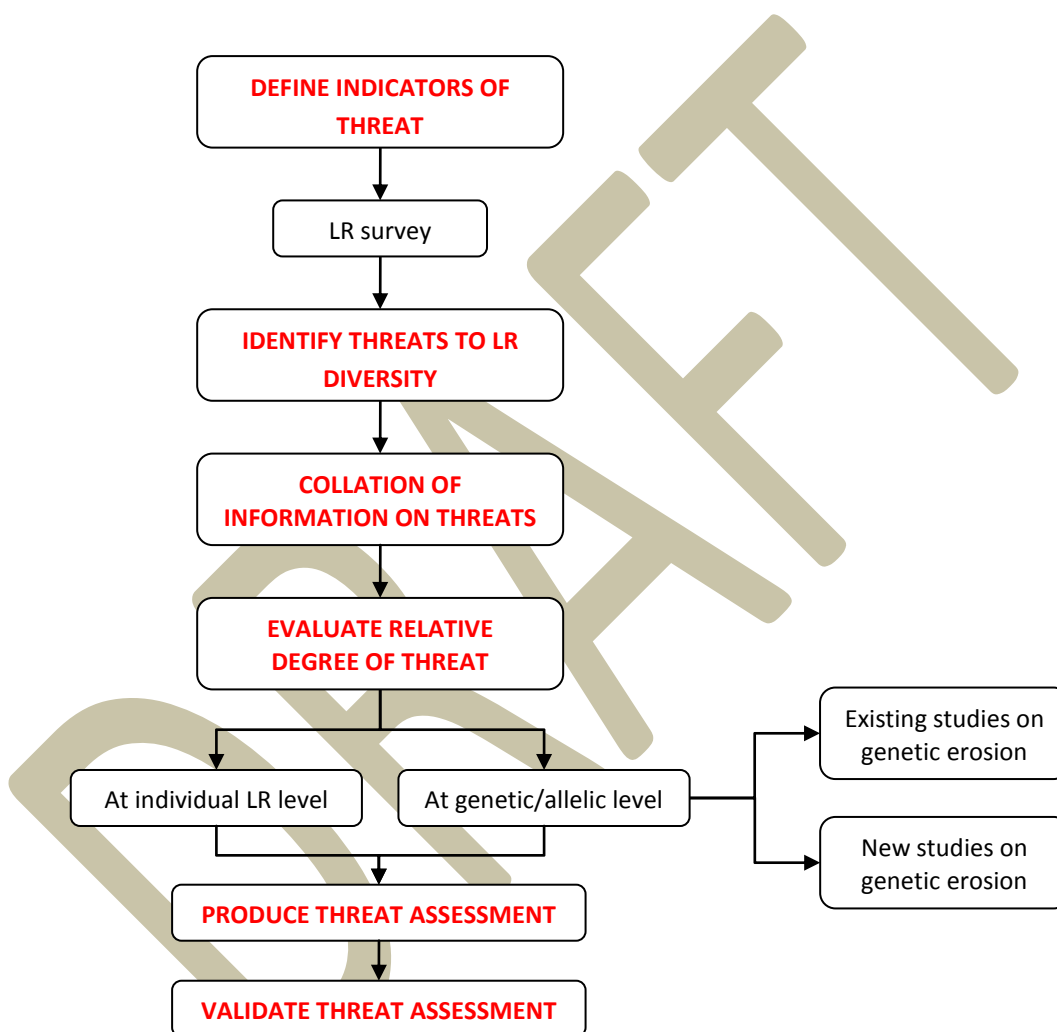


Figure 32. Landrace diversity threat assessment methodology

B.5.2. Methodology for LR threat assessment

- (i) Definition of indicators of threat. The analysis of some of the types of data that should be collated during the LR survey (see Figure 30) together with other indicators can help in estimating relative threat for individual LR (not at the allelic level). These indicators may include:
 - Farmer wealth: whether the LR is grown by a wealthy or a poor farmer/maintainer which will probably influence the likelihood to keep cultivating LR in detriment of new varieties;

- Access to seed planting materials: whether many farmers maintain seed which is easy to access or only few farmers maintain the seeds which are difficult to access;
 - Site/farm area: area dedicated to grow the LR (as a percentage of total regional area of the crop, and versus the number of households that grow the LR), trend for the dedication of new areas to the cultivation of the LR, whether the site is predicted to be negatively affected by climate change;
 - Cultivation system: whether it is subsistence or commercial farming, and whether the farming system is (un)sustainable;
 - Multiplication ability: whether plants produce abundant seeds or are easily propagated vegetatively or, on the contrary, they produce few seeds or are difficult to propagate;
 - Level of plant use: whether most plant parts are used or there's only a limited use of few plant parts;
 - Socio-economic indicators: whether the contribution to the income and nutrition of the LR is significant, market prospects to utilise and commercialise the LR and/or the products manufactured with it, whether there are local or national maintainer incentives, and maintainer-perceived value;
 - Historical indicators: information on the historical availability of a particular LR might be difficult to obtain but may provide baseline information on the previous state of that resource, to show what has changed and the process of degeneration/extinction of LR, and be used as a source of information on the potential for re-cultivation based on the recovery of historical uses that have been lost; these might include: (i) known lost LR (see Table 7 for guiding criteria to detect lost varieties), (ii) the first noted use of a particular LR together with its historical geographical spread and social acceptance, (iii) the date of the first use of that LR, and (iv) the importance and cultivation over a long-term period (e.g. 50-150 years) (long-term trend) compared with a short-term situation (e.g. 10-25 years) (short-term trend);
 - Relative uniqueness of the LR: whether it grows at a single site or it is widespread;
 - LR conservation status: whether it is actively and adequately managed *in situ*, it is cultivated on-farm or in some other form a protected area, it is stored *ex situ*, the methods of selection of seed saved and storage are adequate, the maintainer exchange seeds and how frequent, etc.;
 - Knowledge of genetic diversity: is it known by scientific assessment or perceived by the farmer, this type of data may indicate genetic erosion thus high level of threat;
 - Other indicators: presence in catalogues of seed companies or nurseries, whether it is used in breeding programmes, whether it is known to be resistant to abiotic stresses; a LR that is of value to seed companies, nurseries or for breeding programmes or known to be resistant to abiotic stresses is likely to be less threatened.
- (ii) Identification of threats to LR diversity and collation of this information. For each LR at each occurrence site, threats should be identified using the indicators listed above.
 - (iii) Evaluation of the relative degree of threat. At the individual LR level and at allelic level (based on existing genetic diversity studies or undertake novel genetic diversity studies).
 - (iv) Production of the threat assessment. Based on the outcome of the previous stages, a threat assessment of LR can then be compiled.
 - (v) Validation of the threat assessment. The threat assessment should then be validated with the judgments made by the maintainers of LR; this is particular important for those

LR thought be lost and group discussions, radio broadcasting, newspapers publications, etc. could help gathering more information on those LR and understand whether they are, in fact, lost; on the other hand, and given there are frequently problems regarding the nomenclature and genetic identification of LR (see Box 63), molecular characterization of LR could help detecting LR that were thought to be lost but, in fact, have a different name.

Table 7. Guiding criteria for detecting lost varieties ¹⁵⁷

Was the lost variety an old variety (say at least 30-50 years old)?	<input type="checkbox"/> Yes <input type="checkbox"/> No <input type="checkbox"/> Do not know
Was the variety introduced from neighbouring villages a long time ago (say at least 20–30 years)?	<input type="checkbox"/> Yes <input type="checkbox"/> No <input type="checkbox"/> Do not know
How long since the variety disappeared?	<input type="checkbox"/> Over last 5 years <input type="checkbox"/> Over 5–10 years <input type="checkbox"/> More than 10 years <input type="checkbox"/> Do not know
Was it a sudden loss or a gradual process?	<input type="checkbox"/> Sudden <input type="checkbox"/> Gradual <input type="checkbox"/> Do not know
How popular was the variety?	<input type="checkbox"/> Very popular <input type="checkbox"/> Popular <input type="checkbox"/> Not so popular <input type="checkbox"/> Do not know
Was seed or planting material of the variety obtained through the informal seed system or purchased?	<input type="checkbox"/> Informal <input type="checkbox"/> Purchased <input type="checkbox"/> Both <input type="checkbox"/> Do not know
Do you think it is likely that some custodian farmers in neighbouring villages are still keeping seed or planting material of this variety?	<input type="checkbox"/> Yes, very likely <input type="checkbox"/> No, very unlikely <input type="checkbox"/> Do not know

B.5.3. Examples and applied use

Box 75. Threat assessment of agricultural crops and landraces in Nepal

A method based on population, ecological, social, modernization and use criteria was suggested to undertake threat assessment of crop species. The authors suggested that combinations of criteria in these categories can be used to carry out threat assessment of crop genotypes. In addition, the following threat categories were proposed: Extinct (seed is locally not available for exchange or planting), Endangered or Threatened (few households growing the LR in a small area), Conservation

¹⁵⁷ Padulosi and Dulloo (2012)

Dependent (many households growing the LR in a small area or vice versa), No Risk (commonly grown by many households), and Not Evaluated or Data Not Available.

Source: Joshi *et al.* (2004)

Box 76. Red List of crops

The authors attempted to obtain a list of threatened agricultural and horticultural crop species (excluding ornamentals and forestry species) by matching the list of crops in Mansfeld's Encyclopaedia of Agricultural and Horticultural Crops (Hanelt and IPK Gatersleben 2001, IPK Gatersleben 2003) with the IUCN Red List of Threatened Species. However, this assessment did not consider the threat to LR material within crops.

Source: Hammer and Khoshbakht (2005)

Box 77. Threat assessment of landraces in the Lazio region (Italy)

Five categories of indicators of threat to evaluate genetic erosion and levels of risk of LR were adopted in the Lazio region (Italy). These include: (i) the presence of the product in the market, (ii) the presence in catalogues of the seed companies or nurseries, (iii) number of farmers cultivating the LR, (iv) area under cultivation (as a percentage of total regional area of the species), and (v) trend for the dedication of new areas to the cultivation of the LR.

Source: Porfiri *et al.* (2009)

Box 78. Red List of landraces in Romania

The authors modified the methodology described by Hammer and Khoshbakht (2005) and produced a data sheet model to describe the conservation status of old crop varieties for future Red Listing of the Romanian LR. They included data such as: species and vernacular names, conservation status, chorology, whether the LR is cultivated within protected areas, human-animal conflicts that can threaten LR, surface area of cultivation, cultivation details, seed origin, the main barriers to the conservation of the LR, etc. The authors identified LR threat categories based on the pre-2001 IUCN Red List Categories (IUCN 1994): Extinct On-Farm (ExF), Endangered On-Farm (EF), Endangered for *Ex Situ* (EE), Vulnerable On-Farm (VF), Vulnerable for *Ex Situ* Conservation (VE), Rare, Least Concern (LC) and Indeterminate (I).

Source: Antofie *et al.* (2010)

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B.6. Setting LR conservation priorities

B.6.1. Overview

Why do we need to set LR conservation priorities?

The creation of a national inventory of LR is likely to identify a great magnitude of diversity present, much of which is expected to have been previously unrecognised. Therefore, the process of establishing priorities for conservation is an obvious and essential step in any conservation strategy (but only if the number of LR exceeds the number that can be conserved using the available resources).

The economic value of biodiversity and genetic resources has been defined^{158,159,160} and economists have developed a number of methods for assessing several components of public goods which have been applied to biodiversity. However, the main focus has been on the valuation of ecosystem services rather than genetic resources *per se*.

There has been considerable debate over which criteria should be utilised when undertaking a scheme of species prioritization^{161,162}. Potential criteria to consider include threat of genetic erosion, endemism, rarity, population decline, quality of habitat, intrinsic biological vulnerability, current conservation status, recovery potential, feasibility and sustainability of conservation, taxonomic uniqueness, genetic distinctiveness, ecogeographic distribution, biological importance, socio-economic use, cultural importance, economic factors, legislation, ethical and aesthetic considerations, and priorities of the conservation agency. Although some of these criteria may be applied to LR diversity prioritization, the socio-economic aspects in particular are of fundamental importance in LR conservation and therefore in LR prioritization. In addition, numerous systems and methods for setting priorities have been used to define priorities for the conservation of crop wild relatives but none to LR diversity.

Example of national priority LR	Example of national priority LR

An agreed set of criteria as well as standard methodology for systematic prioritization has yet to be established in order to conserve the highest priority LR diversity. The criteria and methodology used may vary according to the needs of individual countries and/or the conservation agencies that are undertaking the work. Whatever system is used, the total number of target LR must be adjusted to a number that can be actively conserved using the available financial and human resources.

The process of setting priorities for LR conservation can be complex and time-consuming depending on the methodology and criteria used. Methodologically, the starting point of

¹⁵⁸ Flint (1991)

¹⁵⁹ Shands (1994)

¹⁶⁰ Drucker *et al.* (2001)

¹⁶¹ See e.g. Fitter and Fitter (1987)

¹⁶² See Maxted *et al.* (1997c)

prioritization is the national inventory of LR (or the monographic inventory of target crops, or the inventory of all LR from a particular region within the country). Whatever the approach, floristic or monographic, it basically consists of three main steps: (i) Definition of the prioritization criteria, (ii) Definition of the prioritization scheme, and (iii) Application of both the criteria and the methodology to finally obtain the priority LR (see Figure 33).

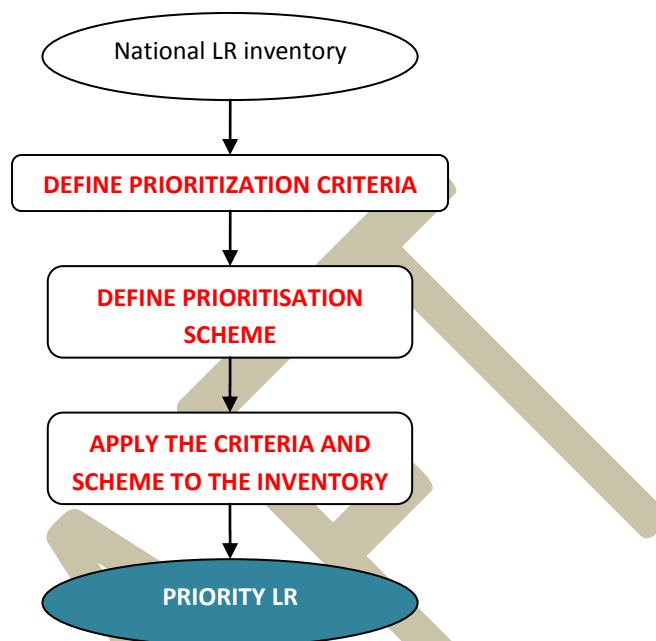


Figure 33. Process of establishing conservation priorities from a national inventory of LR

B.6.2. Methodology for landrace prioritization

(iv) Definition of the prioritization criteria. The prioritization criteria should be defined by the responsible national agency or researcher. The economic value of the crop and the cultural/identity value are likely to be the most important criteria in establishing LR conservation priorities, but there are several other criteria that can be considered. Major categories of LR prioritization criteria include:

- LR diversity: whether a particular LR occurs together with other LR—it is more cost effective to conserve sites that have high numbers of LR rather than sites with a single LR.
- Cultural and identity value: the cultural importance that a particular LR has in a community.
- Farmers' priorities: the priority given to a particular LR by the farmers themselves (for example, based on importance in their diet, special cooking qualities), or an indication of importance estimated by the large number of farmers that grow a particular LR.
- Threat status: whether threat status has been assigned to the LR and/or Information on threats (e.g. obtained from passport data) (see B.5.2 Methodology).
- Historical evidence: a LR that has been cultivated for longer should be prioritised assuming that length of cultivation indicates perceived value by farmers and relative adaptability to environmental as well as to consumer changes.
- Economic value: LR are of direct use, particularly to subsistence or marginal agriculture, and also constitute a potential source of novel genetic diversity for

breeding and other forms of utilization; therefore, the economic importance of both the crop (at national level) and the LR themselves is a good indicator of their value. In other words, whether the crop is nationally important and whether a particular LR is locally important should be taken into account. For these two aspects of economic value, two sub-criteria can be used:

- a. *National economic value of the crop*: for example, crop production quantity and area and/or the number of known crop varieties (including LR) grown at national level;
 - b. *Economic value of the LR*: LR production quantity and area and/or uses (whether the LR is grown for food, fodder, forage, etc.).
- Native status: whether the LR is a primary (autochthonous or allochthonous) or a secondary LR (see *What is a landrace?* In B.1. Introduction).
 - Conservation status: before a LR can be given high priority for conservation, related current conservation activities should be reviewed. If sufficient genetic diversity is already being conserved *in situ* and/or *ex situ*, additional conservation efforts may not be justified, and resources should focus on those LR that are not being conserved. Note however that careful attention to the information obtained from *ex situ* holdings should be paid because: a) researchers often identify LR using merely the name given to the LR by the farmer (assuming that two differently named LR are in fact different), but not only may farmers use the same name for LR that are genetically distinct, they may also use different names for the same LR (see Box 63); b) the material held in gene banks might be incorrectly determined, dead, in poor condition or unavailable to potential users; c) the number of accessions might be misleading because of duplicates; and d) *ex situ* accessions might not be representative of the overall genetic diversity of a LR (see Box 32).
 - National rarity: a LR with limited range within the country is considered rarer than a LR occurring throughout the country; therefore, number of provinces in which each LR occurs can be considered.
 - Agronomic information as noted by the maintainer: beneficial LR characteristics such as ability to cope with altitude, climate, soil type, water stress, pest or diseases and improve yield, size, taste and colour.
 - Other: other criteria that might be useful or considered important include threats to a small niche market or declining use of LR in religious ceremonies.



Recoding of agronomic characteristic with farmers of Mkhalatsong cowpea LR grown in a cotton field in Chingale (Zomba District, Malawi) (photo: Edwin A Chiwona).



Market with “Uzgen” rice (Os province, Kyrgyzstan) (photo: Pavol Hauptvogel).



Market with home garden products in Hebei province (China) (photo: Pavol Hauptvogel).

- (v) Definition of the prioritization scheme. Similar to the selection of prioritization criteria, the choice of the prioritization methodology (or scheme) should be a decision made by the responsible national agency or researcher. The complexity of the scheme will depend on the time available, financial resources, data availability, etc. Prioritization schemes include rule-based, scoring and ranking systems, with or without weighting of criteria, different combinations of criteria, etc. (see Section A.4 to contrast with CWR prioritization).
- (vi) Application of the prioritization criteria and scheme to the inventory: This will culminate in the list of priority LR for conservation.

B.6.3. Examples and applied use of LR prioritization criteria and schemes

Box 79. UK National LR Inventory

The Department of Environment, Food and Rural Affairs (Defra) of the UK government commissioned a national inventory of genetic resources for food and agriculture. The authors primarily used the native status of LR (where high priority was assigned to autochthonous LR), as well as economic national importance of the crop as criteria to prioritise crops to be the focus of a preliminary inventory.

Several LR were identified in Scotland, including: Scots timothy (*Phleum pratense* L.), bere barley (*Hordeum vulgare* L.), black oat (*Avena strigosa* Schreb.), Shetland Black and Lewis Black potatoes (*Solanum tuberosum* L.), and Shetland cabbage (*Brassica oleracea* L.). Given that data on the exact extent of cultivation were not available, and fieldwork fell outside the scope of the national inventory of genetic resources, national distribution and evidence of threat were used to further prioritise Hebridean and Shetland oat and Shetland cabbage LR among all the other LR to assess the extent of current cultivation and conservation.



Figure 34. Distribution of Shetland cabbage landrace maintainers on the Shetland Islands
Source: Scholten *et al.* (2004, 2008), Green *et al.* (2009).



Landrace of *Avena strigosa* (Shetland oat) (photo: Maria Scholten).



Brassica oleracea (Shetland cabbage) landrace on the island of Whalsay, Shetland Islands, Scotland (photo: Maria Scholten).

Box 80. Landraces inventory and prioritization in Romania

The authors attempted to collate all data on Romanian LR conserved on-farm from: (i) the BIOGEN Database designed and managed by the Gene bank in Suceava that includes passport and on-farm descriptors gathered during 20 years of systematic survey and collecting missions, and (ii) a farmers survey of selected villages in three strategic areas: Suceava, Maramures and Apuseni Mountains, where a broad range of genetic diversity of major crops such as wheat, maize, bean, potato and faba bean is known to exist. Agricultural extension services, local authorities, biology and agronomy teachers and local priests helped in identifying the farmers recognized as ‘conservationists’ of LR. These farmers were then directly approached and semi-structured interviews took place. Common bean (*Phaseolus vulgaris* L.) were prioritised for a LR survey based on its importance in rural people’s diet, the high number of LR and the wide distribution in Romania.

Source: Strajeru *et al.* (2009)

Phaseolus vulgaris LR in Romania

Box 81. Bolivian and Peruvian “Payments for Ecosystem Services (PES)” Study

The authors attempted to evaluate whether multiple conservation goals could be optimised together with social equity when paying for the on-farm conservation of LR, so as to generate agrobiodiversity conservation services. The authors selected priority LR in the Bolivian and Peruvian Andes as case studies for the research.

Through a participatory process with local farmers (via community workshops and interviews), and in the absence of adequate status data, LR that were threatened (by replacement by more commercially favoured varieties) as well as those historically important in the livelihoods of farmers and that were extinct from their farming systems, were identified. Local scientists and agricultural extension experts prepared a ranked list of the most threatened LR through consideration of qualitative information on: (1) the area under cultivation for each LR, (2) the number of farmers cultivating a specific landrace, (3) the level of traditional knowledge associated with the utilization of that LR in farming, food preparation, and for socio-cultural purposes, and (4) the amount of farmer stored seeds available for each LR. In addition, as information on genetic traits was not available, a dissimilarity analysis based on their agromorphological characteristics (e.g. colour and size of panicle, size and form of leaves, size of plant), and resistance to specific weather conditions (e.g. frost, drought) was carried out. Grain size and colour were found to be the most important characteristics in distinguishing LR.

Finally, the LR ranked as being most under threat, were further prioritised based on the dissimilarity information. Five priority quinoa LR in Bolivia (Chillpi Blanco, Huallata, Hilo, Kanchis, Noveton) and four in Peru (Misa Quinoa, Chullpi Anaranjado, Janko Witulla, Cuchi Willa) were selected as priorities and were included in a larger study that aimed at understanding whether, when paying for conservation services, conservation goals could be optimised without compromising social equity.

Source: Narloch *et al.* (2011)

Participatory process with local farmers in the Bolivian/Peruvian Andes

Priority quinoa LR from Bolivia/Peru

Box 82. Priority Rice Landraces in Ban Khoang, Sa Pa District (Vietnam)

Rice LR were prioritised from a research site selected in the context of the project "Strengthening the scientific basis of in situ conservation of agrobiodiversity on-farm" in Ban Khoang Commune of Sa Pa District, Lao Cai Province, supported by the International Plant Genetic Resources Institute (IPGRI) and the Vietnam Agricultural Science Institute (VASI). Participatory Rural Appraisal (PRA) methods were used to survey and evaluate LR. Interviews and focus group discussions were conducted in order to understand farmers' rice production systems and help in the design of a questionnaire for a formal household survey. In addition, direct field observations of the farmers' rice fields and household farming systems, as well as management practices, were carried out. Finally, a farm household survey was conducted using the questionnaire for about 40 farms/farmers that were representative of different agroecological conditions, farm size and ethnic groups, in order to obtain farmers' priority ranking of values, evaluation criteria, constraints and opportunities for LR production.

