INTERACTIVE TOOLKIT FOR CROP WILD RELATIVE CONSERVATION PLANNING version 1.0

2017

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Based on Maxted N, Magos Brehm J and Kell S (2013) Resource Book for the Preparation of National Plans of Crop Wild Relatives and Landraces. Food and Agriculture Organization of the UN, Rome, Italy.

Front cover page (clockwise from top left):

Oryza rufipogon Griffin., Laos (Bao-Rong Lu)

Lupinus angustifolius L., Spain (José Iriondo)

Solanum lichtensteinii Willd., South Africa (Livhuwani Auldrean Nkuna)

Coffea mauritiana Lam., Mauritius (Ehsan Dulloo)

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SUMMARY

The Convention on Biological Diversity (CBD), the International Treaty on Plant Genetic Resources for Food and Agriculture (ITPGRFA), the Global Strategy for Plant Conservation (GSPC) and the 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 related to crops and possess beneficial traits that can be bred into new crop cultivars to help agriculture withstand changing environmental conditions and market demands.

CWR are vital plant genetic resources that, if efficiently preserved and sustainably used, can increase food security, alleviate human poverty and improve ecosystem stability. However, their diversity is currently threatened by human environmental mismanagement and socio-political pressures, and is being irreversibly eroded and lost. Despite this, the conservation of these resources remains largely neglected by conservation and agricultural agencies. CWR diversity can be conserved using a range of techniques applied at local, national, regional and global administrative levels. Whichever technique is used and regardless of the administrative level selected for study, it is important that the approach taken is well coordinated to ensure resource conservation is maximized and available for exploitation.

At the national level, CWR conservation planning has so far taken place in only a few countries and only a small number of national strategic action plans (or national strategies) have been developed. Furthermore, systematic implementation of national CWR conservation actions is still very scarce. Thorough CWR conservation planning, together with the use of indicators to assess the efficiency of conservation actions will provide a step change in agrobiodiversity conservation. It will also complement, and make a significant contribution to, local and global goals. The *Interactive Toolkit for CWR Conservation Planning* places particular emphasis on how national strategic action plans (or national strategies) for CWR 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 CWR checklists, (b) prioritization of taxa for active conservation and creation of priority CWR inventories, (c) collation of taxonomic, ecogeographic, genetic and threat data, (d) diversity (distribution, genetic and ecogeographic) analyses, (e) novel IUCN Red Listing threat assessments, (f) *in situ* and *ex situ* gap analyses, (g) climate change analyses of priority CWR, (h) establishment and implementation of complementary *in situ* and *ex situ* conservation recommendations, (i) monitoring of conserved diversity and (j) making the critical link between conservation and use, to ensure the conserved resources are sustainably exploited. Each of these ten stages is a key component in developing and implementing a national strategic action plan.

The Toolkit is divided into four parts. Part 1 provides an introduction to the toolkit. Part 2 defines CWR and describes their value, threats, conservation status and policy context. Part 3 briefly summarizes how a national strategic action plan for CWR conservation and sustainable use can be developed. Finally, Part 4 includes different modules, each corresponding to individual steps in the CWR conservation planning process. Each module contains an overview of the planning step, a recommended methodology, possible challenges and suggested solutions to help overcome them (discussed using applied examples), a list of references used in the text and additional materials that can be used to help the user achieve that particular conservation planning step.

ACKNOWLEDGEMENTS

The **Interactive Online Toolkit for CWR Conservation Planning** is based on the publication Resource Book for the Preparation of National Plans for Conservation of Crop Wild Relatives and Landraces published by the Food and Agriculture Organization of the United Nations (FAO). The Resource Book was then transformed to an interactive and online version in the context of the project In situ *Conservation and Use of Crop Wild Relatives in Three ACP Countries of the SADC Region* project (SADC Crop Wild Relatives for short) co-funded by the European Union and implemented through the ACP-EU Co-operation Programme in Science and Technology (S&T II by the ACP Group of States (grant agreement no. FED/2013/330-210).