Source: Canh *et al.* (2003)

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B.7. Genetic data analysis of priority landraces

B.7.1. Overview

Why it is important to undertake genetic studies of landraces?

- For genetic characterization to help differentiate LR;
- To assess genetic diversity within LR;
- To search for traits of interest for crop improvement;
- To establish the pattern of genetic diversity within LR and enable priorities for conservation to be established within each LR.

(v) *Proxy assessment of genetic characterization.* The LR name is commonly used as a proxy for genetic distinction, yet it is known that farmers may use the same name for LR that are genetically distinct but also use different names for the same LR (see Box 63). Given the complexity of national contexts and scenarios, it is imperative that the relationship between the LR and their genetic distinction is further researched. However, financial resources are regularly absent and assumptions may have to be made. Pragmatically, in general, we can assume that different LR names are different genetic entities.

(vi) *Assessment of genetic diversity within LR.* Typically, conservation biology aims at conserving the maximum number of species and numbers of individuals within a species. However, the conservation of intrinsic genetic diversity within a taxon has also been identified as equally important¹⁶³. The genetic diversity available within a species represents its evolutionary potential, allowing it to evolve and adapt to a changing environment. Unlike, modern varieties, LR are not genetically stable and uniform entities. These characteristics make them not only important gene sources for crop improvement, but also for local food security as they have a broader genetic base making them less vulnerable to changes in the environment. Therefore, the assessment of genetic diversity provides baseline information against which genetic erosion can be detected in the future.

Molecular lab photos	Molecular lab photos
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(vii) *Identifying traits of interest for crop breeding.* Two distinct but complementary components of genetic variation have been identified. The first is related to the functional diversity which has resulted from adaptive evolution due to natural selection. The second relates to neutral alleles which results from neutral evolutionary forces such as migration, mutation and genetic drift. The relative importance of adaptive versus neutral variation in

¹⁶³ Jump *et al.* (2008)

conservation genetics has been extensively debated over the years¹⁶⁴. Adaptive variation refers to alleles (or quantitative traits) that affect fitness. They are the primary targets of natural selection and reflect a species' potential ability to adapt to changing environments¹⁶⁵. Adaptive genetic variation is evaluated in quantitative genetic experiments under controlled and uniform environmental conditions. However, the assessment of adaptive variation is very time consuming and quantitative traits involved in adaptation are sometimes difficult to find. Moreover, since that adaptive variation is the result of environmental and genetic factors, large sample sizes are required (which might not be available for threatened populations) in order to understand the contribution of these components to the overall variation. Neutral genetic diversity on the other hand, refers to those alleles that have no direct effect on a species' fitness and are not affected by natural selection. They do not provide information on the adaptive or evolutionary potential of populations or species. This type of genetic diversity can be assessed using a wide range of molecular markers. They include microsatellites and AFLP (Amplified Fragment Length Polymorphism). The assessment of neutral genetic variation has been frequently used as a shortcut to infer global genetic diversity and to support strategies for the conservation of threatened taxa¹⁶⁶.

The issue of whether a correlation between neutral and adaptive variation exists has been debated and conclusions do not always agree. Some authors have found that neutral and adaptive genetic diversity and differentiation are positively correlated¹⁶⁷, whereas other studies indicate that measurements of neutral diversity have a very limited prediction ability of quantitative variation¹⁶⁸ and thus cannot be used as a surrogate of adaptive genetic data, at least for some traits. Within the context of genetic conservation, especially under threat of climate change, gene conservation strategies should focus on the adaptive capacity of populations (and species) by considering their 'individual plasticity' (i.e. their ability to respond to different environmental conditions), their adaptive genetic diversity and the occurrence of natural selection that acts upon them, as well as their ability to disperse¹⁶⁹. Adaptive variation assessment is therefore particularly important since it allows the identification of the components of genetic diversity responsible for the adaptation of populations to different conditions. Nevertheless, adaptive studies are more time consuming and require more skilled staff. In resume, ideally, an adaptive diversity study should be undertaken. If for reasons of financial resources, time available or lack of skilled staff it is not possible to undertake such studies, and assuming there is a positive correlation between neutral and adaptive genetic diversity, then neutral genetic diversity results can be used as a proxy of adaptive genetic diversity.

(viii) *Establishing population priorities for conservation within a LR.* The amount and patterns of genetic diversity both within and between populations of a species, genetic population structure, and common and localised alleles (see Box 25), are some of the data that can be useful when prioritising populations for conservation. For instance, if a LR of the same name that is grown at several different sites is found to be genetically homogenous, then a single farm could carry out the conservation activity; however, if different populations of a LR with

¹⁶⁴ e.g. Bowen (1999), Fraser and Bernatchez (2001), Merilä and Crnokrak (2001), Reed and Frankham (2001), McKay and Latta (2002), Holderegger *et al.* (2006)

¹⁶⁵ e.g. Falconer and Mackay (1996), McKay and Latta (2002), van Tienderen *et al.* (2002)

¹⁶⁶ e.g. Palacios and González-Candelas (1999), Rottenberg and Parker (2003), Eckstein *et al.* (2006), Watson-Jones *et al.* (2006)

¹⁶⁷ e.g. Merilä and Crnokrak (2001), Pearman (2001)

¹⁶⁸ e.g. Reed and Frankham (2001, 2002)

¹⁶⁹ Lefèvre (2007)

the same name are genetically distinct, several farms would need to be involved in their conservation to ensure all genetic diversity within that particular LR is conserved.

Box 83. Allele types according to their distribution in populations

Marshall and Brown (1975) developed a two-way classification system of alleles based on their frequency in populations (common or rare) and distribution across populations (widespread over many populations or localized to just a few). Marshall and Brown (1975) and Brown and Hardner (2000) defined any allele occurring in $\geq 25\%$ of populations as a widespread allele and those occurring in $< 25\%$ of populations as a localized allele. Marshall and Brown (1975) also suggested the classification of the alleles according to their average frequency in a population as common ($P \geq 0.05$) or rare ($P < 0.05$). Four classes of alleles were then defined: (i) common and widespread (population frequency $P \geq 0.05$, and occurring in $\geq 25\%$ of populations); (ii) common and local (population frequency $P \geq 0.05$, and occurring in $< 25\%$ of populations); (iii) rare and widespread (population frequency $P < 0.05$, and occurring in $\geq 25\%$ of populations); (iv) rare and local (population frequency $P < 0.05$, and occurring in $< 25\%$ of populations). From these four categories, the authors argued that the 'common and local' category is the most important in terms of conservation because it includes those alleles that confer adaptation to local conditions. On the other hand, 'common and widespread' alleles are everywhere so they will inevitably be conserved regardless of the conservation strategy, while 'rare and widespread' alleles will be conserved depending on the total number of sampled plants if *ex situ* accessions are to be sampled or if the conservation area includes most of the population in an *in situ* approach. The 'rare and local' class includes very rare variants and recent or deleterious mutants which are extremely difficult to collect but a fraction will always be included in any conservation strategy.

Source: Marshall and Brown (1975), Brown and Hardner (2000)

Along with taxonomic, ecogeographic, characterization and evaluation data and farmer-based knowledge, a National LR Conservation Strategy should, whenever possible, include genetic information of the LR, not only to differentiate and characterise LR, but also to detect which priority LR populations should be targeted for *in situ* and *ex situ* conservation (i.e. those with the greatest amount of genetic diversity and/or with interesting adapted alleles, etc.), and to help detect and thus prevent LR diversity genetic erosion. Figure 35 illustrates the process of collating genetic diversity data on LR. It is necessary to know: (i) whether there are pre-existing genetic studies on the LR, (ii) whether there are financial resources to undertake (further) genetic studies, (iii) whether staff can carry out a genetic study, (iv) whether farmers' perceived value of a LR can be used as a proxy of genetic information (if resources and expertise are not available for ii and iii). Finally, a genetic erosion monitoring scheme should be implemented in order to detect changes in genetic diversity of the LR (see A.1.

Monitoring of landraces on-farm).

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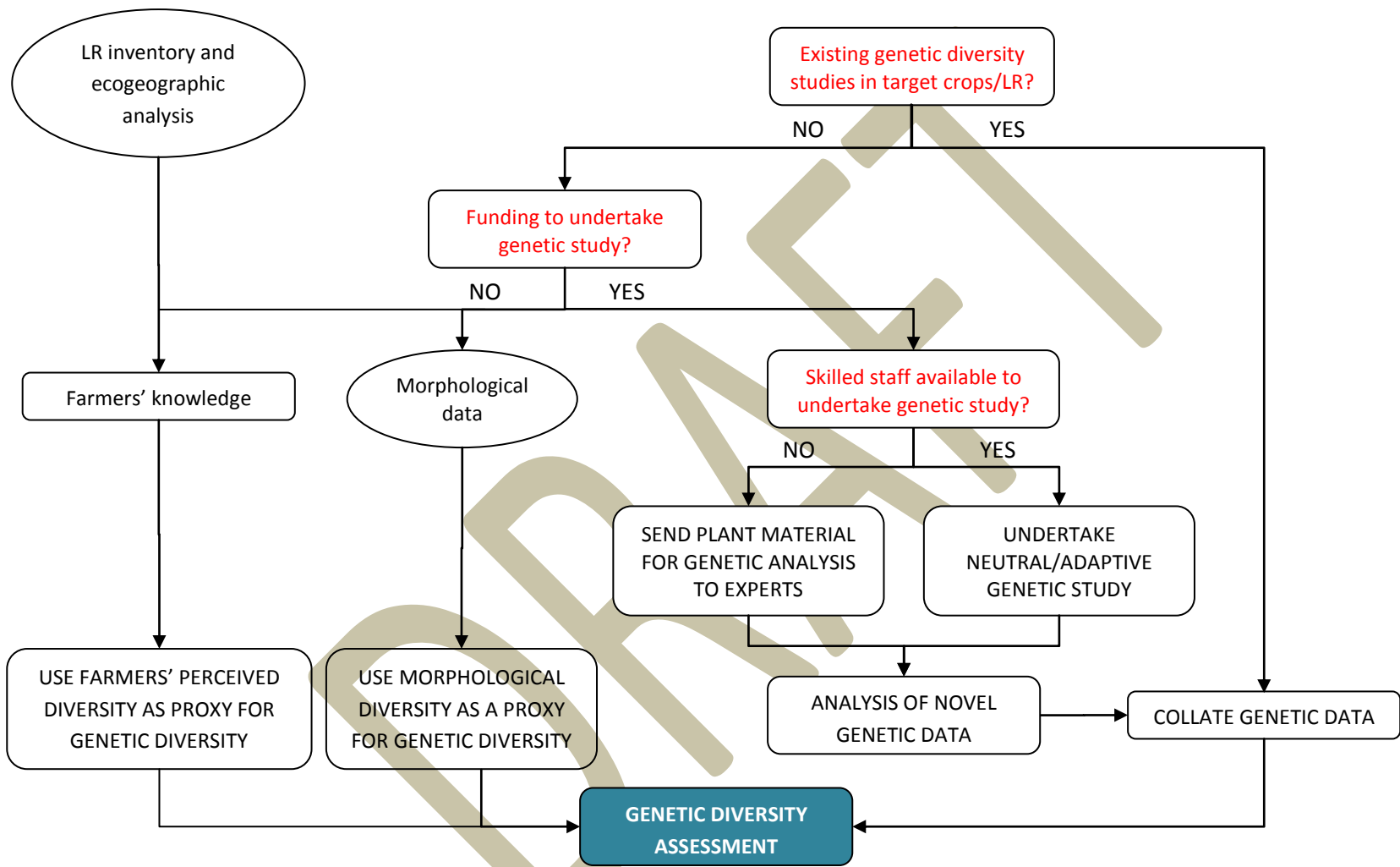


Figure 35. Collation of genetic diversity data of LR

B.7.2. Methodology for LR genetic diversity analysis

The main practical questions that need to be answered in regard to the collation of genetic data are:

- (vi) Are there any genetic studies and genetic information already available for the target crop/LR? If so, then collate all the information obtained which can be useful to understand the species' genetic characteristics. Information on the breeding system should also be gathered as it is crucial in understanding the patterns of distribution of genetic diversity within populations of LR. If no genetic information is available, then if possible a genetic study (on adaptive or neutral diversity) should be carried out.
- (vii) Are there sufficient financial resources to undertake a genetic study (either on adaptive or neutral genetic diversity)?
- (viii) Are there skilled staff able to undertake such a study? If financial resources and expertise are available, a genetic study is thus desirable. If financial resources are available but no skilled staff, plant samples should be collected, then sent to skilled experts to analyse.
- (ix) However, if resources are limited and it is not possible to undertake a genetic diversity study; information on farmer's perceived diversity within their LR can be used as a proxy for genetic data. The main categories of descriptors that can be used to document the diversity perceived by farmers are: distinguishing traits (e.g. colour, shape or size of fruits and/or leaves), agronomic traits (e.g. overall appearance, yield), abiotic stresses (e.g. drought, high temperature), biotic stresses (e.g. susceptibility or resistance to pests and/or diseases), quality traits such as organoleptic (e.g. taste, fragrance) and nutritional qualities (e.g. makes people grow stronger, high sugar content), market traits (e.g. marketability, transportability)¹⁷⁰. Alternatively or additionally, existing or freshly collected morphological data and / or farmers' perceived diversity¹⁷¹ can be used as a proxy for genetic data (different morphological characteristics imply different genetic characteristics). Further, if no other data are available, the ecogeography of the LR may be used to identify potential genetic diversity, the assumption being that genetic diversity will be correlated with ecogeographic diversity.
- (x) Genetic erosion monitoring scheme. Once genetic baseline data have been obtained, a plan to assess genetic diversity regularly over time (in order to detect any genetic erosion events) can be implemented (see A.1.

¹⁷⁰ see Bioversity and The Christensen Fund (2009) for the complete list of farmers' knowledge descriptors

¹⁷¹ see e.g. Mkumbira *et al.* (2003), Chiwona-Karltun *et al.* (2004)

(xi) Monitoring of landraces on-farm).

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B.7.3. Examples and applied use of LR genetic diversity studies

Box 84. Genetic diversity of *Phaseolus vulgaris* L. and *P. coccineus* landraces in Italy

Genetic diversity of 66 *Phaseolus* genotypes (including 14 LR of *P. vulgaris* and 9 LR of *P. coccineus*) collected in Marche, central Italy, were assessed using inter simple sequence repeats (ISSR), nuclear microsatellites and (SSR) and chloroplast microsatellites (CpSSR). *P. vulgaris* showed higher genetic diversity than *P. coccineus* for the SSR and CpSSR, but not for the putative neutral ISSR markers. These data suggested that the diversity in LR of *Phaseolus* has been maintained by farmers' selection and adaptation to heterogeneous environments. In addition, genetic diversity of Marche genotypes was compared to that of American genotypes. 71% of the *P. vulgaris* LR from Marche are of Andean origin.

Source: Sicard *et al.* (2005)

Phaseolus vulgaris LR in Italy

Phaseolus coccineus LR in Italy

Box 85. Genetic diversity of rice accessions from India

Genetic diversity of 35 rice accessions (19 LR, 9 cultivars and 7 wild relatives), was assessed with microsatellite (SSR) markers distributed across the rice genome. The mean number of alleles per locus and percentage of polymorphism were estimated. Cluster analysis based on allelic diversity showed that the LR, cultivars and wild relatives analysed are clearly different. Allelic richness was found to be higher among wild relatives, followed by LR (0.356), and lower for cultivars. Allelic variability among the SSR markers was thus high enough to categorize cultivars, LR and wild relatives of the rice germplasm examined. The results also suggested that genes from LR and wild relatives should be introgressed into cultivars for their improvement.

Source: Ram *et al.* (2007)

Rice LR from India

Rice LR from India

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WWW

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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^{172,173,174,175}. 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 characterization are lacking.

There is now an extensive literature associated with gap analysis which essentially identifies areas in which selected elements of biodiversity are under-represented¹⁷⁶. 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 mentioned¹⁷⁷. 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 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 strategy for the crop gene pool¹⁷⁸. More recently, a gap analysis methodology based on GIS tools has been developed specifically for crop gene pools¹⁷⁹.

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 36 summarises how these types of data feed onto a gap analysis study.

¹⁷² Noss and Cooperrider (1999)

¹⁷³ Eken *et al.* (2004)

¹⁷⁴ Rodrigues *et al.* (2004)

¹⁷⁵ Langhammer *et al.* (2007)

¹⁷⁶ 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)

¹⁷⁷ See Ingram and Williams (1993)

¹⁷⁸ See Maxted *et al.* (2008b)

¹⁷⁹ Bioversity International *et al.* (2009) and also see R-package GapAnalysis available at: http://r-forge.r-project.org/R/?group_id=645

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 17 illustrates both the *in situ* and *ex situ* gap analysis methodologies.



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").

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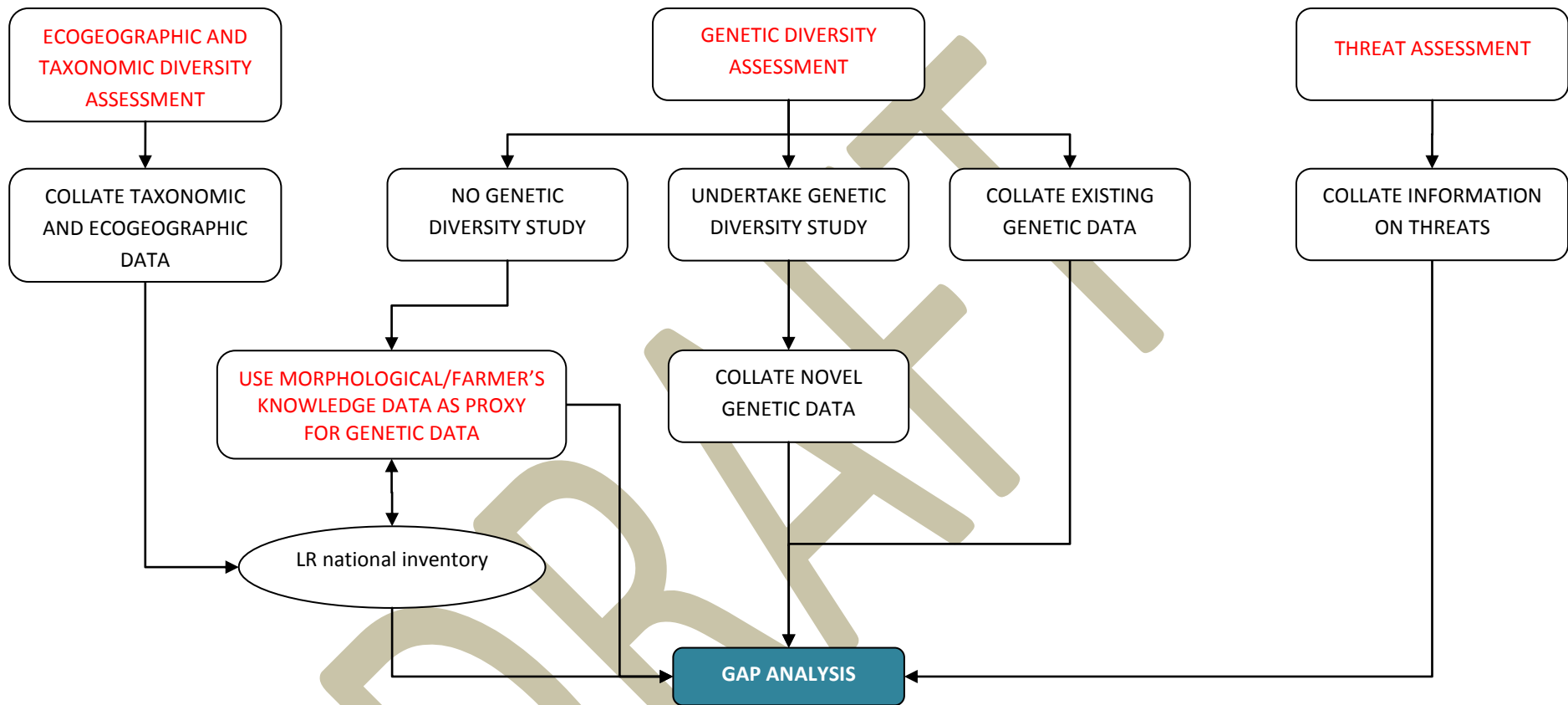


Figure 36. Data collation for LR gap analysis

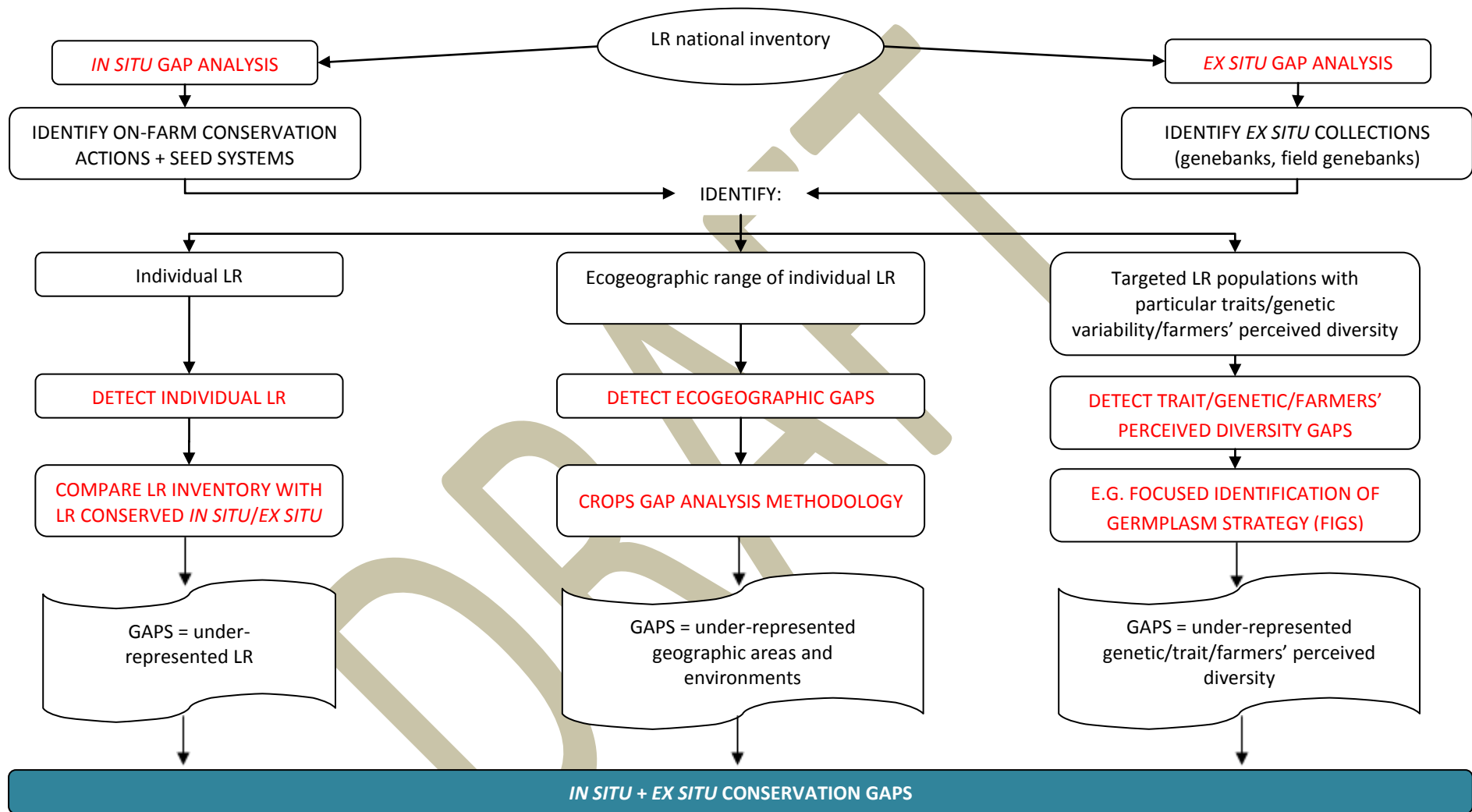


Figure 37. Landrace diversity *in situ* and *ex situ* gap analysis methodology

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 crops⁷⁰.