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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, Valeria Negri, Renzo Torricelli, Joana Magos Brehm, Bao-Rong Lu, Ehsan Dulloo, Achille Ephrem Assogbadjo, Edwin Chiwona, Shelagh Kell, John Wiersema, Tania Carolina Camacho-Villa, Suzanne Sharrock, Nadiya Al-Saadi, Sónia Dias, Nigel Maxted and Heli Fitzgerald.

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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

1 HOME PAGE

The **Interactive Toolkit for Crop Wild Relative Conservation Planning** is designed to provide guidance to plan and implement active *in situ* and *ex situ* conservation of CWR at national level. The conservation recommendations that result from this national CWR conservation planning process are used to develop National Strategic Action Plans (NSAP) (or National Strategies) for the conservation and sustainable use of CWR (to know more about NSAP development, click here).

There is no single method for planning CWR conservation or for developing an NSAP for the conservation of CWR. This is mainly due to factors concerning financial resources, availability of baseline biodiversity data, the country where the NSAP is to be implemented, as well as the focal area and remit of the agencies that are responsible for formulating and implementing the NSAP. Nevertheless, CWR conservation planning can be viewed as a series of steps and decisions that follow the same basic pattern in all countries. This Toolkit and its protocols, examples and resources should thus be viewed as a framework and an aid for planning CWR conservation, not a prescription. It is important to note that the Toolkit can be used for the entire conservation planning process or for individual steps, and that the steps do not necessarily have to be followed in the same order.

BOX 1 WHO THE TOOLKIT IS FOR

Three different groups of users may access and use this Toolkit:

- FAO national focal points.
- Agencies responsible for planning and implementing national strategies, such as national agricultural or environmental agencies.
- NGOs (e.g. farmers' organizations), local institutions (e.g. genebanks, universities, research institutes) and individual scientists.

The mechanisms of delivering the Toolkit to its users and how it can fit into the wider context of PGRFA conservation is illustrated below.

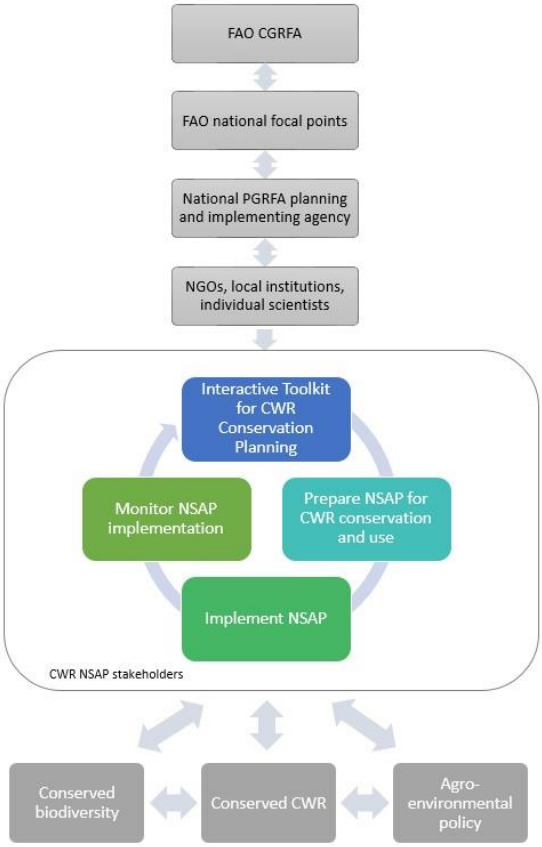


Figure 1 NSAP formulation and implementation and users of the Toolkit.

BOX 2 HOW TO USE THE TOOLKIT

The Toolkit can be used either online or offline. To use it offline, the full content of the Toolkit can be exported by clicking the EXPORT button which appears on the top-right of every page.

Please be aware that in order to access the modules of the Toolkit you will need to register using your email address and to provide some information about the country in which you are based for work, the type of organization you work for and the purpose for using the Toolkit. These data are for statistical purposes only. Once you have registered you can access the Toolkit any time you require using your email address.

The Toolkit is designed as a sequential but flexible process. It is advisable, however, that you first introduce yourself to CWR and to NSAP and then move onto the Toolkit itself and start with the first module on National CWR conservation planning which briefly explains how CWR conservation planning can be undertaken. You can then move onto the different nodules bearing in mind that each individual module corresponds to a particular step in the conservation planning process.

The Toolkit is divided into 12 sections, each of which corresponds to a step in the national CWR conservation planning process. Each section provides a brief introduction to the corresponding step and is then divided into:

(i) Methodology:

- Briefly outlines the different phases for that particular conservation planning step.
- Includes an interactive flowchart (shown by default), which is the central element of this Toolkit. The flowchart is composed of a series of yes/no questions, helping the user move through the various phases and choose the options that are most appropriate given the user's national context. Detailed explanations of each phase are linked to the interactive flowchart and are accessible by clicking on the shapes of the flowchart. In addition, there is a static version of the flowchart which can be consulted at any time and a full written text that exactly matches the information presented in the flowchart.

(ii) Examples and applied use:

- Makes reference to case studies showcasing how that particular CWR conservation planning step has been undertaken.

(iii) References:

- Lists the references used in the preparation of the various texts from the section.

(iv) Additional materials and resources:

- Includes supplementary materials relevant to the section, providing tools and extra practical examples to help the user visualize and understand how to undertake that particular conservation planning step. These materials include:

Books, scientific papers, grey literature.

PowerPoint presentations.

Projects.

Recordings, video files.

Software tools.

WWW

Web links.

Social networks.

2 CROP WILD RELATIVES

Crop wild relatives (CWR) are **wild plant taxa closely related to crops**. They have an indirect use as gene donors for crop improvement due to their relatively close genetic relationship to crops. They are therefore an important socio-economic resource that offers the novel genetic diversity required to maintain future food security. 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 concept, has been proposed as follows: ‘‘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'' (Maxted *et al.* 2006).

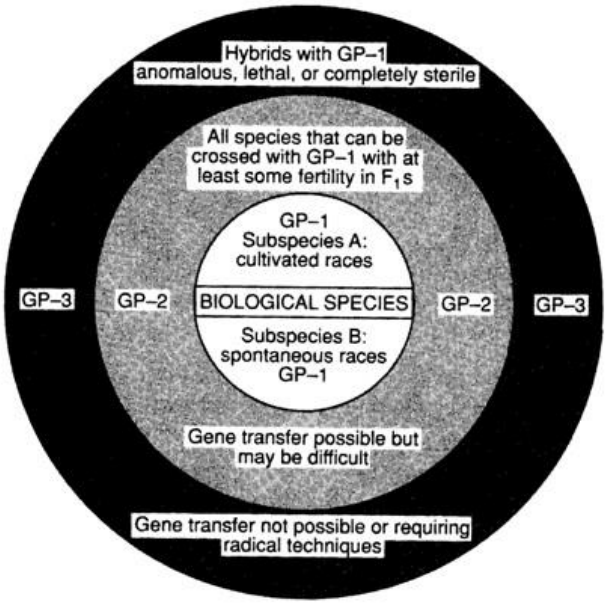


Figure 2 Gene Pool concept: GP1A–cultivated forms of the crop, GP1B-wild or weedy forms of the crop, GP2–secondary wild relatives (less closely related species from which gene transfer to the crop is possible but difficult using conventional breeding techniques), GP3–tertiary wild relatives (species 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).