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) (see Box 86). Focused Identification of Germplasm Strategy (FIGS) is a predictive characterization technique and can be used in this context. The basic steps of a FIGS analysis for LR are:

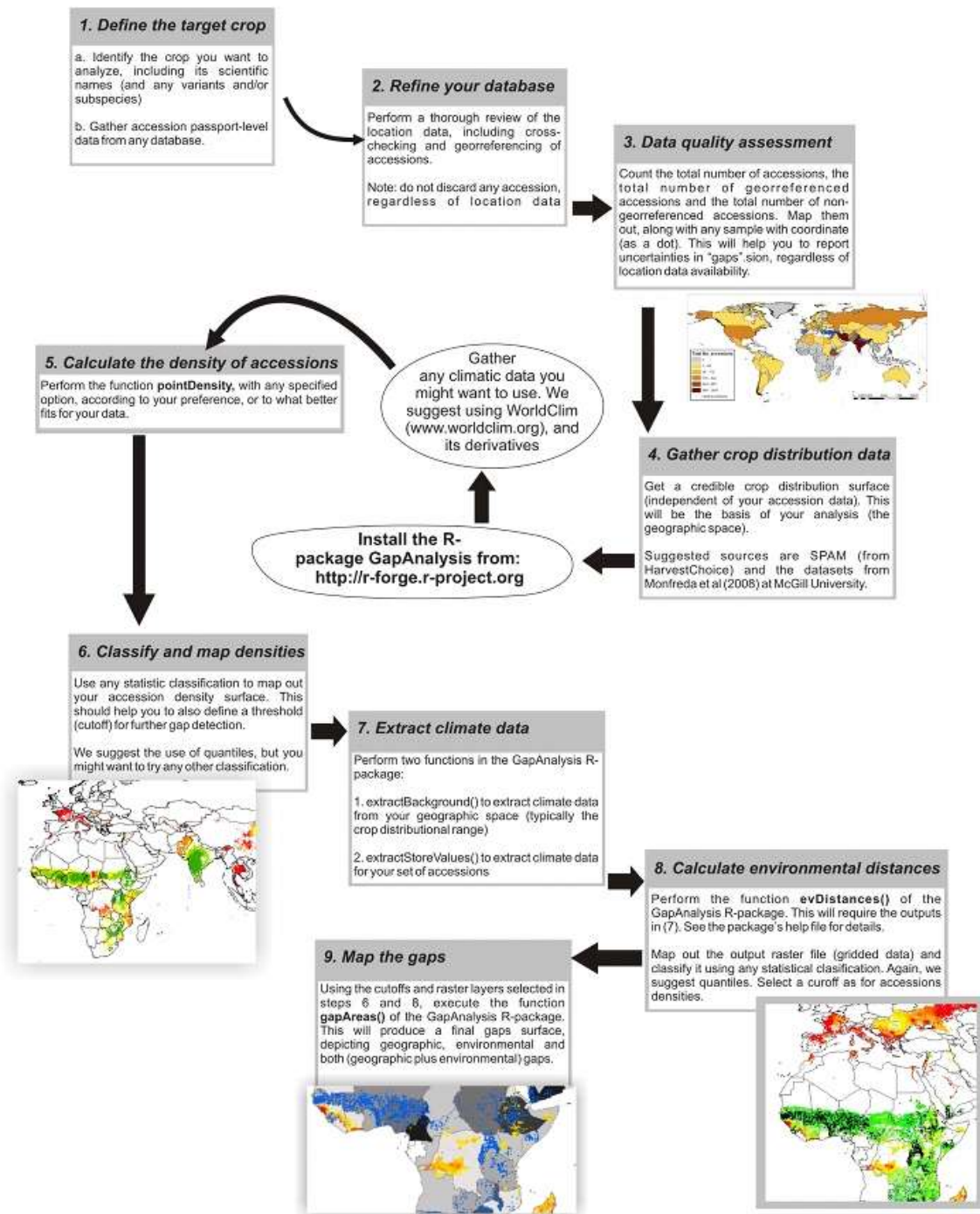


Figure 38. Crops gap analysis methodology at ecogeographic level¹⁸⁰

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

¹⁸⁰ 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 characterization

Predictive characterization 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 characterization 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.

- 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.
- 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 characterization 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: Bioersity International *et al.* (2009)

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B.8.5. Additional materials and resources

Methodological references:



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

Examples of crop gap analysis:

WWW 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):



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

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

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

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

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

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): http://www.ecpgr.cgiar.org/germplasm_databases/central_crop_databases.html.

Biodiversity occurrence data:

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

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

Crop data:

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

Environmental data:

WWW Bioclimatic variables: WorldClim – Global Climate Data: <http://www.worldclim.org/>

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

WWW Topography: The CGIAR Consortium for Spatial Information (CGIAR-SCI)
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WWW BioGeomancer: <http://www.biogeomancer.org/software.html>

WWW GeoNames: <http://www.geonames.org/>

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

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



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

B.9. Establishment of LR *in situ* conservation

B.9.1. Overview

What are the in situ conservation goals of a National LR Conservation Strategy?

A National LR Conservation Strategy aims at the development and implementation of a national network of on-farm sites where long-term active conservation (in order to safeguard their genetic diversity as well as traditional/local knowledge associated with LR maintenance and use) and sustainable use of LR is carried out to contribute to food security, especially in marginal rural communities.

In practice, there is likely to be discussion over whether on-farm sites should target single LR or multiple LR. This choice will ultimately depend on the goals of the National Strategy, the objectives of the commissioning agency, on the financial and human resources allocated to the conservation of LR and, most important of all, on the farmer's willingness to maintain and cultivate LR. The financial resources dedicated to conservation, and especially to the conservation of PGR, is a crucial limitation to the development of targeted actions and management plans that permit efficient conservation and utilization of these resources. So, generally, a multi-LR approach is more viable and realistic and often used in opposition to a single-LR approach because several LR can be conserved at the same time in a single area and unit costs will be reduced. In addition, multi-LR sites may conserve entire farming systems whereas single-LR sites are focused on the value (cultural, religious, for food security, etc.) of each individual LR and on their particular adaptive diversity. However, if a particular LR is of sufficient national, regional or global priority, even if found in isolation from other LR, the establishment of an on-farm site to conserve it may be justified. See B.9.3 Examples and applied use for examples of both multi- and single-LR on-farm sites.

The establishment of LR *in situ* conservation goals involves five main stages (Figure 39): (i) overview of *in situ* conservation gaps, (ii) preliminary selection of on-farm sites (either using a single-LR or multi-LR approach), (iii) incorporation of threat data on the selection of on-farm sites, (iv) final selection of sites, and (v) production of action/management plans (summary of the National LR Conservation Strategy developed for single or multi-LR).

Gaps in on-farm conservation of LR were identified with the gap analysis and should be taken into consideration. When there are no on-farm conservation activities at national level, a preliminary selection of on-farm sites should be carried out either focusing on single-LR or multiple-LR sites. When on-farm conservation activities do exist, *in situ* conservation gaps identified in the gap analysis can be complemented by selecting either single-LR or multiple-LR sites for efficient conservation of nationally important LR (Figure 39). A single-LR approach helps identify the sites that should be targeted for on-farm activities specifically for a particular LR throughout its distribution, whereas a multi-LR approach helps identify sites for on-farm activities of groups of LR.

In both approaches (single- and multi-LR), threats (e.g. climate change) should be taken into account. Priority should be given to those areas whose habitat suitability (for a particular LR) is predicted not to be altered significantly with changes in climate (or not affected by any other threat), or if so, it should be controlled and monitored, thus ensuring their long-term persistence and conservation. Areas that are likely to suffer greater LR erosion as a result of climate change may be more appropriately targeted for *ex situ* conservation. However, these areas may still be worth monitoring as the LR that remain in these areas have the ability to adapt to the changing environmental conditions brought about by climate change and so in themselves may have additional value to breeders.

The network of on-farm sites should be the result of a pragmatic approach in relation to the conservation goal while at the same time ensuring adequate backup *ex situ* conservation for the population(s).



Farmer choosing seeds of beans in Kamen Brjag (Bulgaria) (photo: René Hauptvogel).



The farmer Maria Ninusheva grow all these accessions from many years ago (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").

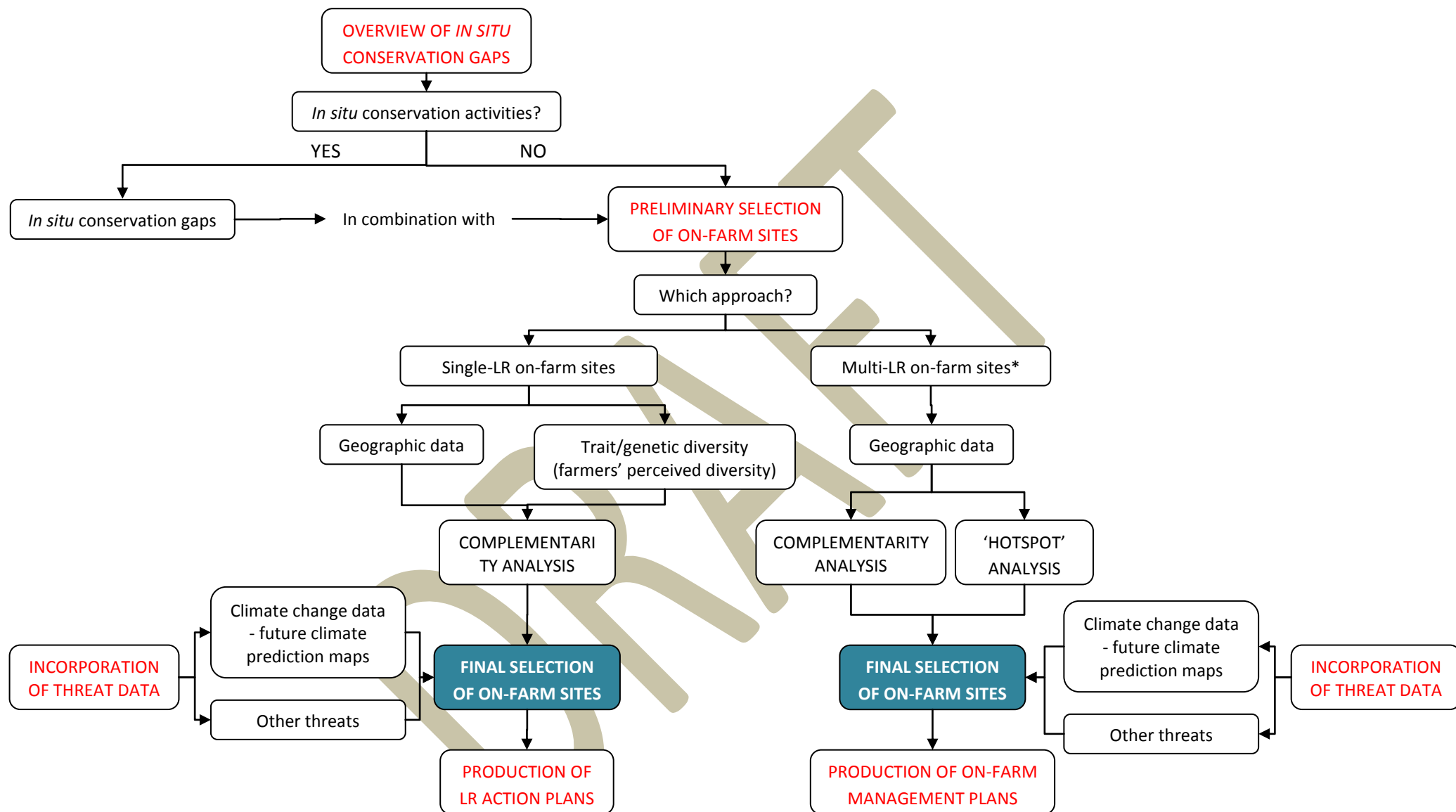


Figure 39. Establishment of LR in situ conservation goals

*The methodology suggested by Negri *et al.* (2012) (see Box 90) can also be used to select multi-LR on-farm sites.

B.9.2. Methodology for establishing LR *in situ* conservation goals

- (v) Overview of *in situ* conservation gaps. *In situ* conservation gaps that resulted from the *in situ* gap analysis should be taken into consideration.
- (vi) Preliminary selection of on-farm sites.

- Multi-LR on-farm conservation sites. A network of multi-LR on-farm conservation sites can be established based on the minimum number of farm areas that contain the optimal sample of LR, either by: (i) identifying LR ‘hotspots’ (areas with high LR richness) or (ii) by identifying the minimum number of sites needed to conserve all priority LR as given by an iterative process of complementarity analysis^{181,182}.

‘Hotspot’ analysis identifies one or more sites that have significantly higher levels of LR diversity regardless of the LR that occur within those sites (i.e. two very LR rich sites can be identified but they may contain the exact same LR, therefore it would not be efficient to actively conserve both sites). Having made this point, where genetic diversity within LR is considered, it may be worth conserving both or multiple sites with an identical array of LR if it is known or predicted by ecogeographic analysis that the samples of genetic diversity contained in each site complements rather than duplicates the diversity at other sites. ‘Hotspot’ analysis can be carried out using DIVA-GIS (<http://www.diva-gis.org/>).

Complementarity analysis identifies the minimum number of sites needed to conserve all priority LR. The first selected grid square (and the on-farm site within that) is likely to be the site that contains the highest concentrations of LR; the second site selected should be the grid square with the highest concentrations of LR not present in the first selected site, and so on^{76,77}. The common LR are likely to be duplicated in multiple on-farm sites. With a goal of maximising the genetic diversity conserved, a certain level duplication of LR will be desirable as long as the sites duplicating LR have complementary genetic diversity. This approach can be used to identify diverse and complementary areas regarding other types of data (e.g. genetic or trait diversity) or used to refine the first complementarity analysis based on geographic data. Two areas may have the same number of LR (hence both priorities for conservation), but the LR in one area may be genetically similar while in the second area they may be very different. Complementarity analysis can be carried out using DIVA-GIS (<http://www.diva-gis.org/>). It is worth noting that no examples of the use of complementarity analysis for LR have been published yet, possible due to the general lack of systematic LR distribution data at the country or regional level.

The complementarity analysis is usually recommended over the ‘hotspots’ approach because it allows the establishment of a network of on-farm sites that covers most (if not all) target LR.

- Single-LR on-farm conservation sites. If we look at particular traits/genetic variability/farmers’ perceived diversity or even ecogeographic diversity, then the multi-LR on-farm conservation sites are unlikely to broadly represent this diversity for each LR; therefore, we would have to look at the single LR level and choose the sites that are more diverse. The main objective for setting up on-farm conservation sites is to ensure that maximum genetic diversity of the target LR is captured; therefore, if financial and human resources are available, a single-LR site for exceptionally important LR can be established. Using this approach, specific LR diversity of interest is more likely to be captured by the national network of on-farm conservation sites.

¹⁸¹ Rebelo (1992a, 1992b)

¹⁸² Rebelo (1994)

Single-LR sites can be based on geographic location or other types of data (e.g. particular trait of interest, genetic variability, farmers' perceived diversity, and ecogeographic diversity data).

Complementarity analysis can be used to identify the minimum number of sites needed to conserve all diversity of interest of a particular LR within the minimum number of sites. The precise number of on-farm sites needed to ensure the conservation of maximum diversity will vary from LR to LR and is dependent on the distribution of the diversity within the LR. To establish the minimum number of sites, there is a need to review the intra-species pattern of diversity and the relative diversity found within and between LR populations. However, this does require possible extensive sampling of LR populations and more in depth studies. If such studies have not been undertaken or resources are not available to carry them out, it is recommended that five LR populations are conserved from the most ecogeographically diverse sites¹⁸³.

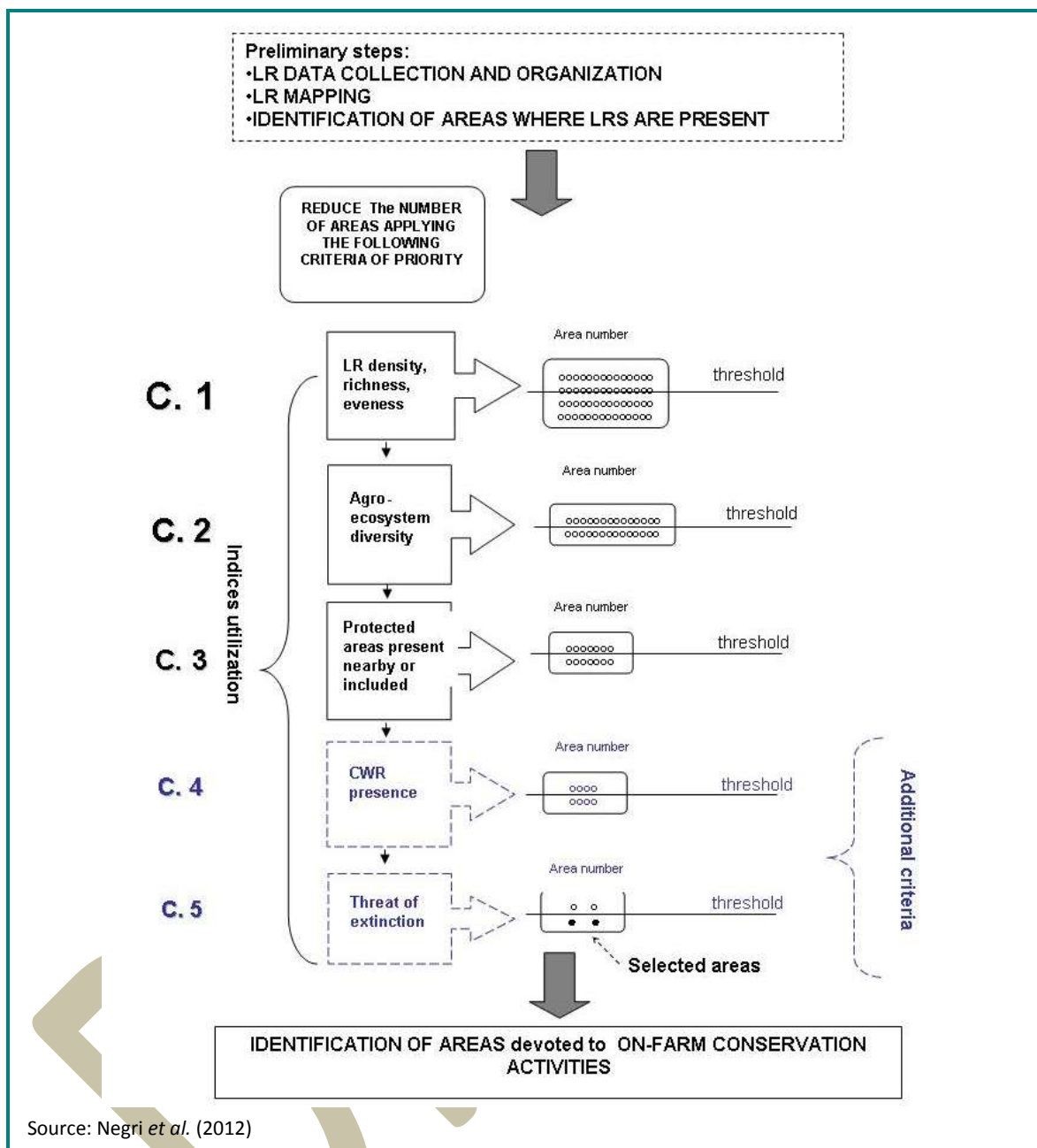
- (vii) Incorporation of threat data in the selection of on-farm conservation sites. Climate prediction maps, whenever available, can be used, as well as knowledge of other existing threats affecting sites. Those non-localised threats, which impact globally and cannot be avoided (such as climate change) should be used to select those areas less affected, hence ensuring the long-term preservation of LR.
- (viii) Final selection on on-farm conservation sites. The final selection of on-farm conservation sites is made after screening the preliminary selection of sites (together with *in situ* conservation gaps that resulted from the gap analysis) with the information on non-localised threats affecting those sites.
- (ix) Production of action plans/managements plans. These summarise the National LR Conservation Strategy developed for single or multi-LR and can be:
 - LR Action Plans: produced when a single-LR approach is carried out; it should contain information on taxonomy, description, image, distribution, ecogeography, current conservation status and action, threat assessment, uses, additional conservation action required, research and monitoring requirements, incorporation in existing national or local conservation initiatives, farmers' knowledge on the production systems, history of cultivation, traits of interest, etc.
 - On-Farm Site Management Plans: produced if a multi-LR site is set up; it should contain information on every LR within the site, including the information listed above for the LR Action Plans as well as information on the management of that specific site as a whole.

B.9.3. Examples and applied use of the establishment of LR *in situ* conservation goals

Box 90. Methodology for identifying sites for on-farm conservation activities

Recently, Negri *et al.* (2012) developed a methodology for the identification of areas devoted to on-farm conservation activities when on-farm activities are scarcely existent, which was applied to LR diversity in Central Italy. This methodology includes: LR data collection and organization, LR mapping, and identification of areas where LR are present. These potential conservation areas for on-farm activities are then prioritised according to: LR density, richness and evenness, agro-ecosystem diversity, protected areas presence, including or nearby CWR presence and threat of extinction (see Figure below). These criteria were applied in sequence and a threshold was defined for each criterion below which potential areas are not admitted to the following criterion.

¹⁸³ Following Lawrence and Marshall (1997).



Source: Negri *et al.* (2012)

Box 91. Site selection for CWR and LR conservation in Vietnam

A GEF project “*In situ* Conservation of Native Landraces and their Wild Relatives in Vietnam” ran from 2002 until 2005 and targeted the conservation of six native LR (rice, taro, tea, mung bean, *Citrus* spp., litchi and longán) and CWR in three areas (the Northern Mountains, Northern Midlands, and Northwest Mountains) in Vietnam and provided technical support to help farmers in effective conservation, development, sustainable management and use of their native LR and CWR. Sites for the conservation of LR and CWR were one of the outputs of this project. The selection of these was carried out in two steps:

1. Identification of genetically important areas based on:
 - presence and genetic diversity of target species,
 - presence of endemic species,
 - overall floristic species richness,

- presence of high numbers of other economic species,
- presence of natural and/or semi-natural ecosystems,
- presence of traditional agricultural systems,
- protection status and/or existence of conservation-oriented farmers or communities that manage a number of species and varieties.