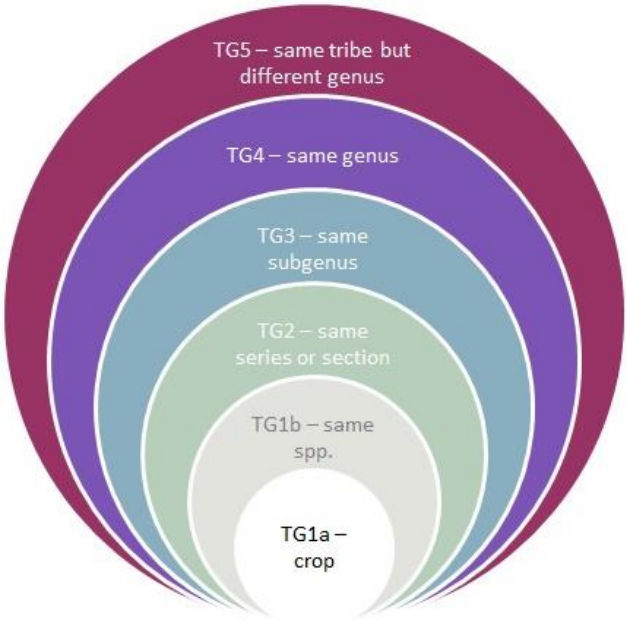


Figure 3 Taxon Group concept: TG1a–crop, TG1b–same species as crop, TG2–same series or section as crop, TG3–same subgenus as crop, TG4-same genus (Maxted *et al.* 2006).

2.1 IMPORTANCE OF CWR

CWR 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—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 (see Hajjar and Hodgkin 2007, Maxted and Kell 2009 for reviews). CWR diversity thus constitutes an important plant genetic resource for food and agriculture that is available for utilization by national, regional and international stakeholders, and which forms the basis of food and livelihood security (Maxted *et al.* 2011). In addition, like any other wild species, CWR are also components of natural and semi-natural ecosystems, and also play a role in ecosystem functioning and in broader environmental sustainability and the maintenance of ecosystem services.

Why should we utilize more and more CWR diversity?

- 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 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.

- Globally, agriculture is being practised 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 CWR diversity.
- There is a continuous and growing demand from breeders for novel diversity to be used in the development of new varieties due to the relatively short-term commercial lifespan of modern cultivars (usually 5–10 years).
- 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 fewer problems with the transfer of unwanted characteristics from exotic CWR material.
- 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.

Figure 4 *Allium altaicum* Pall., in Tien Shan (China) in 2009; it is a tertiary wild relative of common onion (*A. cepa* L.) and primary wild relative of brunching onion (*A. fistulosum* L.), it is also a taxon group 3 relative of Chinese onion (*A. chinense* G.Don.) and of chives (*A. schoenoprasum* L.). (Photo: Vojtech Holubec)

How can current crop varieties cope with changing environments?

While climate change will directly impact CWR diversity, it will also alter the agro-environmental conditions under which our crops grow and will augment the risk of pest and disease spread, thus impacting 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 the wide range of conditions to which they are adapted (FAO 2008). Nevertheless, climatic change can lead to non-analogous climate conditions and their consequences are thus difficult to predict. Therefore, **CWR 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**.

BOX 3 USE OF CWR DIVERSITY IN CROP IMPROVEMENT

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 crop productivity, disease resistance, and tolerance to various environmental conditions, for which CWR are potential sources (Heywood 1997). 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 diversity in the improvement and creation of new varieties.

CWR thus present a tangible resource of actual or potential economic benefit for humankind at national, regional and global levels. Exploitation of its 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 CWR.

Tanksley 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. They also avoided transfer into polyploid crops where transfer was more difficult (e.g. rice, sorghum and sweet potato). The use of CWR diversity in crop improvement programmes for 29 major crops has 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 (see Figure below). The review showed that the degree to which breeders use CWR varies between crops, with CWR use being particularly prominent in barley, cassava, potato, rice, tomato and wheat improvement. Rice and wheat are 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 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 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.