2. Selection of specific sites and communities within larger genetic reserves where socio-economic conditions indicated good prospects for on-farm agrobiodiversity conservation activities. Workshops, stakeholder consultations, and meetings between NGOs, local institutes and farmer groups aided this process. Finally, the community receptivity to sharing traditional knowledge and practices that promote *in situ* conservation was assessed at each site.

The selected sites thus encompass a range of topographic, climatic and socio-economic conditions (e.g., proximity to markets and community-level associations), species and LR.

Eight genetic reserves were selected. Two of them include more than one conservation site (in a cultivated ecosystem and an associated site in an adjoining protected area), and the six remaining reserves consist only of cultivated ecosystems. Most of the targeted sites are both species diverse, maintain more than one crop and are LR diverse within target crops.

Source: <http://www.undp.org.vn/projects/vie01g35/index.htm>

Box 92. Single-LR on-farm example

Sainfoin (*Onobrychis vicifolia*) has been cultivated in the UK since the 18th century and is used as a source of high quality hay. Historically several sainfoin LR were cultivated but today only two LR remain, Cotswold Common and Hampshire Common. The latter is grown solely on the Cholderton Estate in Hampshire (www.cholderton-sustainable.com), where it has been cultivated and seed saved annually since 1720. Currently on the estate 440 hectares are cultivated in a legume/ grass ley – cereals rotation. Four to five tonnes of seed are produced on average per year, the seed being harvested with combine and cleaned off-farm then planted in the following year. The seed was sold off-farm until the 1980's when it became uneconomic due to the costs of certification and maintenance on the National List, leaving the Cholderton Estate as the sole maintainer and grower of Hampshire common sainfoin. In this case although the LR is productive, producing comparable yield to lucerne, it is maintained because of a single grower's enthusiasm for the landrace and the wish not to break the family tradition of growing 'their' LR.

Source: Scholten et al. (2009)

Box 93. Maize landraces in Portugal – multi-LR on-farm example

A total of 51 maize LR and 175 other varieties of associated crops were identified and collected in a collecting mission to several rural communities of central Portugal. The main purpose of this mission was to collect maize LR with technological ability for bread production and to evaluate whether a participatory plant breeding and conservation programme could be established. The production of LR was carried out in small farms with multi-crop, quality oriented, and sustainable systems. The authors showed that farmers maintained between one and three maize LR and that a participatory plant breeding and conservation programme could be possible if local authorities were involved.

Source: Vaz Patto *et al.* (2007)

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B.9.5. Additional materials and resources



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DRAFT

B.10. Implementation of on-farm conservation

B.10.1. Overview

What is the aim of implementing on-farm conservation priorities?

The establishment of the national LR *in situ* conservation goals results in the identification of a national network of LR on-farm conservation sites. These will then need to be implemented at local level and specific decisions will have to be made in order to effectively conserve the LR *in situ* the landraces.

The establishment of the national LR *in situ* conservation goals results in the identification of a network of LR on-farm conservation sites. Thus far, the process has been focused at the national level (and global priorities, if they have been integrated in the National Strategy) and specific decisions will require implementation at the local level. However, the implementation of LR on-farm conservation priorities can be complicated in most countries because a national network of agro-biodiversity conservation areas does not already exist (like protected areas do for wild species).

The most important element in the implementation of a national network of on-farm conservation sites is the farmer who decides whether to keep maintaining the LR and has the knowledge about its/their management and uses. The acknowledgement of local people/farmers/maintainers by the conservation and policy communities as well as the building of inter-community relationships is thus fundamental to conserve LR diversity. However, it is important to highlight that farmers face a number of constraints in the conservation and use of LR. These are mainly related to the availability of crop diversity within the production systems and its accessibility to farmers, the valuation of crop genetic resources among them, as well as the actual recognition of the benefits to them by using these resources (see Figure 40). Also in many developed countries legislative issues around seed certification and the registration of varieties on the national list may also cause serious constraints. These constraints are thus major impediments in the implementation of national on-farm conservation priorities.



Storage of rice LR (Os province, Kyrgyzstan) (photo: Pavol Hauptvogel).



Air seed cleaning of “Uzgen” LR in Sorobasat (Os province Kyrgyzstan) (photo: Pavol Hauptvogel).

The implementation of on-farm conservation priorities broadly may be separated into nine stages (Figure 41): (i) Find out whether the target farmers have socio-economic conditions to maintain LR, (ii) Reformulate the *in situ* conservation goals (if needed), (iii) Integrate on-farm conservation priorities with national/international agri-environmental schemes, (iv) Convince farmers to use and maintain LR, (v) Find out whether the priority target on-farm sites occur within formal protected areas (as these areas already have a conservation ethos), (vi) Ensure LR diversity exists in sufficient quantities within the production systems, (vii) Ensure LR diversity is accessible to farmers, (viii) Ensure LR diversity is valued by farmers, and (ix) Ensure farmers benefit from the use of LR diversity.

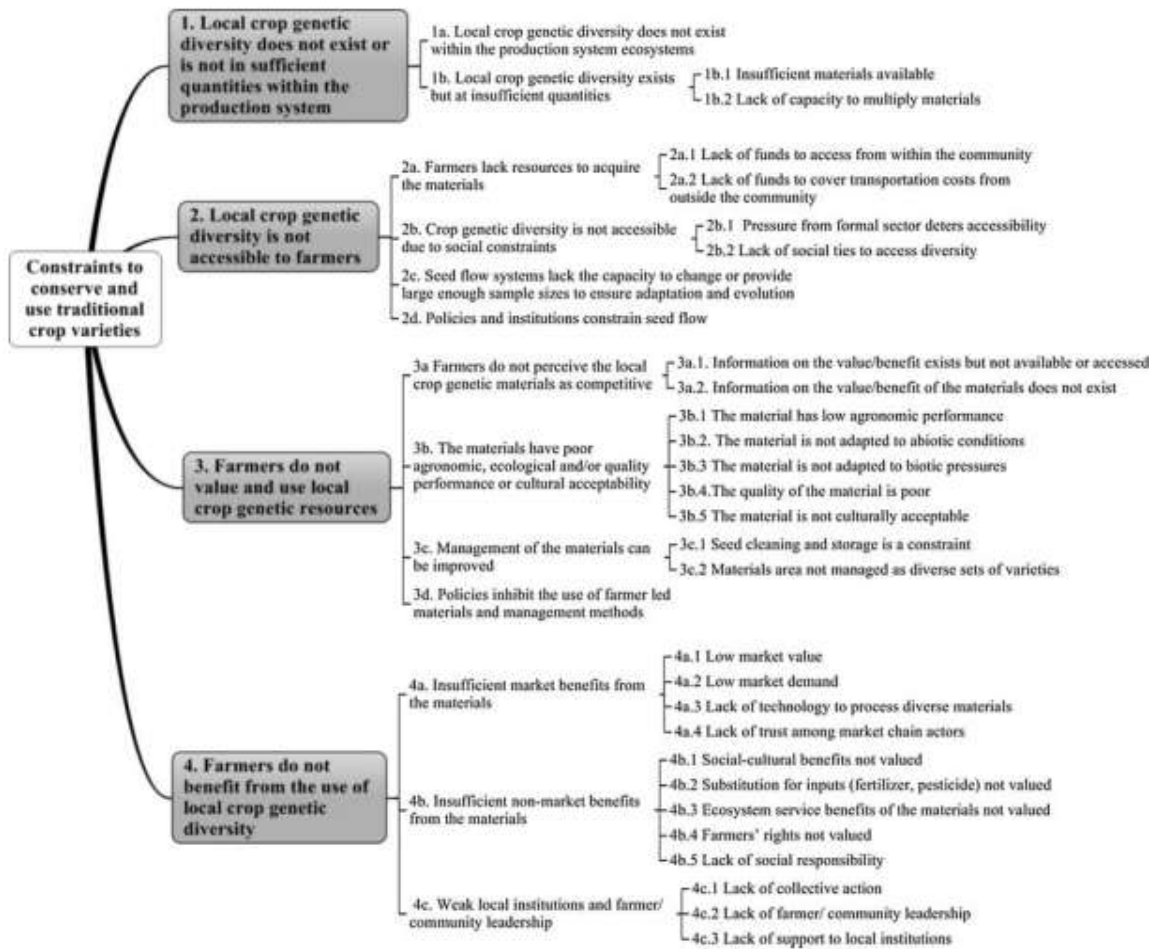


Figure 40. Heuristic framework for identifying LR constraints¹⁸⁴

B.10.2. Methodology for the implementation of on-farm conservation priorities

- (vii) Find out whether the target farmers have socio-economic conditions to maintain LR. Those farmers that grow LR and are willing to be involved in their long-term maintenance as well as those that have socio-economic conditions favourable to maintain LR should be targeted.
- (viii) Reformulate the *in situ* conservation goals (if needed).

¹⁸⁴ From Jarvis *et al.* (2011)

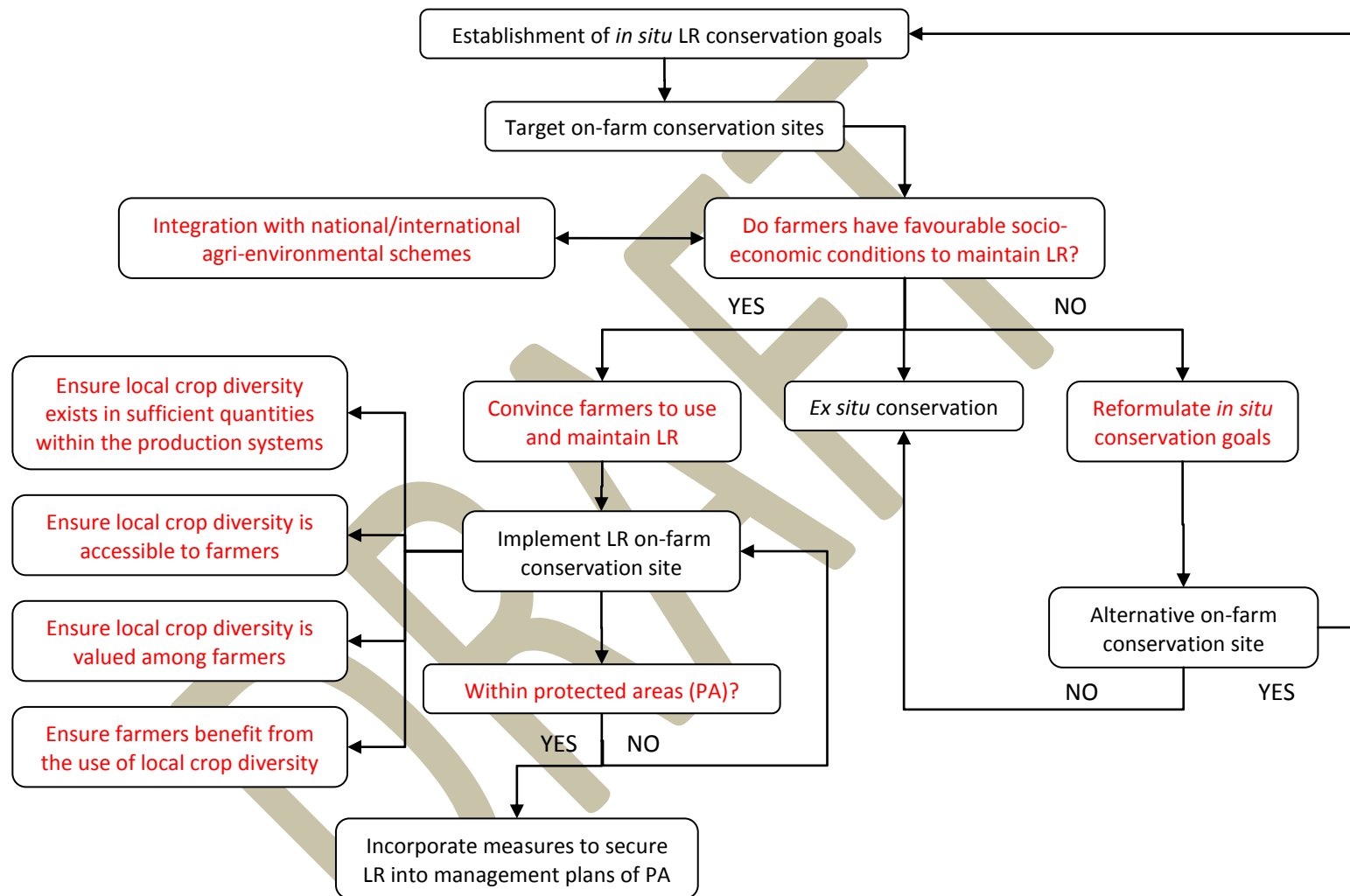


Figure 41. Implementation of on-farm conservation priorities

- (ix) Integrate on-farm priorities with national/international agri-environmental schemes. Ideally, a national network of on-farm conservation sites should be incorporated within agri-environmental schemes such as those funded by the European Commission or other regional agencies, to ensure that their management is properly coordinated and the conservation of the target LR is effective. A growing effort to strengthen the relationship between agriculture and the provision of ecosystem services has been registered¹⁸⁵. *In situ* and on-farm PGRFA conservation activities are now being set up as a result of Payment for Environmental Services (PES) schemes in an attempt to encourage and reward farmers and rural communities for their role in conserving and managing PGRFA for the future. However, the actual implementation of these schemes remains a significant challenge.
- (x) Convince farmers to use and maintain LR. Promoting the involvement of local communities in on-farm management and conservation is crucial for it to be effective, perhaps more so than any other form of conservation as here the farmers are the actually implementers of the conservation actions. Therefore, traditional knowledge and traditional cultivation practices that have been used to maintain LR for millennia will be critical to their preservation. Although it is recognised increasingly that LR are also maintained in non-traditional cultivation systems such as organic production systems, museum demonstration plots or those used for niche markets where the link to traditional cultivation practices is not critical. Raising the profile of LR amongst the agricultural community is needed and this will only be sustainable in the long-term if the farmer benefits. Thus, the following points of this methodology (vi, vii, viii, ix) should be used as arguments in order to convince them that the sustainable use and conservation of LR is the best option to tackle food security problems. For instance, the promotion of the search for innovative market niches and new commercial opportunities is vital. Development centres (e.g. the International Development Research Centre – IDRC and the Development Evaluation Research Centre – DEVRA) have been working on supporting NGOs and other organizations in the developing world in promoting self-sufficiency, so they could help to promote the maintenance of LR among farmers and other LR maintainers.

¹⁸⁵ FAO (2009)



Traditional farmer holding a panicle of “Zomba” sorghum LR in Manjalende Village (Phalombe District, Malawi) (photo: Edwin A Chiwona).



Farmer shelling bean legumes (photo: Vojtec Holubec).



Farmers in West Tatry (Zuberec, Slovakia) (photo: Pavol Hauptvogel).



Farmer Haci Salman (Quba district, Azerbaijan) (photo: Mirza Musayev).

- (xi) Find out whether the priority target on-farm conservation sites occur within formal protected areas. Many protected areas (PAs) contain considerable areas of agricultural

land where numerous LR have been maintained by farmers. However, it is highly unlikely that management plans of those areas incorporate measures to secure LR diversity. By conserving locally important LR, PAs can add another dimension to their conservation commitment by also contributing to food security. Either within PAs or outside them, a national network of on-farm sites to conserve national LR diversity is desirable. Conservation agencies and NGOs, namely those in charge of managing land for conservation, should include conservation and management plans for LR in the management plans of those areas, and also establish community seed banks for local LR to help ensure their continued availability and use.

- (xii) Ensure local crop diversity exist in sufficient quantities within the production systems. Lack of sufficient diversity within production systems can be due to several reasons (Figure 40). See Table 8 for actions that can be performed to overcome such constraints.
- (xiii) Ensure local crop diversity is accessible to farmers. Access to diversity may be constrained by several factors (Figure 40). See Table 8 for actions that can be performed to overcome such constraints.
- (xiv) Ensure local crop diversity is valued among farmers. Farmers may not value local crop diversity for several reasons (Figure 40). See Table 8 for actions that can be performed to overcome such constraints.

Community seed banks	Community managed nurseries
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- (xv) Ensure farmers benefit from the use of local crop diversity. Farmers may not benefit from the use of local crop diversity for several reasons (Figure 40). The provision of government incentives is a possibility and if they are to be used, they must be linked to some form of guarantee from the landowner to ensure the LR thrives; therefore, a management agreement including a conservation prescription is required. See Table 8 for actions that can be performed to overcome such constraints.

Finally, the location and establishment of specific LR on-farm conservation sites will ultimately be pragmatic—it will be dictated by the financial resources available for *in situ* conservation and governmental will.



Portuguese LR and American yellow dent varieties in a farmers meeting regarding the perception of farmers for maize kernel, related with maize bread quality (participatory plant breeding) (Coimbra, Portugal) (photo: Manuel Paulo).



Woman selling mixed cowpea LR at Zomba Market (Zomba District, Malawi) (photo: Edwin A Chiwona).



Market of LR in Svetlen (Bulgaria) (photo: René Hauptvogel).



Market with home products in Funchal (Madeira, Portugal) (photo: Pavol Hauptvogel).



Eco-farmer with flax (*Linum usitatissimum*) in Rim (Bela Krajina, Slovenia) (photo: Pavol Hauptvogel).



Prizes won by Mr Meireles for his “Pigarro” and “Fandango” maize LR until 2005 in the regional contest “Sousa Valley Best Ear” initiated in 1992 in Paredes (North of Portugal) with the objective of electing the best maize ears within the Sousa Valley Region (photo: Pedro Mendes-Moreira).



Creation of home products using traditional varieties in Nitra (Slovakia) (photo: Pavol Hauptvogel).



Maize bread "Broa" made with Portuguese maize LR (photo: Pedro Mendes-Moreira).

Table 8. Actions that promote on-farm conservation ¹⁸⁶

GENERAL CATEGORY	ACTIONS	STEPS			
		(vi) Ensure local crop diversity exists in sufficient quantities within the production systems	(vii) Ensure local crop diversity is accessible to farmers	(viii) Ensure local crop diversity is valued among farmers	(ix) Ensure farmers benefit from the use of local crop diversity
Improving availability of material	Reintroduction of materials from <i>ex situ</i> collections (national or community gene banks)	X	X		
	Reintroduction of materials collected from farmers from similar environments into local informal seed systems	X	X		
	Seed cooperatives for collection, distribution and multiplication of seeds	X	X		X
	Community seed / gene banks	X	X	X	X
	Community managed nurseries	X	X	X	X
	Diversity field fora (where farmers discuss and experiment in crop analysis, management and improvement)	X	X	X	X
	Diversity kit (diverse LR made available to farmers to allow them to select those that suit their conditions and need)	X	X	X	X
	Diversity fairs	X	X	X	X
	Seed vouchers	X	X	X	
	Reduction of transportation costs of traditional variety as material is already closer to farmer communities		X		
	Cross site visits for farmers and local extension workers	X	X	X	
	Microfinance or credit schemes to enable purchase of local materials		X		
Improving information and	On-farm experimental diversity blocks	X	X	X	X
	Field or lab trials comparing traditional and modern varieties	X	X	X	

¹⁸⁶ Adapted from Jarvis *et al.* (2011).

GENERAL CATEGORY	ACTIONS	STEPS			
		(vi) Ensure local crop diversity exists in sufficient quantities within the production systems	(vii) Ensure local crop diversity is accessible to farmers	(viii) Ensure local crop diversity is valued among farmers	(ix) Ensure farmers benefit from the use of local crop diversity
availability of information	Community Biodiversity Register			X	X
	Literacy training, particularly for poor and vulnerable groups			X	X
	Variety information databases made in farmer friendly formats			X	X
	Setting up information systems and internet connections for farmer access to information		X	X	X
	Small weather stations that can be linked to internet sites			X	X
	Rural radio programmes that includes talks on the importance of crop diversity			X	X
	Drama, music and poetry travelling shows that have crop diversity as a theme			X	X
	Painting and art competitions that reward farmer groups for knowledge and descriptions of agricultural diversity			X	X
Improving and management of traditional varieties materials	Participatory crop improvement (Participatory Plant Breeding, Participatory Varietal Selection)		X	X	X
	Using genomics to improve <i>in situ</i> crop populations		X	X	X
	Changing the formal breeding institutions to increase the use of farmer selected materials and traditional varieties in their programmes		X	X	X
	Planting of intra-specific mixtures to reduce pests and diseases		X	X	X
	Improve seed storage facilities and methods			X	X
	Seed cleaning/treatment			X	X

GENERAL CATEGORY	ACTIONS	STEPS			
		(vi) Ensure local crop diversity exists in sufficient quantities within the production systems	(vii) Ensure local crop diversity is accessible to farmers	(viii) Ensure local crop diversity is valued among farmers	(ix) Ensure farmers benefit from the use of local crop diversity
Improved processing	Shift retailers to use different processing equipment that can use diversified materials			X	X
	Training of producers in improved processing techniques and providing credit to acquire processing equipment			X	X
Alternatives and modifications to seed certification systems	Plant varieties common knowledge (VCK)		X	X	X
	Registration and release of farmers' varieties with acceptance of enhanced bulk varieties		X	X	X
	Geographic indications		X	X	X
	Quality declared seed (QDS) (that certify the vendor rather than the seed)		X	X	X
	Truthfully labelled seed laws that focus on seed quality rather than seed purity		X	X	X
	Registries of native crops		X	X	X
	Links between intellectual property rights protection and benefit-sharing				X
	Plant variety protection systems adapted to farmers varieties			X	
Market creation and promotion	Market promotion through taxes and subsidies				X
	Market creation for traditional varieties or products from traditional varieties including niche markets		X	X	X
	Education and financial support to farmer's groups to develop a marketing strategy			X	X
	Micro-credit facilities to set up small businesses, particularly for rural men and women				X

GENERAL CATEGORY	ACTIONS	STEPS			
		(vi) Ensure local crop diversity exists in sufficient quantities within the production systems	(vii) Ensure local crop diversity is accessible to farmers	(viii) Ensure local crop diversity is valued among farmers	(ix) Ensure farmers benefit from the use of local crop diversity
	Advertisement campaigns to improve consumer and retailer awareness of important traits (nutritional, adaptive, etc.)			X	X
	Cook books with traditional recipes; gardening books that promote traditional varieties for particular management practices			X	X
	Fair trade price premiums – Eco-labelling (paying the full production value through price premiums)		X	X	X
Building partnerships and trusts	Organization of meetings involving market-chain actors to discuss how to enhance market potential			X	X
	Private and public partnership for the construction of small infrastructure for the production of a better quality product			X	X
	Strengthened and cooperative extension services that include farmers are more demand driven or establishment of new farmers'-governed local institutions	X	X	X	X
Changing norms	Advertising and social campaigns that promote better adapted varieties that reduce the need for chemical inputs to change social norms such as nutritional cultural values of food			X	X
	School biology <i>curriculum</i> include traditional crop varieties as agricultural resource and ecosystem service	X		X	X
	Gender sensitive response policy	X	X	X	X
Promoting ecological land	Environmentally sensitive areas (ESA) include high agro-biodiversity areas			X	X
	Agro-biodiversity Zones			X	X

GENERAL CATEGORY	ACTIONS	STEPS			
		(vi) Ensure local crop diversity exists in sufficient quantities within the production systems	(vii) Ensure local crop diversity is accessible to farmers	(viii) Ensure local crop diversity is valued among farmers	(ix) Ensure farmers benefit from the use of local crop diversity
management practices	Agro-biodiversity Ecotourism			X	X
	Organic farming and organic seed breeding with traditional variety used as planting materials		X	X	X
	Investment in agricultural research that includes the use of agricultural biodiversity within the production system	X	X	X	X
	Biodiversity included in Environmental Impact Assessment of individual projects, policies and programmes	X	X	X	X
Payment schemes for ecosystem services	Payment for Environmental Services (PES)		X	X	X
	Linking upstream and downstream communities		X	X	X
	Sharing of monetary benefits				X

DRAFT

B.10.3. Examples and applied use of the implementation of on-farm conservation priorities

Box 94. Methods of supporting conservation and use of traditional crop varieties

Farmers appear to find that LR diversity of both major staples and minor crops remain important to their livelihoods, despite earlier expectations that these varieties would rapidly disappear from production systems when outcompeted by modern high-yielding cultivars. The reasons for maintenance are complex and likely to be associated with adaptation to marginal and low input agriculture, stable performance, the socio-economic conditions of many small-scale farmers, or existence of niche markets whose requirements cannot be met by modern cultivars. However, to understand and underpin LR maintenance it seems important not only to understand better the nature and contribution of LR to the production strategies of rural communities around the world, but also ways in which they are maintained and managed. This can then help in the development of ways of improving the use of these varieties and their contribution to rural livelihoods. It is likely that studies of (i) on-farm diversity, (ii) access to diversity and information, (iii) the extent of use of available materials and information, and (iv) benefits obtained by the farmer or farming community from their use of local crop diversity, will be at the core of the maintenance of traditional varieties and crop genetic diversity within their production systems. Jarvis *et al.* (2011) concluded that: firstly, it is essential to develop an appropriate understanding of the extent and distribution of diversity in a system and how it is maintained through local institutions and practices; secondly, the analysis of the interaction between LR diversity and farming practice is likely to lead to the identification of a number of complementary supporting actions; and thirdly, the success of any actions will depend centrally on local knowledge, the strength of local institutions and the leadership of farmers and communities. So that farmers and their maintenance practices are as much the focus of on-farm conservation as the LR diversity the conservationist wishes to conserve; the importance of on-farm policies (whether implemented by local, national and international organizations and agencies) and the support for local institutions should enable farmers to take a greater role in the management of their resources and if the farmers are successful, then LR diversity should be maintained.