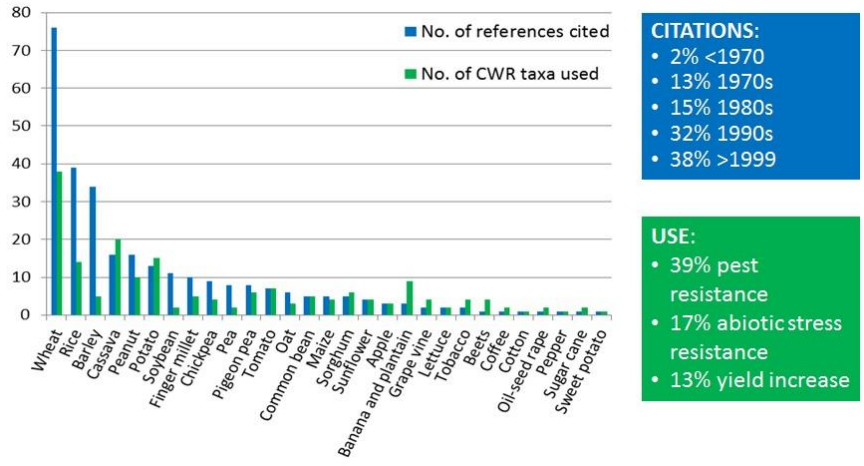


Figure 5 Number of references citing the use of CWR in crop improvement (Maxted and Kell 2009).

BOX 4 WHAT IS THE MONETARY VALUE OF CWR?

The particular food security value of CWR has been recognized at least since Darwin discussed their study and conservation (Darwin 1868), but it was Vavilov (1926) who was the first to promote their systematic conservation in practical terms. However, CWR conservation have 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, it has been estimated 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). 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).

A recent study commissioned by the Millennium Seed Bank Partnership, Kew (MSB), and carried out by PricewaterhouseCoopers (PwC), UK, has estimated that the **wild relatives of 29 crops prioritized by the MSB have a value of $42 billion, with a potential of $120 billion in the future in terms of their potential for improving productivity or stress resistance in commercial crops** (PwC 2013). If maize, soya bean and sugarcane are included, the current and potential values increase to $68 billion and $196 billion, respectively. These results were based on analyses from seed development to farmgate sales of four crops (wheat, rice, potato, and cassava) and extrapolated to the target 29 crops.

Figure 6 *Aegilops tauschii* Coss., a secondary wild relative of bread and durum wheat, as well as a number of other cultivated wheats; it is a drought-tolerant species and a possible gene source for pest and disease resistance; it has contributed traits to bread wheat for good baking qualities and winder hardiness. (Photo: Vojtech Holubec)

2.2 THREATS AFFECTING CWR

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 (spread of allelic diversity) of common local alleles, or the loss of combinations of alleles over time in a defined area**. Genetic erosion can affect **wild populations** but can also affect **populations conserved *in situ* and accessions conserved in *ex situ* collections** (i.e. when the *ex situ* collection goes through the regeneration process and accessions are inadvertently selected to suit the regeneration site). It is important to distinguish between genetic changes that are detrimental to populations and the 'normal' background levels of change. Any loss of diversity through genetic erosion means the individual is less likely to be able to adapt to a changing environment and means that potentially useful traits will be unavailable to the breeder.

Figure 7 Habitat of *Vicia bithynica* (L.) L., a tertiary wild relative of faba bean and potential gene source for rust resistance and other diseases, being invaded by *Carpobrotus edulis* ((L.) N.E.Br. in Ericeira, Portugal. (Photo: Joana Magos Brehm)

Why are CWR threatened?

There are numerous factors that negatively impact wild plant populations (including CWR) resulting in genetic erosion, and potentially the 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).
- Habitat destruction, degradation, homogenization 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, hybridize with, cause physical or biological damage to, or kill native species).
- Natural calamities (floods, landslides, soil erosion etc.).

- Climate change (which is expected to directly affect phenology and lead to extinction of wild plant species, particularly in drier regions where certain CWR may already be at the edge of their distribution) (e.g. Parmesan and Yohe 2003, Root *et al.* 2003, Thuiller *et al.* 2005, Jarvis *et al.* 2008, Lenoir *et al.* 2008).
- Lack of education and awareness of the importance of CWR and the need to conserve them.
- War and political instability.
- Lack of knowledge regarding CWR breadth, location and real use potential.
- Lack of conservation action for CWR. For instance, 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.
- Environmental mismanagement.