Source: Jarvis *et al.* (2011)

CBR in Nepal	CBR in Nepal
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Box 95. Community biodiversity register in Nepal

A project that aimed at developing methods and models for on-farm agrobiodiversity management was carried out in Nepal and implemented jointly by the Nepal Agricultural Research Council (NARC) and Local Initiatives for Biodiversity, Research and Development (LI-BIRD) in Nepal and coordinated globally by the International Plant Genetic Resources Institute (IPGRI).

The main objective was to implement a Community Biodiversity Register (CBR) in 40 farmers' groups of Kaski and Bara districts of Nepal, whose farms represented mid-hills and Terai agro-ecosystems, respectively. A total of 1325 households were directly involved in data recording of six crops: rice, finger millet, taro, cucumber, sponge gourd and pigeon pea.

The implementation of the CBR included the following steps:

1. Preparation of the CBR protocol: the below issues were discussed with the farmers and community based organizations (CBO).

- Objectives of the project clearly stated: “documenting farmer’s knowledge on crop genetic resources and monitoring the status of crop diversity that could possibly increase community awareness on the values and benefits associated with them”;
 - Outline of the format documentation;
 - List of the crops and their selection criteria;
 - Implementation modality for documentation, analysis and information sharing;
 - Sustainability and ownership issues over CBR data.
2. Getting prior informed consent of communities: via village level workshops, the CBR protocol was shared to know their interest in participating, to get their consent and to obtain feedback.
 3. Setting CBR objectives at the community: the communities endorsed the CBR by a local project management team (LPMT) and community level meetings took place in order to discuss several issues:
 - Objectives of the CBR;
 - Benefits of the CBR to the communities;
 - The basic unit for CBR documentation;
 - Information to be recorded;
 - Who should record the CBR;
 - Target crops;
 - Where CBR should be maintained and registered.
 4. Formulating local institutions for CBR: at each project site, a committee for CBR was formed (with representative farmers of the CBOs); its role was to monitor, coordinate and supervise the CBR implementation.
 5. Capacity development of communities: the LPMT provided training on CBR documentation to CBOs and CBR guidelines were developed in local languages.
 6. Data recording: a register for each CBO was provided together with a CBR kit (bag, pen, note book) to handle the CBR register.
 7. Collation and validation: after completing the information in the registers, the CBR committee members collected the registers from the CBOs and deposited in the CBO office.
 8. Data entry and analysis: the data were entered into a computer program and several types of analysis were carried out (e.g. farmer maintaining highest diversity, total number of cultivars grown by each farmer).
 9. Results sharing: meetings with the CBR committee were organized to identify ways of presenting farmers the results (e.g. tables and pie-charts)
 10. Facilitating community decisions and piloting conservation actions: a village level workshop was organized so the community would endorse the priority community action plans into their annual plans.
- Local crop diversity was thus documented by the CBR methodology in order to avoid knowledge erosion. It also improved awareness and the empowerment of farmers’ decision-making, facilitating access to traditional knowledge and materials, as well as monitoring local crop diversity to strengthen on-farm agrobiodiversity management.
- Source: Subedi *et al.* (2005)

Box 96. Strategies for sustainable conservation and use of legumes in Ghana

In this study, strategies aiming at the conservation of legumes, including their collection, characterization and evaluation, are presented. Among specific issues regarding *ex situ* conservation (e.g. collection of germplasm, characterization, preliminary and further evaluation, improving longevity of seeds, development of core collections, molecular characterization), the authors also explored strategies that improve seed flow within and between communities and the *in situ* characterization of

LR for the genetic improvement of legumes. These include: diversity fairs, diversity theatres, participatory breeding, diversity blocks, community biodiversity register and biodiversity fairs.

Diversity fairs: local seed markets and fairs that constitute an important seed and local knowledge exchange system. These fairs are threatened by the formal sector of seed production and distribution. In Ghana, national farmers' days are usually held to honour selected farmers who display their produce. However, the selected farmers usually produce high yielding varieties, but some of them may still cultivate LR. Diversity fairs are thus organized to: (i) recognize knowledgeable farmers, (ii) locate areas of high diversity, (iii) identify and locate endangered LR, (iv) identify key farmers who maintain high diversity of cultivars, (v) prepare an inventory of crop genetic resources, and (vi) empower local communities in controlling their genetic resources and develop the concept of community gene banks that link formal and informal seed supply system.

Diversity theatres: help raise awareness about the importance of local crop resources while celebrating local culture. They may be based on traditional stories and myths that involve local crops, and are usually organised by local actors and community groups. Workshops, rural poetry, folk song competition and local food fairs can also be included.

Participatory breeding: involves both farmers and researchers in the conservation and improvement of crop resources (Amanda 2000). Participatory plant breeding and participatory varietal selection are used to develop varieties based on farmers' preferences with access to germplasm and technologies from the gene bank. The role of the farmer in plant breeding is therefore acknowledged by the formal plant breeding sector (Sthapit 2001). Through this activity, researchers locate diversity, identify uses for different crops, and characterise the traits that farmers perceive as valuable (Sperling and Berkowitz 1994).

Diversity blocks: through the involvement of local communities, this allows the characterization of LR under farmer management conditions. While farmers use traditional management practices, researchers observe and record agromorphological characteristics. The characterised diversity may then be selected for diversity fairs.

Community biodiversity register (CBR): this is a mechanism that allows local communities to keep records about local crop diversity and associated knowledge. The register is maintained and can be accessed by farmers or local institutions acting as a tool for biodiversity conservation (Sthapit 2001). Information in the register may include: LR names, name of donors, associated local knowledge and uses, the traditional and non-traditional passport data (e.g. agro-morphological characteristics, agro-ecological characteristics, and cultural importance). The information is provided by farmers and maintained centrally, whereas the seeds are stored by individual farmers that allow access to all community members.

Source: Aboagye (2007)

Diversity fairs in Ghana

Participatory breeding in Ghana

Box 97. Gender: increasing access, participation and decision-making in Vietnam

In Vietnam, women represent 65% of the labour force in the total population and provide 54% of the total agricultural labour. With an increased rate of migration of men to the cities, women's responsibility

in improving agricultural yields is growing. Studies show that although much of the work in agriculture is done by women (up to 70%), they are not the recipients of agricultural extension support services nor have they been given training in new technologies and new knowledge.

This study aimed at examining gender role differentiation in making decisions on maintaining genetic diversity on-farm in six villages. The specific objectives were to:

- Determine the time allocation and division of labour of men and women in major farming households at each site;
- Identify what resources men and women in plant genetic diversity conservation can command to carry out their activities, and the benefits they derive from such activities;
- Ascertain factors affecting gender division:
- Assess the possible effects of such gender role differences on opportunities or constraints for men's and women's participation in the project;
- Create training opportunities for women's participation in the project.

Data were collected by direct observation and interviews. All activities relate to rice farming and growing other crops—home gardens were included. Different group discussions (men, women, age groups) were conducted for collecting and analysing data. The data collected from men and women were finally compared.

As farmers, the women are responsible for growing, collecting, processing and storage of food crops. As mothers, they are also responsible for domestic affairs and for gathering and utilizing food, fodder, fuel, medicinal plants, fibre for textile and housing materials. They usually do more housework than men and receive no salary. Women often select which varieties to keep for home consumption and which to sell at the local market. However, determining what crop varieties will be grown next season is done by men.

Both men and women often select different morphological traits in varieties: while women are particularly interested in seed size, aroma and good cooking quality and tolerance to disease, men are usually concerned with market traits such as high yield and good processing.

Women possess important knowledge of the value and uses of the plants they grow and collect so their perception has important implications for on-farm conservation of agrobiodiversity. They are important decision-makers and key sources of expertise in managing crop resources, while men have only showed a small part of the farmers' perception data on crop genetic diversity. For these reasons, group interviews should be segregated by gender.

In order to enhance women's role in participatory *in situ* conservation, women's perceptions should be raised through short training courses and farmers' fairs, and they should be key actors in Participatory Plant Breeding (PPB). This study has indirectly recommended that the government should be aware about the crucial role that women play in sustainable agricultural development and in *in situ* conservation to alleviate poverty in study sites.

Source: Cuong and Hue (2011)

Farmer (women)/participatory plant breeding/training courses in Vietnam	Farmer (women)/participatory plant breeding/training courses in Vietnam
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DRAFT

B.11. Establishment and implementation of *ex situ* LR conservation

B.11.1. Overview

What are the ex situ conservation goals of a National LR Conservation Strategy?

A National LR Conservation Strategy aims at the development and implementation of a national network of on-farm sites where long-term active conservation of LR is carried out. In parallel, *ex situ* conservation should be undertaken as a conservation backup (for reintroduction in case of crop loss) but also to permit easy access to these materials for crop improvement and research. *Ex situ* and *in situ* conservation should, therefore, be seen as complementary strategies that contribute to food security and poverty alleviation.

The Convention on Biological Diversity¹⁸⁷ changed the relative focus of conservation efforts so that subsequently *ex situ* conservation was seen primarily as a safety backup strategy to provide security for the favoured *in situ* conservation. However, it should be stressed that both *ex situ* and *in situ* techniques have their advantages and disadvantages, and they should not be seen alternatives but as complementary strategies. While recognising that it would be remiss to implement a National LR Conservation Strategy and establish key national *in situ* on-farm conservation areas without a safety backup to help guarantee long-term conservation of the populations, this proposition fails to recognise the unique situation of PGRFA conservation. In all PGRFA conservation the end goal is not only the maximum diversity conserved but also the sustainable use of that diversity. Unlike broader biodiversity conservation, there is a use imperative, PGRFA is conserved because it has direct use value and the dual goal of conservation and use should be intimately linked. The justification of conservation *ex situ* as an *in situ* backup also fails to recognise the fact that crop diversity has historically almost exclusively been conserved *ex situ*, perhaps not even for its conservation value *per se* but because it provides the most practical means of access for the germplasm user community. At present few plant breeders approach on-farm maintainers for germplasm to use in their breeding programmes, why would then if the diversity is available from easily accessible gene banks?

There are a range of *ex situ* conservation techniques available (Box 52), but because the vast majority of LR have orthodox seeds (i.e. seeds that can be dried and stored at -18°C without loss of viability) and seed storage is a relatively cheap conservation option, *ex situ* seed conservation in gene (= seed) banks predominates. Therefore, in parallel to the establishment and implementation of the *in situ* component of the National LR Conservation Strategy that identifies and establishes national LR on-farm conservation sites, there is also a need to locate, sample, transfer and store samples of priority LR diversity for *ex situ* conservation.

The *ex situ* seed conservation of LR may be split between: formal gene (seed) banking and community seed banks (Figure 42). The establishment and implementation of formal *ex situ* LR seed conservation in gene banks includes three steps: (i) Overview of *ex situ* conservation gaps, (ii) Selection of LR and farms for targeted collecting, and (iii) Collecting and curation standard procedures of a gene bank. Similarly the implementation of community seed banks must address similar issues but here the goal is more to provide a buffer against individual seasonal crop failure and loss of seed for subsequent sowing; the community seed bank offers a buffer against the bad years, as well extending LR access to the broader community. As such

¹⁸⁷ CBD (1992)

community seed banks have an important role in ensuring food security, especially in arid or semi-arid lands where food is in short supply after extended periods of drought. Therefore, in a global change scenario where climatic changes are already happening, community seed banks are of the utmost importance. Also community seed banks provide an important means of raising awareness of the National LR Conservation Strategy and the promotion of local LR diversity conservation and use.

Box 98. *Ex situ* conservation of LR

Ex situ conservation is the conservation of components of biological diversity outside their natural habitats (CBD 1992). The application of this strategy involves the location, sampling, transfer and storage of samples of the target taxa away from its native habitat (Maxted *et al.* 1997b). LR seeds can be stored in gene banks, *in vitro* or in field gene banks as living collections.

Examples of major *ex situ* collections include the International Maize and Wheat Improvement Centre (CIMMYT) gene bank with more than 160,000 accessions (i.e., samples collected at a specific location and time), the International Rice Research Institute (IRRI), which holds the world's largest collection of rice genetic resources, and the Millennium Seed Bank at the Royal Botanic Gardens, Kew, which holds the largest collection of seed of 24,000 species, primarily from global drylands. Important national/regional collections include: coffee in Côte d'Ivoire, Ethiopia, Cameroon, Kenya, Madagascar and Tanzania; sesame in Kenya; cassava in Malawi, Zambia and Tanzania, and sweet potato in Mauritius, Zambia, Swaziland and Tanzania (Global Crop Diversity Trust 2007), as well as China's largest seed bank, the Germplasm Bank of Wild Species (GBWS).



Ex situ field gene bank of “Pigarro” LR of maize (*Zea mays*) at ESAC (Coimbra, Portugal) (photo: Pedro Mendes-Moreira).

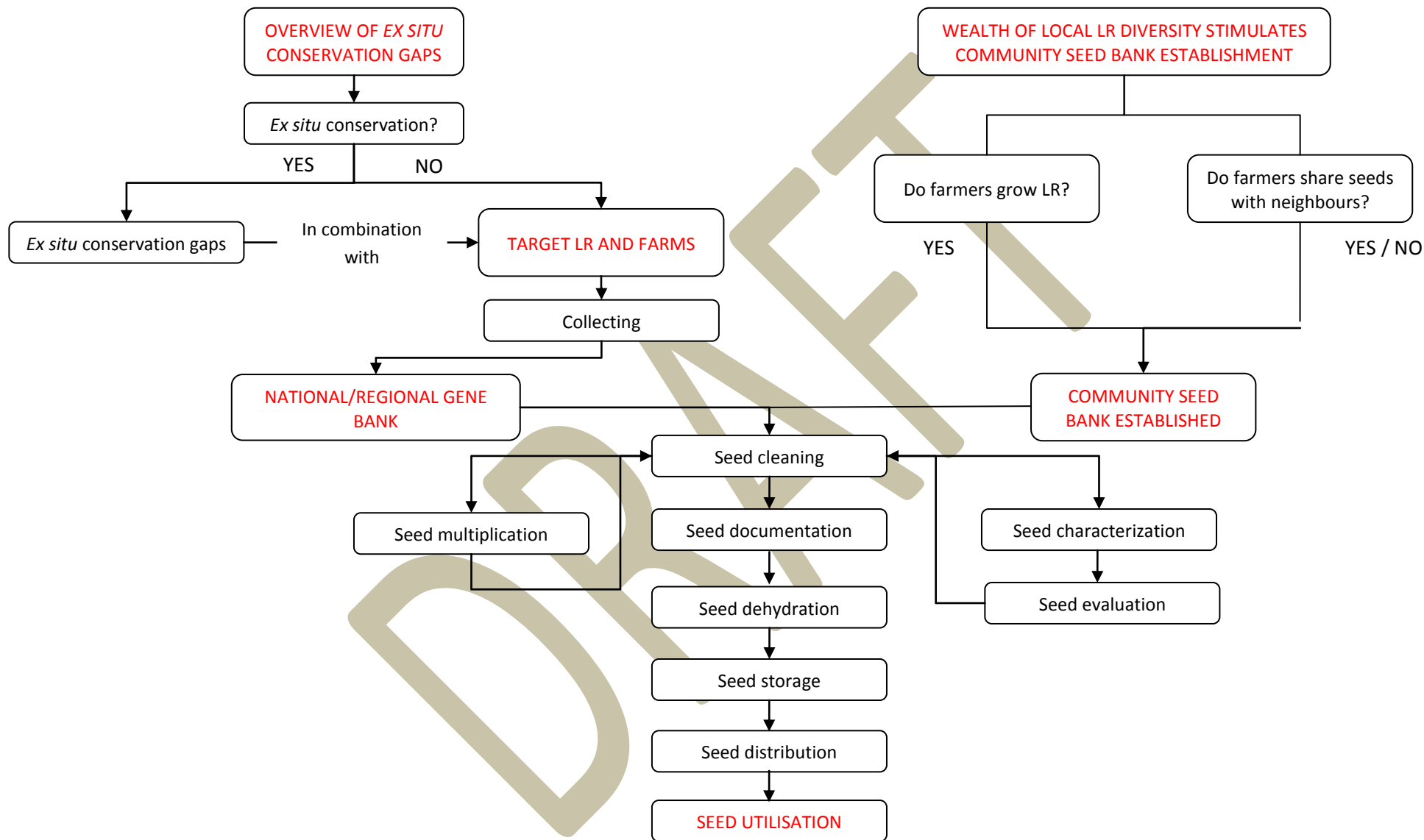


Figure 42. Establishment and implementation of *ex situ* LR conservation

B.11.2. Methodology for establishing and implementing *ex situ* LR conservation

Formal *ex situ* conservation (national/regional gene bank):

- (i) Overview of *ex situ* conservation gaps. *Ex situ* conservation gaps that resulted from the *ex situ* gap analysis should be taken into consideration.
- (ii) Selection of LR and farms for targeted collecting. Priority collecting should target individual LR that are not conserved *ex situ* or *in situ*, as well as LR populations that are not represented in gene banks at ecogeographic, trait, genetic diversity (or farmers' perceived diversity) levels (see Figure 1742).
- (iii) Collecting and curation standard procedures of a gene bank. These include seed cleaning, dehydration, characterization, packaging and storage. See 'Additional materials and resources' for gene bank methodologies.

Informal *ex situ* conservation (community seed bank):

As is shown in Figure 42, although gene banks and community seed bank serve slight different purposes related to the scope of diversity conserved, broadly geographically categorised as national / regional versus local, and the user communities served, the actually internal seed conservation management will follow the same schedule; although the level of technology involved is likely to differ between the two sectors. It would be wise to ensure that community seed bank accessions are duplicated in formal gene bank sector that have possibly greater security of funding and the formal gene bank sector may also be able to provide training to aid effectively implement of the community seed bank.

B.11.3. Examples and applied use

Box 99. Centre for Indian Knowledge Systems (CIKS) community seed bank

CIKS has been actively involved in setting up farmers' seed banks in villages in different parts of Tamilnadu, India. 125 villages in four districts are covered, involving around 3000 farmers. More than 130 varieties of rice and 50 vegetable varieties are being conserved in farmers' fields and experimental farms. These farmers' community seed banks allow efficient seed exchange, distribution, utilization, evaluation, characterization and multiplication of traditional varieties, as well as the survey, collection and documentation of existing varieties. Farmers are encouraged to grow these traditional varieties organically, and marketing is supported through a marketing scheme. As the main result, the community seed bank facilitates the conservation of traditional varieties which eventually will be managed by the farming community itself. In addition, an *in situ* conservation centre was set up and serves as a model from which other farming communities can learn.

Source: CIKS (unknown date)

Box 100. Community seed banks in the Taraka District, Kenya

Community seed banks were implemented in the Tharaka District (Kenya) —a marginal drought-prone area where agriculture is dominated by smallholder farmers—in order to ensure the availability of local varieties after extended drought periods, thus enhancing food security. Long periods of drought lead to crop failure and consequently to unavailability of seeds for planting the following year. In addition, poor farm households are usually so desperate for food that they use seed stocks for food. Community seed banks were set up and seeds were collected. Each farmer deposited two portions of at least 1kg of seed of each variety they grow: one portion for their own use and one for the group. The portion allocated to the group was used for income generation or delivered to other farmers who seek new varieties. Seed quality is controlled and varieties are properly documented. Farmers identified their training needs,

such as leadership skills and group development, and attended training workshops. These workshops were also useful to identify other local varieties and efficient traditional storage practices, to select the most suitable varieties for bulking, and to train farmers in for instance, seed crop husbandry, soil fertility, pests and diseases, seed harvesting and post-harvest management of seed (e.g. treatment against pest damage and cleaning). These community seed banks have enabled community members to gain access to seeds, thus enhancing food security. Conservation of local PGRFA has been achieved and awareness of seed security has been raised. Communities have developed close links among them and improved their confidence in their potential for self-development.

As an example, in 1997, a community seed bank was formed covering two villages, which provides seeds of food staples such as sorghum, millet and cow peas, but also other minor crops. Since 1997 it has expanded its collection from 57 to 140 varieties.

Source: Intermediate Technology Development Group (unknown date)

Box 101. Landrace protection scheme, Scotland

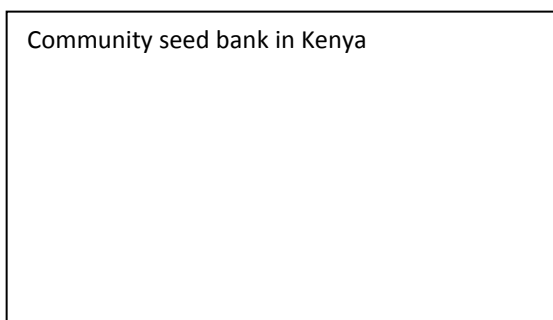
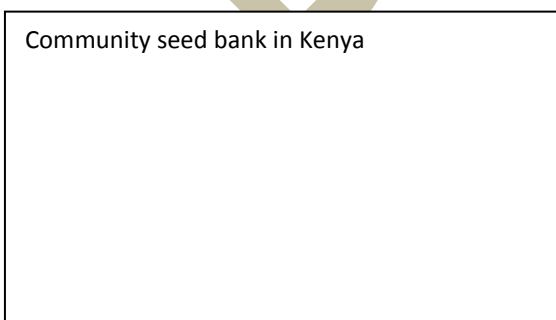
The Scottish Landrace Protection Scheme (SLPS) was launched by Science and Advice for Scottish Agriculture (SASA) in 2006 to provide a safety net for the continued use of landraces by storing seed produced by each grower each year. In the event of poor harvest, a grower can request some of the seed already deposited and stored. With the consent of the donor, the remaining seed can be made available for research, breeding and education. On receipt at SASA, each collected or donated seed sample is registered, examined for seed health and tested for germination. The growers are informed of the results and consent is sought for general distribution of seed. Seed is then cleaned, dried and stored at 22°C and a sub-sample is removed for safety duplication. Each stored sample is notionally divided with the aim of conserving a sufficient quantity of seed for emergency regeneration, monitoring (germination and vigour of seed in store), re-supplying the donor (the quantity being dependent on the size and quality of the original sample), morphological and molecular characterization and general distribution for bona fide research, breeding, education or further evaluation. To meet the above aims, a minimum seed quantity is required for participation in the SLPS and for making seed available for general distribution.

The SLPS supports:

- *in situ* regeneration by community networks of the seed donors;
- establishment of an *ex situ* safety duplication with the provision that growers can have their own seed back in case of a seed crop failure;
- provision of information to growers about germination, diseases and husbandry;

To date the SLPS has been used by Shetland cabbage from Shetland and Small Oat and Rye LR maintainers from the Western Isles.

Source: Green *et al.* (2009).



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B.11.5. Additional materials and resources

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B.12. Monitoring of landraces on-farm

B.12.1. Overview

What is monitoring of landraces on-farm and why it is important?

Monitoring of plant populations means the systematic collection of data over time to detect changes, to determine the direction of those changes and to measure their magnitude¹⁸⁸. The monitoring of LR thus constitutes an important early warning mechanism for detecting varietal extinction and genetic erosion. The monitoring of LR populations aims at:

- Registering changes in varietal diversity,
- Assessing trends in population size and structure,
- Detecting changes in the genetic diversity of LR,
- Determining the outcomes of management/farming practices on populations and to guide management decisions.

Once the on-farm conservation sites are established they provide an opportunity to monitor and assess short and longer term changes in LR diversity, which can help form the basis of assessing levels of LR diversity and so address the goals of the CBD Strategic Plan¹⁸⁹ of reducing loss of genetic diversity, particularly of crop species. Therefore, a monitoring scheme should be included in the site management plans, and should start immediately after site establishment (Figure 43). Monitoring of genetic erosion can be carried out using the materials conserved *ex situ*.

LR monitoring can be carried out at two levels: (i) individual LR, and (ii) LR genetic diversity. In addition, LR can be monitored for evolution and adaptation to environmental conditions.

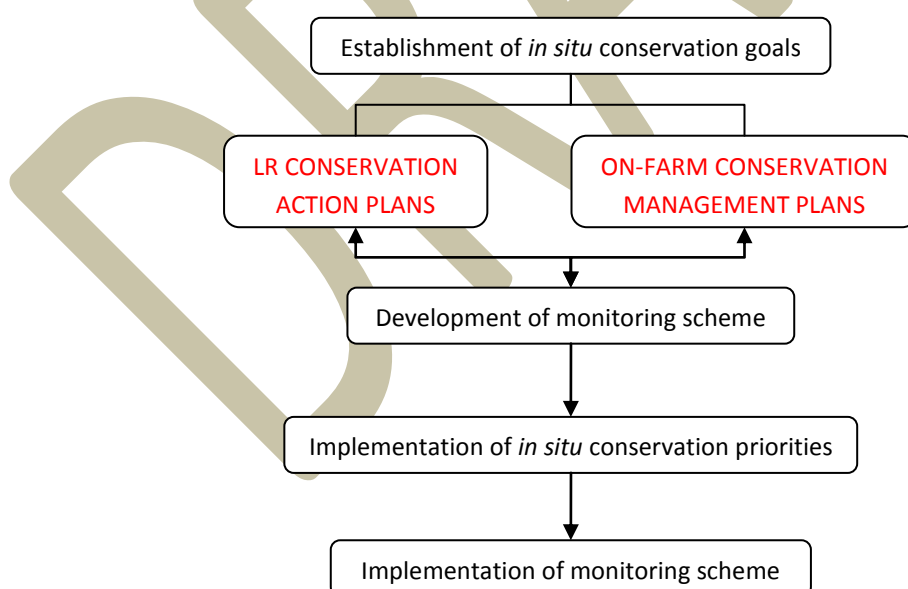


Figure 43. Monitoring of LR diversity *in situ*

¹⁸⁸ Iriondo *et al.* (2008)

¹⁸⁹ CBD (2010b)

B.12.2. Methodology for monitoring LR on-farm

The on-farm conservation sites should be surveyed regularly in order to detect any change in the LR grown. The time between surveys depends on the perception the researcher has during the first survey. That is to say, if the farmer has shown a desire to change to modern varieties in the near future, then surveying should take place after 1 or 2 years after the first survey, but otherwise a gap of 5 to 10 crop generations is advisable. However, the minimum periodicity of monitoring to ensure LR diversity is maintained has yet to be evaluated scientifically. Although having provided guidance on the minimum periodicity of monitoring it should be stated that more regular interaction between the maintainer and conservationist is desirable to ensure problems with pests and diseases or other causes of crop losses are overcome and at the same time check the farmer is continuing to grow the LR. In addition, a comparison between *ex situ* accessions (collected in previous years) and/or between *ex situ* accessions and extant on-farm populations (of the same LR and from the same farm) can also be undertaken in order to assist monitoring of changes in the genetic composition of LR. See Table 9 for further recommendations for monitoring changes in LR diversity.

Monitoring	Genetic monitoring
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Table 9. Monitoring LR to detect changes in diversity

LEVEL OF MONITORING	METHODOLOGY	PARAMETERS TO MEASURE	OBJECTIVES	INDICATORS
Individual LR	1. Compare LR inventories from the same farm in different years: <ul style="list-style-type: none"> Direct observation (farmers' interviews, etc.) Community Biodiversity Registers; Participatory field observations (participatory transect walks) in different years. 	<ul style="list-style-type: none"> Number of LR grown; Area allocated to each LR; Richness indexes e.g. Shannon Weaver Index (H')¹⁹⁰, Simpson Index (D)¹⁹¹; Management practices; Threats. 	<ul style="list-style-type: none"> To monitor changes in LR maintained. To monitor changes in the areas allocated to each LR. To monitor farming practices. To register farmers' perceptions and reasons for changes in varietal diversity. To register changes in specific field-plots. 	<ul style="list-style-type: none"> Decrease in the numbers of farmers growing each LR. Decrease in the area covered by a LR. Decrease in the number of LR. Decrease in H' or D. Increase of the annual replacement of LR with modern varieties in specific field-plots.
	2. Focus group discussions	-	<ul style="list-style-type: none"> To validate the reasons for varietal changes and genetic erosion from comparing the inventories and field observations. To discuss the reasons for varietal change and loss of LR diversity. 	-
Genetic erosion within	1. Genetic analysis – neutral diversity	Genetic diversity (expected heterozygosity) (richness of	To detect changes in the genetic composition within a population of a LR.	Decrease in richness of diversity.

¹⁹⁰ $H = -\sum_{i=1}^s p_i \ln p_i$, where p_i represents the relative proportion of the individuals in group i ; and s is the number of categories (varieties). The greater the value of the index, the more diverse the community.

$$D = 1 - \sum_{i=1}^s \left(\frac{n_i}{N}\right)^2$$

¹⁹¹, where N represents the total number of organisms of all species; n_i is the number of individuals in the i th variety; it ranges from 0 to 1. The closer to 0 the index, the more diverse the community.

LEVEL OF MONITORING	METHODOLOGY	PARAMETERS TO MEASURE	OBJECTIVES	INDICATORS
a LR		diversity).	To detect changes in the genetic composition among different populations of the same LR.	Decrease in evenness of diversity.
		Average number of alleles per locus (evenness of diversity).		
		Linear regression of the above variables against the fixed variables of the year (of collection) surveyed and population size (where population size varied).		
		Analysis of molecular variance (AMOVA) (to compare variances among populations)	To assess population differentiation over time.	Significant population differentiation between samples collected in different years.
Evolution and adaptation	Genetic analysis – adaptive diversity or perceived diversity	<ul style="list-style-type: none"> ▪ Response to variation in agronomic practices ▪ Response to pathogen incidence. ▪ Response to variation in agronomic practices ▪ Response to planting in disease nurseries, etc. 	<ul style="list-style-type: none"> ▪ To detect changes in the genetic composition. ▪ To detect changes in cross-breeding with other varieties and wild relatives. 	Changes in any of the parameters mentioned.

B.12.3. Examples and applied use of LR monitoring on-farm

Box 102. Potential loss of rice landraces in Nepal

A study was undertaken to detect changes in rice LR diversity in a Terai community in Nepal (Kachorwa, Bara) in the context of an IPGRI coordinated project “Strengthening the scientific basis of *in situ* conservation of agro-biodiversity on-farm”. A baseline survey was undertaken between 1998 and 1999 which allowed the documentation of crop diversity as well as socio-economic and agro-ecological factors. The extent and distribution of rice-growing households was assessed based on the distribution of farmer-named varieties (within number of households and the crop area). Threats of genetic erosion were also assessed based on area and number of farmers growing each LR. Later in 1999 and in 2001, rice-growing households were monitored in order to detect the changes in diversity of LR maintained and the areas allocated to each by comparison with the baseline information from 1998. In 1999, 2000 and 2001, participatory transect walks were conducted in order to monitor changes in rice varieties and land allocations. During these visits, farmers’ reasons for changes in varietal diversity were registered. Additionally, changes in specific field-plots regarding the LR diversity grown and annual rate of replacement of landraces with modern varieties were recorded. Focus group discussions were carried out in order to validate the findings for varietal changes and genetic erosion from the previous methods (monitoring, field observations, participatory transect walks) and findings were discussed.

Genetic erosion was estimated based on the numbers of farmers growing each LR as well as the area covered by different LR in different years. In addition, the Shannon Weaver Index (H') and the Simpson Index (D) were calculated and compared between years.

As a major conclusion, it was found that local rice LR were gradually being replaced by modern varieties. In addition, LR were suffering from a decline in the richness and evenness of genetic diversity which is an indication of genetic erosion.

Source: Chaudhary *et al.* (2004)

LR in Nepal monitoring

Box 103. Genetic erosion of rice landrace diversity in South and Southeast Asia

Almost 13,000 *ex situ* accessions of rice LR from Bangladesh, Cambodia, India, Indonesia, Lao PDR, Philippines, Taiwan, Thailand and Vietnam, collected over a 33 year period (1962–1995) and conserved at the International Rice Research Institute (IRRI) were studied regarding their genetic diversity using 12 allozyme loci. Individual LR accessions were grouped according to the date of collection, or when absent, according to the date of acquisition by IRRI (as a proxy of the date of collection). Nei’s expected heterozygosity (genetic diversity) (Nei 1978) and average number of alleles per locus (Lewis and Zaykin 2001) were estimated, and linear regression of these variables was performed against the fixed variables of the year of collection and population size (where population size varied). Additionally, analysis of molecular variance (AMOVA) was used to compare variances among populations and to assess population differentiation over time.

In contrary to what was expected, the authors did not detect significant reduction of available genetic diversity in the studied material. In addition, a strong link between numbers of LR collected (and therefore extant) and genetic diversity was found. Hence, it can be used as an indicator to detect loss of genetic diversity in the future.

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B.13. Promoting the use of conserved LR diversity

Why is it important to promote the use of landrace diversity?

Landrace on-farm conservation is the active management of LR diversity usually but not exclusively within the traditional agricultural systems where they have developed their unique characteristics. The use may be broadly characterised as individual farmer use and broader stakeholder use. Individual farmers continue to grow the LR, maintain the LR diversity and possess the knowledge concerning its cultivation, management and uses, because that LR continues to meet their economic, food security and cultural requirements. The continued growth of the LR by individual farmers has a broader stakeholder use to the agricultural community as a whole as the maintenance of LR provides plant breeders with the diversity they continue to require to meet changing consumer demands, and environmental and market demands. Therefore, the maintenance of LR diversity by farmers is private and public good and should be stimulated to ensure LR preservation.

The conservation of agro-biodiversity is not an end in itself. There is an explicit link between genetic conservation and utilization: genetic conservation must facilitate utilization, either now or in the future. This point is highlighted in the text of the CBD⁸⁴ which states that utilization should be "sustainable" and "meet the needs and aspirations of present and future generations". No conservation action takes place in an anthropogenic vacuum—in other words, whether an on-farm conservation site is to be established or a particular LR population sampled for *ex situ* conservation, there are likely to have been traditional or local users of that resource. Therefore, no conservation action can be successful without the support of the local community. Where possible, traditional or local community utilization should not be restricted or infringed by active LR conservation because conservation cannot succeed without local community support. However, local communities do not always manage their resources sustainably, even if mismanagement is likely to adversely impact their longer-term interests. Therefore, the conservationist's role when formulating conservation actions may be just as much resolving conflicts between local community and practical conservation implementation, ensuring continued local community use of their PGR resources, while achieving sustainable conservation.

LR can be used by farmers, general, and professional users (Table 10). The work of professional users, the general public and local people can be linked through partnership within NGOs, which could contribute with conservation volunteers, and could be involved in sustainable rural development or the use of resources in accordance with traditional cultural practices. Raising public and professional awareness of the value of and need for LR conservation is likely to engender specific conservation action in LR rich areas, as well as promoting general conservation sustainability. All partners should therefore share the goals of sustainable use of biological resources taking into account social, economic, environmental and scientific factors which form a cornerstone of the nations' proposals to implement Agenda 21.

Farmer utilization

Farmers or other crop maintainers may have an extensive history of individual LR cultivation. They usually possess a great deal of knowledge on traditional cultivation techniques and directly utilise LR. See Table 10 and B.10. Implementation of on-farm conservation for more details.



Farmer showing her “Mawangamanga” (coloured seeds) sorghum LR in Chimatiro village (Chingale, Zomba District, Malawi) (photo: Edwin A Chiwona).



Farmer holding a panicle of “Mchesa” sorghum LR in his sorghum garden in Mateyu village (Chikwawa District, Malawi) (photo: Edwin A Chiwona).



Jim McEwan, Production Director at Bruichladdich Whisky Distillery in Islay, Scotland tasting spirit made from bere, a Scottish landrace (photo: Bruichladdich Distillery).

General utilization

The general users of LR are people at large, whose support may be essential to the long-term political and financial viability of a conservation site. Commonly, the general public ultimately finances the establishment and continuation of a network of on-farm conservation sites through taxation. In addition, some members of the general public may wish to visit the on-farm site (Table 10).

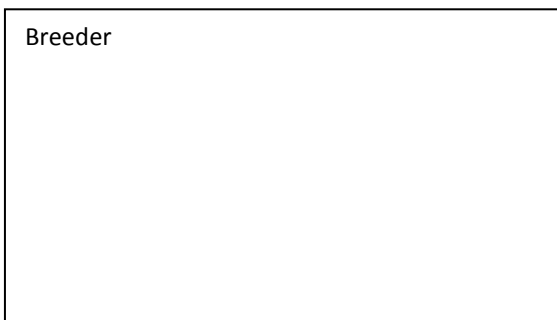


Museum of *Phaseolus* in Smilyan (Bulgaria) (photo: Tsvetelina Stoilova).

Professional utilization

Professional users include researchers, pre-breeders and breeders who characterise, evaluate and screen PGRFA for novel traits using various techniques such as morphological analysis, genomics, transcriptomics, metabolomics, high-throughput phenotyping and GIS-based predictive characterization (see Box 86) as the basis for improved crop breeding (Table 10). Professional users can utilise LR conserved in the on-farm conservation sites but more often they will utilise the samples of these populations stored *ex situ* in gene banks.

LR on-farm conservation sites can act as *in situ* research platforms for field experimentation. There is a real need for a better understanding of species dynamics within conservation areas to aid the sustainable management of the specific taxa, but also as a more general experimental tool for ecological and genetic studies of *in situ* conserved LR. Research activities based on the material conserved should be encouraged as they provide another use for the material conserved and another justification for establishing the conservation site. Monitoring studies (such as of genetic diversity changes), as required by the COP to the CBD adopted strategic plan¹⁹² would be facilitated. This way, we could detect changes associated with future habitat management scenarios; hence take action immediately in order to reduce the current rate of diversity loss.



¹⁹² CBD (2010b)



Researcher taking physiological measurements in a field experiment at IPGR, Sadovo (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").



Morphological characterization of cowpea LR in 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").



Morphological observations and physiological measurements of beans in Cherni Osam, 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").

Table 10. Methods of utilization and promotion of LR use

TYPE OF UTILIZATION	TARGET COMMUNITY	UTILIZATION	PROMOTING USE
Farmer	Farmers and other crop maintainers	Home consumption, commercialization	Diversity fairs, community seed banks, etc. (see Table 8)
General	General public	Consumption, leisure	Media, farmers' market, formal and informal education, cook books, agro-biodiversity ecotourism, art competitions, fair trade
Professional	Researchers, pre-breeders, breeders	Characterization and evaluation, including Focused Identification of Germplasm Strategy (FIGS), field experimentation,	Publication of characterization and evaluation data, web-enabled Trait Information Portal of

		monitoring	characterization and evaluation data
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B.13.2. Additional materials and resources

See Focused Identification of Germplasm Strategy (FIGS) ‘Additional materials and resources’ in B.8.5.

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Promoting the use of landraces:



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B.14. Information system and data management

B.14.1. Overview

Why is data critical to landrace conservation and use?

It is widely accepted within the PGRFA conservation and user community that one major factor hindering effective conservation and use of PGRFA is the lack of easy access to data, as well as obstacles to information exchange due to the many different approaches in managing data. If we are to inventory and build national LR conservation strategies then consistent data collation and management is required.

Historically as noted above there have been many obstacles to information exchange between projects involved in the inventory and establishment of national LR conservation strategies, the few projects that have addressed these tasks have developed stand-alone information systems to manage their LR related data. However in recent years the adoption of data collection and information management standards has been achieved to a large degree for the management of *ex situ* collections data using standard data descriptors such as the FAO/IPGRI Multi-crop Passport Descriptors (MCPD) version 2 published in June 2012 ([http://www.biodiversityinternational.org/index.php?id=19&user_biodiversitypublications_pi1\[showUId\]=6901](http://www.biodiversityinternational.org/index.php?id=19&user_biodiversitypublications_pi1[showUId]=6901)). But even these standards do not adequately cater for the full range of data types that are of relevance to landrace conservation and use.

The EC funded PGR Secure project (see <http://www.pgrsecure.org/>) has as its dual goal agrobiodiversity conservation and the promotion of its sustainable use. One element of which is to develop (i) Europe-wide LR inventory, (ii) Exemplar national LR inventories and (iii) European LR conservation and use strategy. Each of these three deliverables requires extensive data management and intra- and inter-project data exchange. Thus significant progress was required and a set of minimum descriptors for the documentation of on-farm conservation and management activities have been developed, Descriptors for web-enabled national *in situ* landrace inventories (see http://www.pgrsecure.bham.ac.uk/sites/default/files/documents/helpdesk/LRDESCRIPTORS_PGRSECURE.pdf)¹⁹³. The published descriptor list includes fields related to the inventory identification, taxon identification, landrace/population identification, site and location identification, landrace characteristics and finally fields concerning conservation and monitoring actions to be taken in favour of the landrace diversity maintenance. These descriptors have been designed to record the landrace(s) present on-farm, as well as to describe aspects of farm management practices (e.g., agricultural system, cropping management and farm labour division by gender). Descriptors to describe the seed supply system, the farmer's criteria for distinguishing landraces, selection criteria, seed storage practices and crop uses, amongst others, are included. PGR Secure will within the context of the national LR inventories that are planned in Finland, Italy and the United Kingdom will test and refine the descriptors, but the methodology used for data collation and the descriptors are deliberately generic so that they will have applicability globally.

B.14.2. Methodology

Information on landraces is available from wide range of sources, but retrieving it presents a number of challenges. Firstly, in existing databases, such as those managed by plant gene

¹⁹³ Negri et al. (2012)

banks, landrace accessions are generally not distinguished from modern varieties, although this issue should not arise if the FAO/IPGRI Multi-crop Passport Descriptors are used as the SAMPSTAT descriptor allows for the distinction between LR and other types of collection sample. Secondly, different scientists use different definitions of LR, so what is a LR to one is not to another. Thirdly, the crop variety name can sometimes be used to guide decisions as to whether a variety is a LR (for example, if the name of a LR is directly associated with a particular geographic location), but this is not a reliable method because modern varieties can also be given similar names. Furthermore, obtaining information about varieties that people grow for business purposes can be hindered by issues of commercial sensitivity, concerns about the potential legal repercussions associated with national listing of unregistered varieties and insufficient time and resources available to the business to respond. These challenges are not insurmountable but they do demand a carefully considered and tested approach (particularly with regard to obtaining information from commercial enterprises) and a considerable amount of time.

LR Data were collated from various sources, including LR, maintainers, PGR experts, governmental documents, NGOs, commercial companies, gene banks, websites and the literature. The types of data collated will fall into four basic types:

- Ecogeographic data (taxonomic, ecological, geographic and genetic: passport),
- Field population data (passport),
- Conservation management data (curatorial),
- Characterization and evaluation data (descriptive).

Each of these data types are collated using some type of standard descriptor. A descriptor may be defined as “any attribute referring to a population, accession or taxon which the conservationist uses for the purpose of describing, conserving and using this material”. Descriptors are abstract in a general sense, and it is the descriptor states that conservationists actually record and utilise. Standard descriptors for ecogeographic, field and conservation management data are included in the Descriptors for web-enabled national *in situ* landrace inventories¹⁹⁴, while formal characterization and evaluation descriptors are associated with various standardized ‘Crop descriptor lists’ published by FAO, Bioversity, UPOV (see <http://www.bioversityinternational.org/publications.html>). It is important to stress that standard lists of descriptors should be used when they are available. The use of well-defined, tested and rigorously implemented descriptor lists for scoring descriptors considerably simplifies all operations concerned with data recording, such as updating and modifying data, information retrieval, exchange, data analysis and transformation. When data are recorded, they should be classified and interpreted with a pre-defined list of descriptors and descriptor states to consult. This clearly saves a considerable amount of time and effort associated with data entry. The use of lists ensures uniformity, while reducing errors and problems associated with text synonyms.