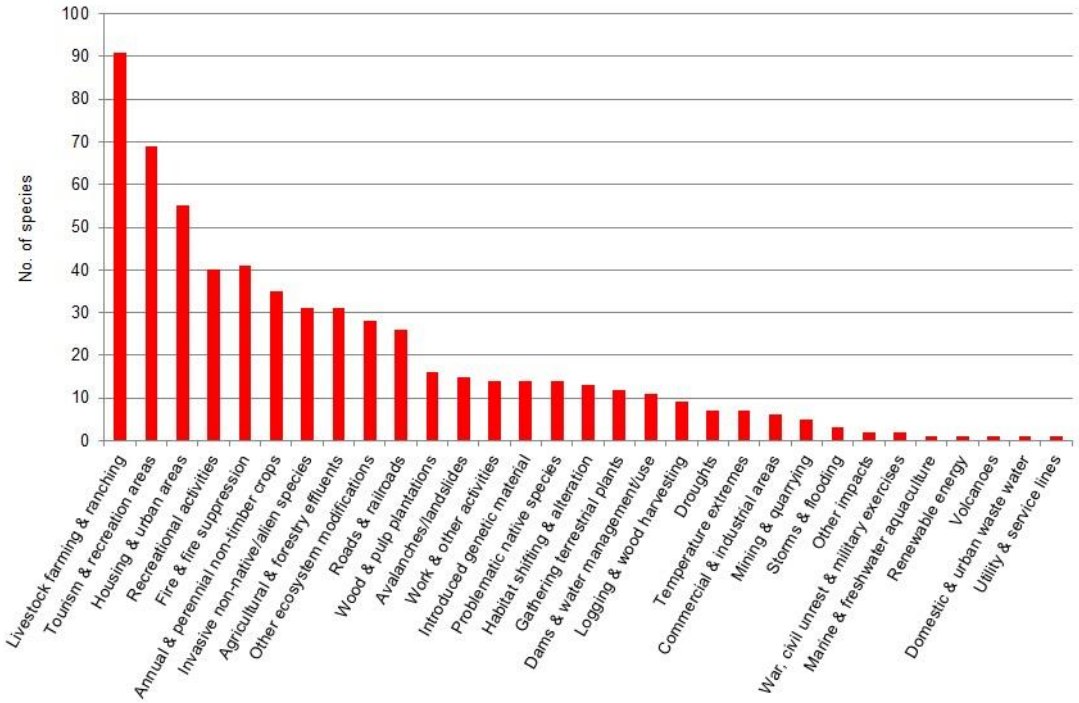


Figure 8 Major threats that affect European CWR (source: Kell *et al.* 2012).

What are the concrete 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 which implies inability to adapt to changing environmental conditions.
- A decrease in the availability of genes and alleles that may confer microhabitat adaptation, disease and pest resistance, yield enhancement traits etc., for crop improvement (e.g. to develop better or newly adapted varieties), which will restrict breeder's options and have a fundamental impact on future food security.

BOX 5 THREAT ASSESSMENT OF CWR DIVERSITY—CURRENT STATUS

Significant progress has been made in assessing the loss of botanical diversity, particularly in regions where the flora is well known. It has been estimated that about 268,000 flowering plant taxa exist globally and, of these, 19,206 were assessed as part of the IUCN Red List by 2015 with 10,551 of them classified as threatened. At European level, there are over 20,000 flowering plants (Euro+Med Plantbase 2006–2011), of which 11,117 were assessed for the IUCN Red List by 2015.