B.14.3. Examples and applied use

There are few examples of data management within the context of the production of a National LR Conservation Strategy. However, one reported example is the Vegetable landrace inventory of England and Wales will be made available via the UK’s Information Portal on

¹⁹⁴ Negri et al. (2012)

Genetic Resources for Food and Agriculture (<http://grfa.org.uk/>)¹⁹⁵. The methodology applied¹⁹⁶ involved:

Experts' meeting

An experts' meeting was called involving all those stakeholders with knowledge or interest in LR conservation and use to discuss the general project strategy and to share existing knowledge of how to obtain information on UK vegetable landraces, how to make contact with landrace maintainers, and a possible strategy for obtaining germplasm samples for *ex situ* conservation. The specific objectives of the meeting were to:

1. Provide an introduction to the project and discuss the proposed project strategy, including the following specific objectives:
 - a. Review official government documentation and scientific/popular literature
 - b. Review NGO and commercial company knowledge and holdings of landrace diversity
 - c. Review *ex situ* seed bank holdings of landraces
 - d. Discuss LR diversity with LR maintainers.
2. Share knowledge of how to achieve each of the above objectives (e.g., specific contacts, literature sources, government documents, relevant NGOs, commercial companies and seed banks).
3. Discuss a procedure for obtaining germplasm samples for *ex situ* conservation and outline a strategy for ensuring sufficient material is duplicated in the appropriate seed banks.
4. Provide examples of existing successful on-farm vegetable LR conservation projects in the UK (or elsewhere) that can be used for reference purposes when formulating conservation recommendations for other vegetable LR.
5. Provide examples of the use of LR germplasm in formal crop improvement programmes that can be used for reference purposes in the final report to Defra.

¹⁹⁵ Kell et al. (2009)

¹⁹⁶ Maxted et al. (2009)

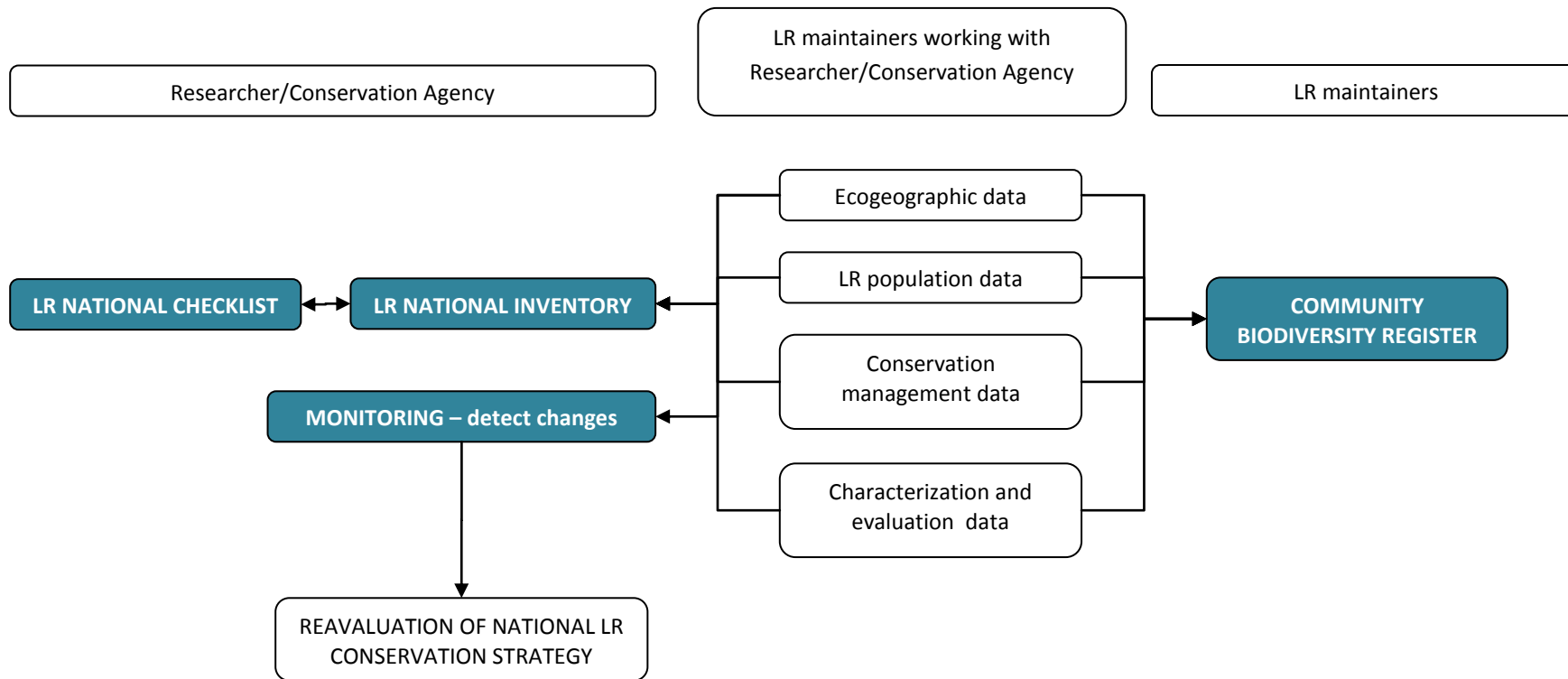


Figure 44. Summary of data flow in LR conservation

Agree scope of the inventory—defining ‘landrace’

It was necessary to discuss and agree a working of a landrace to be used in the project, and it was agreed that keeping an open definition from the outset was desirable in order to capture as full a range of traditional vegetable varieties in the inventory as possible. Furthermore, there is not always a clear defining line between a ‘landrace’ *sensu stricto* and a ‘traditional variety’ or ‘old variety’, nor between crops grown on a subsistence basis or on a small scale for local commerce or seed production. So anything considered a LR by a stakeholder was included.

Designing the landrace database: descriptors and structure

There was a necessary requirement of the government agency funding the research to make the LR information collated available to all stakeholders post-project and this involved designing a database to manage landrace information. A simple database structure was designed and recommendations on the data standards for the collation and management of landrace data, with the long-term aim of providing an information system that can continue to be developed and updated as further information becomes available. The descriptor standards used were the FAO/IPGRI Multi-crop Passport Descriptors version 1 (MCPD) (http://www.biodiversityinternational.org/Publications/pubfile.asp?ID_PUB=124) and the minimum descriptors for the documentation of on-farm conservation and management activities (see http://www.ecpgr.cgiar.org/Networks/Insitu_onfarm/Docs/OnfarmDescr_DRAFT271107.pdf).

Note both these sets of descriptors have now been superseded and the current version of the descriptors should be used (see discussion above). However, critically, these descriptors included provision for recording both site environmental data, which are important for characterization of landraces, and socio-economic data, which are vital for continued maintenance of populations *in situ*. The vegetable landrace inventory of England and Wales will be made available via the UK’s Information Portal on Genetic Resources for Food and Agriculture (<http://grfa.org.uk/>). The database is relational and all crop population records are referenced to a landrace maintainer via site locations. Environmental data are described in a separate table for each site recorded, while socio-economic data, cultivation details and conservation status are related to individual crop population records. Figure 45 shows the overall structure of the database and Figure 46 shows the LR data entry module.

Strategy for accessing landrace information

Data were collated from various sources, including PGR experts, governmental documents, NGOs, commercial companies, gene banks, websites, literature and landrace maintainers.

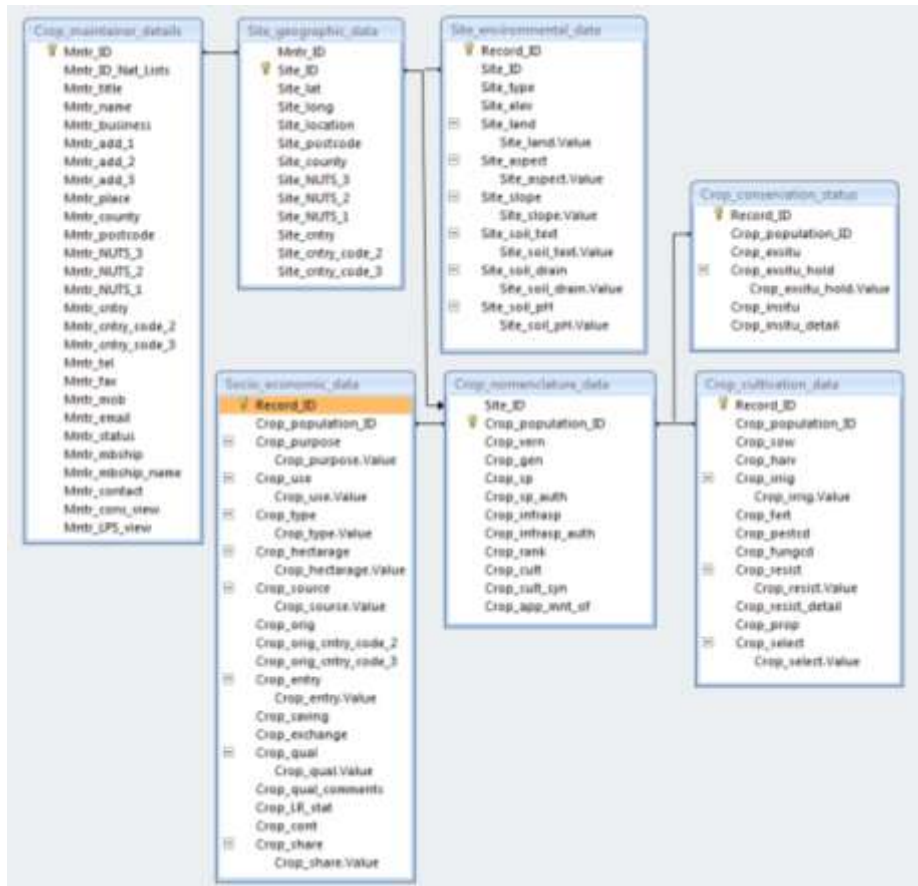


Figure 45. English and Welsh vegetable LR inventory database structure

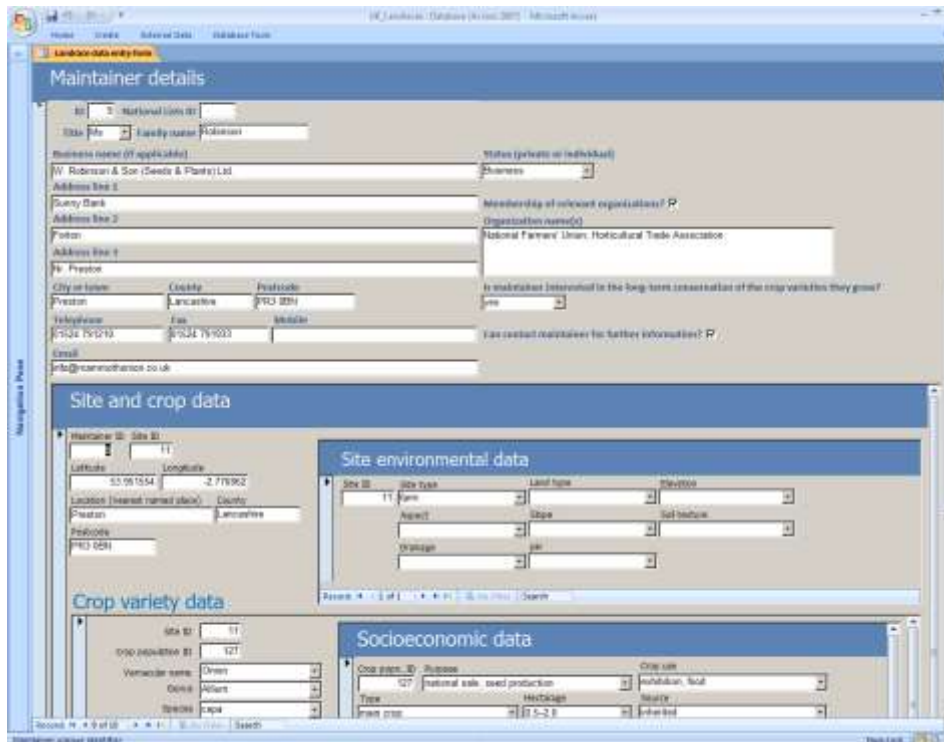


Figure 46. English and Welsh vegetable LR inventory LR data entry module

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B.14.5. Additional resources and materials



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WWW

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SECTION C. CONCLUSIONS AND RECOMMENDATIONS

C.1. Summary of conclusions

There is concern among agrobiodiversity conservationists involved in the effective conservation of CWR and LR diversity as to how they can meet the demand by plant breeders for a broader range of genetic diversity. This diversity is required to mitigate the impact of the rising human population and the changing climate. Nature conservationists (particularly PA managers) for CWR and farmers for LR diversity are recognising the broader ecosystem services provided by the *in situ* conservation of the diversity they manage. As promoted in the CBD Strategic Plan and often implemented through national legislative instrument, like agroenvironmental stewardship schemes or other subsidies, it offers to agrobiodiversity managers a means of linking human well-being to biodiversity conservation. As the general public (through their taxes) fund most conservation activities, showing that conservation expenditure can have a direct benefit to the general public underlines that the funds are well spent and will engender public support.

Like many other elements of biodiversity, CWR and LR are subject to increasing levels of threat in their host habitats, as a result of human environmental mismanagement. However, the responsibility for CWR and LR conservation tends to fall between two conservation sectors—the general nature conservation sector focuses its efforts on rare or threatened species and on habitat conservation, while agricultural conservationists focus on more advanced crop material. As a result, CWR particularly and to a lesser extent LR have been neglected in conservation planning (Maxted 2003). It is now vital that this lack of conservation effort is redressed through systematic CWR and LR conservation at local, national, regional and global levels. It can be argued that the national level is most critical to this refocusing of conservation action, because: post-CBD nations have sovereignty over their agrobiodiversity; there is an obligations on nations to conserve their agrobiodiversity under the provisions of the CBD and ITPGRFA for ratifying countries; the bulk of agrobiodiversity conservation expenditure is at the national level; and even global and local agrobiodiversity conservation action is most commonly implemented via national agencies. The protocols and examples provided in this Toolkit are designed to help meet the demand for practical tools to assist national PGRFA programmes in the development and implementation of CWR and LR conservation strategies, but in doing so, they are also likely to contribute to local, regional and global agrobiodiversity conservation.

The national conservation of CWR and LR does however presents new challenges to the conservation sector—that of requiring (a) nature and agricultural conservationists to work more closely together and integrate conservation actions, and (b) agricultural conservationists to work more closely with farmers. For too long the two conservation sectors have largely worked in isolation, focusing on distinct and different elements of biodiversity, attending alternative conferences and even publishing in different sets of journals. While agrobiodiversity conservationists have often worked with farmers, the relationship has historically primarily been based on short visits to collect seed samples, but regular LR monitoring and helping traditional farmers sustain production is increasingly required. The farmer's ultimate goal is to generate commercial profit rather than to specifically conserve the diverse resource that generates the profit itself; therefore, to jointly fulfil conservation and development goals, the conservationist requires diverse skills (development, marketing, sociological, economic, etc.). In practice ensuring sustainable LR conservation may involve the conservationists working alongside a range of stakeholders and specialists as well as the farmers, but the collaboration goes well beyond the purely scientific.

Therefore, CWR and LR conservation is unique in the sense that it is the shared responsibility of multiple stakeholders and it is now widely recognised that conservation goals cannot be achieved in isolation by any one of them. Ultimately, although agricultural conservationists

may be responsible for establishing priorities for CWR conservation, the actual genetic diversity of CWR will primarily be conserved *in situ* in PAs managed by nature conservationists, just as LR will primarily be conserved *in situ* in cultivation systems by farmers, householders and other maintainers. In this real sense, the approach to CWR and LR conservation is holistic.

There is a growing imperative facing national biodiversity coordinators to meet the obligations of governments under international treaties which encompass legally binding legislative instruments (e.g., notably the CBD and ITPGRFA) and associated strategies (e.g., the GSPC and GPA). In this context, national biodiversity coordinators recognize the need to “develop national strategies, plans or programmes for the conservation and sustainable use of biological diversity” and more specifically for plants, this obligation is inherent in the GSPC and ITPGRFA. As concluded by Balmford *et al.* (2005), progress is being made towards assessing change (usually loss) of biodiversity in various domains (birds, insects, fish, amphibians, coral reefs, forestry and non-PGRFA plants, etc.), but relatively little progress was made to meet the CBD 2010 targets. While some progress has been made under the aegis of the FAO GPA to define indicators for monitoring change, there remains a lack of practical and inexpensive methodologies for measuring change in genetic diversity over time, and assessing real as opposed to proxy genetic erosion.

So how might both national biodiversity coordinators and individual conservationists address their responsibilities for CWR and LR diversity conservation and promote its sustainable exploitation? One answer could be to adopt the approach outlined in this Toolkit for the development of National CWR and LR Conservation Strategies. For the national biodiversity coordinator and policy makers the background and context to developing a National CWR or LR Conservation Strategy that incorporates the promotion of use is outlined in Part 1 of the Toolkit, while Part 2 outlines the practical steps involved in achieving this goal. Both Parts 1 and 2 assume that one end achievement will be an integrated network of national CWR genetic reserves and LR on-farm conservation sites, with systematic *ex situ* collections available to act as a safety backup and provide a point of access for the germplasm user community. These national CWR and LR conservation networks will also feed into a broader global network to maximize conservation efforts.

The network of national CWR genetic reserves and LR on-farm conservation sites not only fulfils the commitment to improved CWR and LR conservation, but also through individual site management offers a routine means of monitoring taxonomic, demographic and genetic diversity changes. This means that the new CBD 2020 target of a significant reduction in the current rate of biodiversity loss at national level should be met for national CWR and LR diversity, we can show clearly through monitoring that it has been met and it will also make a significant contribution to the reduction in global and regional biodiversity losses. The protocols and examples presented in this Toolkit will help both national biodiversity coordinators and individual conservationists meet their agrobiodiversity conservation commitments and aspirations.

In developing the protocols and providing examples, the desire was to assist national PGR programmes develop and implement National CWR or LR Strategies, particularly in developing countries where the bulk of CWR and LR diversity is found and where conservation expertise is least well developed, from initial planning through to Strategy implementation. However, it is worth emphasizing that the toolkit can be used for the entire process or individual steps can also be consulted and applied. Either way the end goal is National CWR or LR Conservation Strategy implementation.

Sustainability for *in situ* CWR conservation or on-farm conservation sites can only be enhanced by use of the diversity they contain and therefore stimulating interest among user stakeholders in the conserved agrobiodiversity is central to the Strategy. Just as botanic gardens often stimulate interest among the general public by displaying specimens of exotic

crops—for example, to show what banana, coffee or rice plants are like in the ‘flesh’—so the PA or on-farm managers can raise the profile of the site by drawing particular attention to the CWR or LR that occur there. Advertising their presence and promoting exploitation of CWR and LR diversity to the potential user communities will help sustain their conservation. The onus is on PA or on-farm managers, just as it is on gene bank managers, to promote utilization of the material in their care.

Finally, the current rate of human population increase, which is linked to the many direct threats (including climate change) to biodiversity and agrobiodiversity, means that a more effective programme for global and national CWR and LR conservation is not a matter of choice but a matter of necessity. Preserving and sustainably using CWR and LR resources will increase food security, alleviate poverty and improve economic and ecosystem stability. The tools to efficiently conserve CWR and LR diversity are available—now we need to act!

C.2. Recommendations

Key recommendation 1: The FAO Commission on Genetic Resources for Food and Agriculture considers the requirement for the establishment of a global network for *in situ* conservation of CWR and LR diversity.

Given the known value of CWR and LR in crop improvement and their potential value in climate change mitigation and future food security, it is perhaps surprising that there has to date been no systematic attempt at global level to conserve CWR and LR diversity. For CWR diversity this has largely been because they fall between the remit of the nature conservation community who mainly focus on rare or threatened wild plant species and habitats, and the agrobiodiversity conservation community who focus on conservation of intra-crop variation. While for LR diversity so little is known about global levels of LR diversity and the task to understand that diversity for all crops is so gargantuan that it has yet to be tackled. In many cases, the selection of global PAs has been *ad hoc*, depending largely on previous land use, ownership or human habitation, recreation and tourism, or historical protection—CWR or LR conservation has not been a consideration. Stolten *et al.* (2006) listed PAs reported to contain CWR species and while this list provides a useful initial indication of which CWR may be found within existing PAs, it is important to stress that in these cases the CWR themselves are unlikely to be actively managed. CWR have the benefit of being wild plant species, so much of the information available for CWR is a result of botanical study not specific study as CWR species, LR do not have the same advantage and therefore, there is no record of which LR are cultivated in existing PAs.

It is obvious from the growing threats that CWR face globally, coupled with the increased requirement for their genetic diversity in attempting to counter climate change, that CWR genetic diversity is currently far from secure and more concerted *in situ* and *ex situ* conservation action must be a priority. The Global Crop Diversity Trust and partners have recently launched a ten year project to ensure priority CWR are conserved *ex situ*; however, *in situ* conservation remains the preferred option because of the need to retain dynamic evolutionary interactions, the sheer number of CWR involved, and the need to conserve their full range of genetic diversity. Therefore, there is a need for complementary *in situ* action through the establishment of a Global Network of CWR Genetic Reserves to ensure that the full range of CWR genetic diversity of the highest priority species for food security is conserved. The Commission has already published a background study for the establishment of a Global Network of CWR Genetic Reserves (Maxted and Kell, 2009)—now the recommendations from this study need to be translated into concrete actions.

Although there are many more LR accessions conserved *ex situ*, it is unlikely that they reflect the true levels of LR diversity maintained by farmers, householder or other maintainers globally

for all crops. There is a need for a thorough review of global LR diversity, together with concerted *in situ* and *ex situ* conservation action to ensure the diversity is secured and available to the user community. National LR reviews in Europe have found LR are often but not exclusively maintained in agriculturally marginal areas and this relationship could be explored further, particularly within the Vavilov Centres to help identify globally important sites to form part of a Global Network of LR On-farm Conservation Sites.

Key recommendation 2: Reaffirm the need for collaboration and coordination among national, regional and international levels to promote on-farm management and *in situ* conservation of plant diversity.

The point has been stressed throughout the Toolkit that effective CWR and LR conservation requires a coordinated effort at national, regional and global levels, as well as between those engaged in their conservation and use. Although the Toolkit is focused at the national level, the integration of national on-farm and *in situ* conservation with the local and international level action is key to maximising conservation efficiency. So on-farm sites and genetic reserves will be situated within a local community and should be grounded within the local community to integrate agrobiodiversity conservation with local benefit and so engender support for the conservation. While individual on-farm sites and genetic reserves via national networks may also contribute to global networks as global conservation action must be implemented in nations and at individual location. As pointed out above global and local conservation action is most commonly implemented via national agencies, so there is need to establish good inter-geographic level linkage.

The effective establishment of a network of CWR genetic reserves and LR on-farm sites will also necessitate a coordinated approach between the professional PGRFA conservation community and the nature conservation community. The threats facing CWR and LR diversity are evident and the need for active conservation is urgent. However, there is a continuing need for stakeholder collaboration in planning and overseeing effective implementation of conservation and use strategies as their sustainability relies not only on solid conservation science, but on the commitment and actions of the entire stakeholder community, including nature and agrobiodiversity conservationists, farmers and other maintainers of genetic resources, and the broad user community, including plant breeders.

Key recommendation 3: The FAO Commission on Genetic Resources for Food and Agriculture considers the requirement for the establishment evidence base for CWR and LR conservation.

In the broader biodiversity conservation community there is now an acceptance of the need to base conservation action on evidence based knowledge, rather than anecdotal advice or a continuation of traditional practices that may inhibit the development of scientific management and effective project planning. The quality of conservation action often reflects the ratio between the information that the conservationist has at hand compared to the sum total of relevant information that is potentially available; the more background information (evidence) the better the decision. The evidence-based framework aims to inform decision makers about the likely outcome of alternative conservation actions. The features of such an evidence based system would be (a) systematic reviews and evaluation, (b) explicit assessment of effectiveness, and (c) web delivery to practitioners (see <http://www.environmentalevidence.org/>). While the advantages of using evidence based system are efficient, unbiased, systematic, scientific conservation, a formalised method to identify areas where evidence is lacking, clear statement of best practice and a needs-led research agenda. Currently the such a system is unavailable for agrobiodiversity conservation but it would undoubtedly improve conservation planning and implementation.

To illustrate the point with a specific example for LR conservation, as discussed above LR conservation is often linked to securing a niche market for the LR and without such a niche market the current LR maintainers may switch production to modern cultivars. Wouldn't it be

useful if those planning LR conservation could look up the evidence base for methodologies for niche market promotion on a web site and find a systematic review of past evidence related to niche marketing that would help them decide how to implement a niche market for the LR they are trying to promote. The evidence-based link to CWR conservation is already established as CWR are wild plant species and evidence-based conservation is now widely used by the natural conservation community for planning plant conservation.

ANNEXES

Annex 1. ITPGRFA Annex 1 Priority crops¹⁹⁷

FOOD CROPS		
Crop	Genus	Observations
Breadfruit	<i>Artocarpus</i>	Breadfruit only
Asparagus	<i>Asparagus</i>	
Oat	<i>Avena</i>	
Beet	<i>Beta</i>	
Brassica complex	<i>Brassica</i> et al.	Genera included are: <i>Brassica</i> , <i>Armoracia</i> , <i>Barbarea</i> , <i>Camelina</i> , <i>Crambe</i> , <i>Diploaxis</i> , <i>Eruca</i> , <i>Isatis</i> , <i>Lepidium</i> , <i>Raphanobrassica</i> , <i>Raphanus</i> , <i>Rorippa</i> , and <i>Sinapis</i> ; this comprises oilseed and vegetable crops such as cabbage, rapeseed, mustard, cress, rocket, radish, and turnip; the species <i>Lepidium meyenii</i> (maca) is excluded
Pigeon Pea	<i>Cajanus</i>	
Chickpea	<i>Cicer</i>	
Citrus	<i>Citrus</i>	Genera <i>Poncirus</i> and <i>Fortunella</i> are included as root stock
Coconut	<i>Cocos</i>	
Major aroids	<i>Colocasia</i> , <i>Xanthosoma</i>	Major aroids include taro, cocoyam, dasheen and tannia
Carrot	<i>Daucus</i>	
Yams	<i>Dioscorea</i>	
Finger Millet	<i>Eleusine</i>	
Strawberry	<i>Fragaria</i>	
Sunflower	<i>Helianthus</i>	
Barley	<i>Hordeum</i>	
Sweet Potato	<i>Ipomoea</i>	
Grass pea	<i>Lathyrus</i>	
Lentil	<i>Lens</i>	
Apple	<i>Malus</i>	
Cassava	<i>Manihot</i>	<i>Manihot esculenta</i> only
Banana / Plantain	<i>Musa</i>	Except <i>Musa textilis</i>
Rice	<i>Oryza</i>	
Pearl Millet	<i>Pennisetum</i>	
Beans	<i>Phaseolus</i>	Except <i>Phaseolus polyanthus</i>
Pea	<i>Pisum</i>	
Rye	<i>Secale</i>	
Potato	<i>Solanum</i>	Section <i>tuberosa</i> included, except <i>Solanum phureja</i>
Eggplant	<i>Solanum</i>	Section <i>melongena</i> included

¹⁹⁷ FAO (2001)

FOOD CROPS		
Crop	Genus	Observations
Sorghum	<i>Sorghum</i>	
Triticale	<i>Triticosecale</i>	
Wheat	<i>Triticum</i> et al.	Including <i>Agropyron</i> , <i>Elymus</i> , and <i>Secale</i>
Faba Bean / Vetch	<i>Vicia</i>	
Cowpea et al.	<i>Vigna</i>	
Maize	<i>Zea</i>	Excluding <i>Zea perennis</i> , <i>Zea diploperennis</i> , and <i>Zea luxurians</i>

FORAGE CROPS	
Genera	Species
LEGUME FORAGES	
<i>Astragalus</i>	<i>chinensis</i> , <i>cicer</i> , <i>arenarius</i>
<i>Canavalia</i>	<i>ensiformis</i>
<i>Coronilla</i>	<i>varia</i>
<i>Hedysarum</i>	<i>coronarium</i>
<i>Lathyrus</i>	<i>cicera</i> , <i>ciliolatus</i> , <i>hirsutus</i> , <i>ochrus</i> , <i>odoratus</i> , <i>sativus</i>
<i>Lespedeza</i>	<i>cuneata</i> , <i>striata</i> , <i>stipulacea</i>
<i>Lotus</i>	<i>corniculatus</i> , <i>subbiflorus</i> , <i>uliginosus</i>
<i>Lupinus</i>	<i>albus</i> , <i>angustifolius</i> , <i>luteus</i>
<i>Medicago</i>	<i>arborea</i> , <i>falcata</i> , <i>sativa</i> , <i>scutellata</i> , <i>rigidula</i> , <i>truncatula</i>
<i>Melilotus</i>	<i>albus</i> , <i>officinalis</i>
<i>Onobrychis</i>	<i>viciifolia</i>
<i>Ornithopus</i>	<i>sativus</i>
<i>Prosopis</i>	<i>affinis</i> , <i>alba</i> , <i>chilensis</i> , <i>nigra</i> , <i>pallida</i>
<i>Pueraria</i>	<i>phaseoloides</i>
<i>Trifolium</i>	<i>alexandrinum</i> , <i>alpestre</i> , <i>ambiguum</i> , <i>angustifolium</i> , <i>arvense</i> , <i>agrocicerum</i> , <i>hybridum</i> , <i>incarnatum</i> , <i>pratense</i> , <i>repens</i> , <i>resupinatum</i> , <i>rueppellianum</i> , <i>semipilosum</i> , <i>subterraneum</i> , <i>vesiculosum</i>
GRASS FORAGES	
<i>Andropogon</i>	<i>gayanus</i>
<i>Agropyron</i>	<i>crisatum</i> , <i>desertorum</i>
<i>Agrostis</i>	<i>stolonifera</i> , <i>tenuis</i>
<i>Alopecurus</i>	<i>pratensis</i>
<i>Arrhenatherum</i>	<i>elatius</i>
<i>Dactylis</i>	<i>glomerata</i>
<i>Festuca</i>	<i>arundinacea</i> , <i>gigantea</i> , <i>heterophylla</i> , <i>ovina</i> , <i>pratensis</i> , <i>rubra</i>
<i>Lolium</i>	<i>hybridum</i> , <i>multiflorum</i> , <i>perenne</i> , <i>rigidum</i> , <i>temulentum</i>

FORAGE CROPS	
Genera	Species
<i>Phalaris</i>	<i>aquatica, arundinacea</i>
<i>Phleum</i>	<i>pratense</i>
<i>Poa</i>	<i>alpina, annua, pratensis</i>
<i>Tripsacum</i>	<i>laxum</i>
OTHER FORAGES	
<i>Atriplex</i>	<i>halimus, nummularia</i>
<i>Salsola</i>	<i>vermiculata</i>

Annex 2. Major and minor food crop genera¹⁹⁸

Genus	Genus	Genus
<i>Allium</i>	<i>Fortunella</i>	<i>Ribes</i>
<i>Ananas</i>	<i>Fragaria</i>	<i>Saccharum</i>
<i>Arachis</i>	<i>Glycine</i>	<i>Secale</i>
<i>Avena</i>	<i>Gossypium</i>	<i>Sesamum</i>
<i>Bertholletia</i>	<i>Helianthus</i>	<i>Setaria</i>
<i>Beta</i>	<i>Hordeum</i>	<i>Solanum</i>
<i>Brassica</i>	<i>Ilex</i>	<i>Sorghum</i>
<i>Cajanus</i>	<i>Ipomoea</i>	<i>Spinacia</i>
<i>Camellia</i>	<i>Juglans</i>	<i>Theobroma</i>
<i>Capsicum</i>	<i>Lablab</i>	<i>Tripsacum</i>
<i>Carica</i>	<i>Lactuca</i>	<i>Triticum</i>
<i>Carthamnus</i>	<i>Lens</i>	<i>Vavilovia</i>
<i>Chenopodium</i>	<i>Lupinus</i>	<i>Vicia</i>
<i>Cicer</i>	<i>Lycopersicon</i>	<i>Vigna</i>
<i>Citrullus</i>	<i>Malus</i>	<i>Vitellaria</i>
<i>Citrus</i>	<i>Mangifera</i>	<i>Vitis</i>
<i>Cocos</i>	<i>Manihot</i>	<i>Xanthosoma</i>
<i>Coffea</i>	<i>Musa</i>	<i>Zea</i>
<i>Colocasia</i>	<i>Olea</i>	
<i>Corylus</i>	<i>Oryza</i>	
<i>Cucumis</i>	<i>Panicum</i>	
<i>Cucurbita</i>	<i>Pennisetum</i>	
<i>Cynara</i>	<i>Persea</i>	
<i>Daucus</i>	<i>Phaseolus</i>	
<i>Digitaria</i>	<i>Phoenix</i>	
<i>Dioscorea</i>	<i>Pimenta</i>	
<i>Echinochloa</i>	<i>Piper</i>	
<i>Elaeis</i>	<i>Pistacia</i>	
<i>Elettaria</i>	<i>Pisum</i>	
<i>Eleusine</i>	<i>Potentilla</i>	
<i>Ensete</i>	<i>Prunus</i>	
<i>Ficus</i>	<i>Pyrus</i>	

¹⁹⁸ Groombridge and Jenkins (2002)

Annex 3. Consolidated list major and minor crop genera

Genus	Approx Sp No.	ITPGRFA (FAO 2001)	Groombridge and Jenkins (2002)
<i>Aegilops</i>	23	X	
<i>Agropyron</i>	15	X	
<i>Allium</i>	750		X
<i>Ananas</i>	1		X
<i>Arachis</i>	69		X
<i>Armoracia</i>	6	X	
<i>Artocarpus</i>	45	X	
<i>Asparagus</i>	120	X	
<i>Avena</i>	25	X	X
<i>Barbarea</i>	22	X	
<i>Bertholletia</i>	1		X
<i>Beta</i>	13	X	X
<i>Brassica</i>	40	X	X
<i>Cajanus</i>	34	X	X
<i>Camellia</i>	119	X	X
<i>Capsicum</i>	10		X
<i>Carica</i>	1		X
<i>Carthamnus</i>	55		X
<i>Chenopodium</i>	100		X
<i>Cicer</i>	44	X	X
<i>Citrullus</i>	4		X
<i>Citrus</i>	25	X	X
<i>Cocos</i>	1	X	X
<i>Coffea</i>	100		X
<i>Colocasia</i>	7	X	X
<i>Corylus</i>	18		X
<i>Crambe</i>	35	X	
<i>Cucumis</i>	52		X
<i>Cucurbita</i>	13		X
<i>Cynara</i>	8		X
<i>Daucus</i>	22	X	X
<i>Digitaria</i>	250		X
<i>Dioscorea</i>	630	X	X
<i>Diploaxis</i>	28	X	
<i>Echinochloa</i>	45		X
<i>Elaeis</i>	2		X
<i>Elettaria</i>	7		X

Genus	Approx Sp No.	ITPGRFA (FAO 2001)	Groombridge and Jenkins (2002)
<i>Eleusine</i>	9	X	X
<i>Elymus</i>	150	X	
<i>Ensete</i>	6	X	X
<i>Eruca</i>	1	X	
<i>Ficus</i>	850		X
<i>Fortunella</i>			X
<i>Fragaria</i>	330	X	X
<i>Glycine</i>	19		X
<i>Gossypium</i>	49		X
<i>Helianthus</i>	51	X	X
<i>Hordeum</i>	32	X	X
<i>Ilex</i>	400		X
<i>Ipomoea</i>	650	X	X
<i>Isatis</i>	50	X	
<i>Juglans</i>	20		X
<i>Lablab</i>	1		X
<i>Lactuca</i>	75		X
<i>Lathyrus</i>	160	X	
<i>Lens</i>	4	X	X
<i>Lepidium</i>	220	X	
<i>Lupinus</i>	220		X
<i>Lycopersicon</i>			X
<i>Malus</i>	40	X	X
<i>Mangifera</i>	60		X
<i>Manihot</i>	99	X	X
<i>Musa</i>	43	X	X
<i>Olea</i>	33		X
<i>Oryza</i>	24	X	X
<i>Panicum</i>	300		X
<i>Pennisetum</i>	80	X	X
<i>Persea</i>	200		X
<i>Phaseolus</i>	60	X	X
<i>Phoenix</i>	13		X
<i>Pimenta</i>	15		X
<i>Piper</i>	1050		X
<i>Pistacia</i>	9		X
<i>Pisum</i>	4	X	X
<i>Potentilla</i>			X

Genus	Approx Sp No.	ITPGRFA (FAO 2001)	Groombridge and Jenkins (2002)
<i>Prunus</i>	200		X
<i>Pyrus</i>	15		X
<i>Raphanus</i>	3	X	
<i>Ribes</i>	200		X
<i>Rorippa</i>	85	X	
<i>Saccarhum</i>	40		X
<i>Secale</i>	3	X	X
<i>Sesamum</i>	19		X
<i>Setaria</i>	130		X
<i>Sinapis</i>	7	X	
<i>Solanum</i>	1250	X	X
<i>Sorghum</i>	30	X	X
<i>Spinacia</i>	3		X
<i>Theobroma</i>	20		X
<i>Tripsacum</i>	12	X	X
<i>Triticosecale</i>			
<i>Triticum</i>	48	X	X
<i>Vavilovia</i>	1		X
<i>Vicia</i>	160	X	X
<i>Vigna</i>	104	X	X
<i>Vitellaria</i>	1		X
<i>Vitis</i>	65		X
<i>Xanthosoma</i>	57		X
<i>Zea</i>	16	X	X

Annex 4. FAO/Bioversity Multi-Crop Passport Descriptors V.2

Annex 5. Extended List of Ecogeographic Data Descriptors¹⁹⁹

FIELD NAME	DESCRIPTION	EXAMPLE
id	Record unique identifier	1
taxon_id	Taxon identifier for linkage with Species table (Vincent et al. 2012)	46
metadata_id	Metadata unique identifier	154
filename	Original filename holding the records	PH_finalformat_CK.xlsx
username	Username. Suggested format is [first letter of first name][lastname]	ncastaneda
collection	Name of the collection to which this specimen belongs	Plants of America
source	Source of the record. Takes any of the following values: -G: Germplasm bank -H: Herbaria	H
is_expert	Use value 1 if record was provided by expert	1
institute_name	Name of institute where specimen was seen	Smithsonian Institute
institute_id	ID of institute where specimen seen Use valid herbarium and genebank standard codes.	US
provider_name	Name of institute that provided the record	
provider_institute_id	ID of institute that provided the record Use valid herbarium and genebank standard codes.	CIAT
source_url	Source URL if coming from internet	http://www.si.edu
unique_number	Code given by the institution to each specimen/accession stored	DC34566
image	Path where the picture is stored	US/Priority/Vigna/IMG6578.JPG
barcode	Barcode of the specimen or sample	A0928873874
vno_1	Any other identifier in the specimens	9876
vno_2	Any other secondary identifier in the specimens	
botrecat	Sight record or vouchered record	Voucher

x1_family	The family name appropriate to the genus name field, entered in full with capitalization of the first letter only. If the family is unknown leave blank.	Fabaceae
x1_genus	Generic name should be entered in full with the first letter capitalized.	Vigna
x1_sp1	The species epithet of the plant must be entered in full, all lowercase, no embedded spaces. It may contain one or two hyphens. If the plant represents a new species that has not been formally described, then sp. nov., sp. A, sp. 1 (or other acceptable codes) should be entered, if possible followed by a unique identifier, such as the collector's name and number or the locality.	angularis
x1_author1	Use standard author names as given in IPNI	(Willd.) Ohwi & Ohashi
x1_rank1	Enter the rank of the second specific epithet if there is one.	
x1_sp2	The species epithet of the plant must be entered in full, all lowercase, no embedded spaces. It may contain one or two hyphens. If the plant represents a new species that has not been formally described, then sp. nov., sp. A, sp. 1 (or other acceptable codes) should be entered, if possible followed by a unique identifier, such as the collector's name and number or the locality.	
x1_author2	Use standard author names as given in IPNI	
x1_rank2	Enter the rank of the second specific epithet if there is one.	

¹⁹⁹ Castañeda Álvarez *et al.* (2011)

x1_sp3	As for second species epithet (see field x1_sp1)	
x1_author3	Use standard author names as given in IPNI	
x1_detby	Name of most recent determinator (name of a person). This field is used to store the name of the botanist who last named the specimen. The format is "surname, initials". Use a ; to separate two names.	Maxted
x1_detdate	The format should be: YYYY-MM-DD Also this format: YYYY/MM/DD	
x1_detdd	Day of most recent determination	12
x1_detmm	Month of most recent determination	10
x1_detyy	Year of most recent determination	1980
x1_detstat	Determination source: determinator or folder	Specimen
x2_family	(See field x1_family)	Fabaceae
x2_genus	(See field x1_genus)	Vigna
x2_sp1	(See field x1_sp1)	unguiculata
x2_author1	(See field x1_author1)	
x2_rank1	(See field x1_rank1)	
x2_sp2	(See field x1_sp2)	
x2_author2	(See field x1_author2)	
x2_rank2	(See field x1_rank2)	
x2_sp3	(See field x1_sp3)	
x2_author3	(See field x1_author3)	
x2_detby	Name of penultimate determinator. The format is "surname, initials". Use a ; to separate two names.	Maxted
x2_detdate	The format should be: YYYY-MM-DD Also this format: YYYY/MM/DD	
x2_detdd	Day of penultimate determination	5
x2_detmm	Month of penultimate determination	6
x2_detyy	Year of penultimate determination	1965
x2_detstat	(See x1_detstat)	Specimen
x3_family	(See field x1_family)	
x3_genus	(See field x1_genus)	
x3_sp1	(See field x1_sp1)	
x3_author1	(See field x1_author1)	
x3_rank1	(See field x1_rank1)	
x3_sp2	(See field x1_sp2)	
x3_author2	(See field x1_author2)	
x3_rank2	(See field x1_rank2)	
x3_sp3	(See field x1_sp3)	
x3_author3	(See field x1_author3)	
x3_detby	Name of antepenultimate determinator. The format is "surname, initials". Use a ; to separate two names.	
x3_detdate	The format should be: YYYY-MM-DD Also this format: YYYY/MM/DD	
x3_detdd	Day of antepenultimate determination	
x3_detmm	Month of antepenultimate determination	
x3_detyy	Year of antepenultimate determination	
x3_detstat	(See x1_detstat)	

annotated_specimen	Boolean field (1 if annotated, 0 if not)	1
collector	Name of collector (name of a person)	Maxted, N.
addcoll	Name of any additional collectors	
collnumber	collnumber = prefix + number + suffix	
prefix	Collection prefix	F
number	Collection specimen ID	310
suffix	Collection suffix if any	C
colldate	colldate = colldd, collmm, collyy	
colldd	Collection day	3
collmm	Collection month	7
collyy	Collection year	1954
country	Country of collection	Ethiopia
old_country		
iso2	This is the ISO of the country that is linked to Countries table	ETH
adm1	Name of the state/province where specimen was collected	Affar
adm2	Name of the county/district/municipality where specimen was collected	Asaita
adm3	Further administrative level details (level 3)	
adm4	Further administrative level details (level 4)	
local_area	Recognized areas smaller than county/district (i.e., national park, forest reserves, river deltas)	

locality	Full locality description	Asaita, 5km to the office of the Mile Serdo Wildlife Reserve
coord	Any provided coordinates (any system)	
lat_deg	Latitude (degrees)	9
lat_min	Latitude (minutes)	2
lat_sec	Latitude (seconds)	0
ns	North or South (N or S)	N
latitude	Latitude in decimal degrees	9033333
long_deg	Longitude (degrees)	38
long_min	Longitude (minutes)	42
long_sec	Longitude (seconds)	0
ew	East or West (E or W)	E
longitude	Longitude in decimal degrees	38.7
llorig	Latitude/Longitude original source	Specimen
lldatum	Latitude/Longitude datum (i.e., WGS84)	WGS84
alt	Altitude at which specimen was observed	100
alt_max	Maximum altitude (if a range is specified, then the MIN should be in the "alt" field)	120
habitat_txt	Description of habitat	Occurs in grasslands
cult_stat	weedy, cultivated, wild	Wild
origin_stat	Native, introduced, naturalized	Native
soil	Description of soil conditions at site if available	Deep soils
slope	Slope of site if available	Around 20 degrees slope

aspect	Aspect of site if available	Hilly and steep
plant_description	Free text description of the plant, including info as: Life Form; Size; Leaves; Stems; Flowers; Fruits; Bark; other unique characters	Purple flowers
frequency	How abundant is the specimen at the collection site?	Very abundant in the collecting site
fl_code	Flowering information	1
fr_code	Fruiting information	1
info_graminea	Phenological information (only for Graminae/Poaceae)	0
vernacular	Vernacular (common) name	Cowpea
language	Language or tribal name of common name	
uses	Uses as recorded on label	Fodder, medicinal
type_memo	Type info is different from determinant	
voucher_id	ID of the voucher specimens	US897505
notes	Any additional info on the label	Seeds stored in the fridge
dups	Any other known herbarium codes	K, BM, COL
availability	Availability of germplasm (Is the accession truly available to the public?)	0
field_collected_data	Boolean field (1=yes, 0=no). Specifies if this specimen is the product of a field visit of this project.	1

data_public_access	Boolean field (1= yes, 0=no). This field will be used to specify whether the record can be available or not to the general public. This will be filled according to data-donor agreement.	1
type	If this is a Type (Type = Y; not a Type = N)	0
comments	Use in case you need to register any issue in the digitization of the specimen	All specimens were collected under the funding of the Global Crop Diversity Trust