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). A review of Red List assessments using the current and most detailed IUCN Red List Categories and Criteria (IUCN 2001) showed that, of the 25,000 CWR species present in Europe, less than 1% had been assessed by 2008 (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, because 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 also likely to be threatened. More specifically, for European CWR, an IUCN Red List assessment was recently undertaken for 591 European CWR species representing 25 crop gene pools/groups (Bilz *et al.* 2011). It found that 11.5% (66) of the 591 species are considered to be threatened, with 3.3% (19) Critically Endangered, 4.4% (22) Endangered and 3.8% (25) Vulnerable—a further 4.5% (26) of the species are classified as Near Threatened.

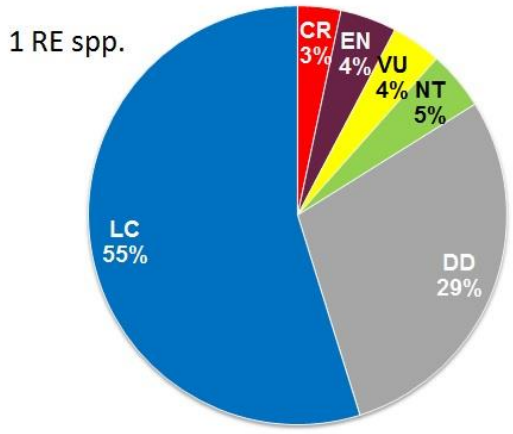


Figure 9 Red list assessment of European CWR (source: Kell *et al.* 2012).

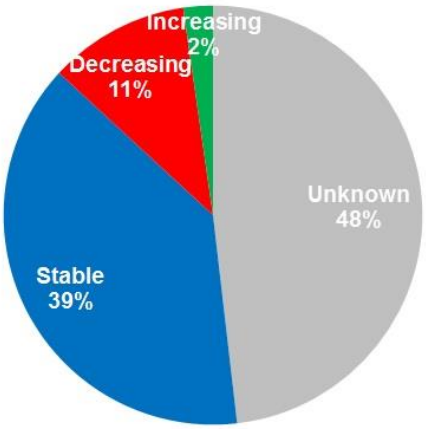


Figure 10 Population trends of European CWR (source: Kell *et al.* 2012).

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. Ecogeographic data for 36 CWR genera and over 310 CWR species were then collated and threat assessments undertaken. It was found that 14.6% (45) of the species are considered threatened, with 2.3% (7) 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.

BOX 6 CWR AND CLIMATE CHANGE

Climate change is predicted to have a great impact on diversity (Thomas *et al.* 2004). Global mean surface temperature is predicted to rise by 0.3–0.7°C between 2016–2035 (IPCC 2013), with the highest prediction set at a rise of 4.8˚C for the year 2100 compared to current mean temperatures (Prather *et al.* 2013), causing considerable disturbance to regional and seasonal patterns of precipitation. 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 on ecosystems and species, including significant range shifts towards the poles or upwards in altitude with gradual earlier spring events (e.g. Parmesan and Yohe 2003, Root *et al.* 2003, Lenoir *et al.* 2008, Thomas *et al.* 2012).

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. Additional 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 1,350 plant species and concluded that more than half of the species are predicted to be threatened by extinction by 2080 if they are unable to disperse. On the other hand, plant taxa have the ability to respond to climatic changes, and this has been evident in the large-scale distribution shifts already observed in the Quaternary period (Huntley 1990). 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.

Looking specifically at CWR, a comparative study of the likely impact of climate change on three crop gene pools (Jarvis *et al.* 2008) found 16–22% of CWR species are likely to be extinct by 2055. Furthermore, it is predicted that the majority of species will lose greater than 50% of their current distributional range and that the range that remains will be highly fragmented.

The effect of climate change will have direct consequences on the establishment of *in situ* and *ex situ* conservation priorities and the active management of CWR. For *in situ* conservation this means accommodating plant distribution range shifts when selecting new areas for active conservation. It will also involve upgrading the current, highly static protected area system to incorporate both current and future projected distributions (Midgley *et al.* 2003). For *ex situ* conservation it may mean prioritizing for collection those populations that are likely to be negatively affected by climate change and/or those at the edge of species distributions to try and capture the genetic diversity that is under threat.

2.3 *IN SITU* AND *EX SITU* CONSERVATION OF CWR

Systematic conservation of CWR diversity involves the complementary application of *in situ* and *ex situ* strategies. The precise combination of *in situ* and *ex situ* techniques will vary according to the taxon being conserved, resources available for conservation and the potential value and use of the species.

***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). For wild taxa such as CWR, *in situ* conservation involves the establishment of genetic reserves. Genetic reserve establishment 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.* 2008b).

Since the inception of the CBD, *in situ* conservation has been indentified as the primary conservation strategy, with *ex situ* employed as a backup. This is because, in contrast to *ex situ* conservation, *in situ* conservation promotes natural gene exchange and continued evolution of CWR populations (CBD 1992, Maxted *et al.* 1997a, FAO 2001, Heywood and Dulloo 2005, Stolton *et al.* 2006).

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 can be established.

***Ex situ* conservation**: 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).

Figure 11 Erebuni State Reserve (Armenia), a genetic reserve dedicated to the conservation of wild wheat, including *Triticum urartu* Tumannian ex Gandilyan, *T. boeoticum* Boiss., *T. araraticum* Jakubz and *Aegilops* spp. (Photo: René Hauptvogel)

Figure 12 *Ex situ* conservation of CWR (project 'Adapting agriculture to climate change: collecting, protecting and preparing crop wild relatives' led by the Global Crop Diversity Trust and the Royal Botanic Gardens, Kew, UK) at the António Luís Belo Correia Seed Bank (National Museum of Natural History, University of Lisbon, Portugal). (Photo: Sara Lobo Dias)

Are CWR already conserved?

Both the *in situ* and *ex situ* conservation of CWR is currently inadequate.

***In situ* conservation**:

- CWR are found in existing protected areas but are not monitored or actively managed.
- There are very few examples of active *in situ* CWR conservation.
- The *Second Report on the State of the World's Plant Genetic Resources for Food and Agriculture* (SoWPGR-2) (FAO 2010a) highlights the relatively little progress made in conserving wild PGRFA outside protected areas.

***Ex situ* conservation**: although efforts to conserve PGRFA have historically been focussed on *ex situ* conservation (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), the SoWPGR-2 has noted that while the total number of *ex situ* accessions has increased since the first report (FAO 1998), CWR diversity is still under-represented. For example, only about 7.6% of *ex situ* PGR accessions reported by EURISCO are from wild populations (137,639 out of a total of about 1,800,000 accessions).

BOX 7 EXAMPLES OF CWR GENETIC RESERVES

The list below presents positive examples of *in situ* CWR conservation. Nevertheless, 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 in the quality standards for genetic reserve conservation of CWR (Iriondo *et al.* 2008, 2012).

Armenia

- Erebuni State Reserve (89 ha) – wild wheat, including *Triticum urartu*, *T. boeoticum*, *T. araraticum* and *Aegilops* spp. (Avagyan 2008).

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) (Mulongoy and Gidda 2008).

Costa Rica

- Corcovado National Park (47,563 ha) – avocado (*Persea americana*), nance (*Byrsonima crassifolia*) and sonzapote (*Licania platypus*) (Mulongoy and Gidda 2008).
- Central Valley – wild bean populations (*Phaseolus* spp.) (Zoro Bi *et al.* 2003, Baudoin *et al.* 2008).

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*) (Mulongoy and Gidda 2008).

India

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

Iran

- Touran protected area which comprises a national park and a biosphere reserve (1,102,080 ha) – wild relatives of barley (*Hordeum* spp.) (Mulongoy and Gidda 2008).

Israel

- Amniad reserve, eastern Galilee (380 ha) – wild emmer wheat (*Triticum dicoccoides*), *Hordeum spontaneum*, *Beta vulgaris* and *Olea europaea* as well as a rich grassland (with > 400 spp.) (Anikster *et al.* 1997, Safriel *et al.* 1997, Kaplan 2008).

Kyrgyzstan

- Besh-Aral State Nature Reserve (63,200 ha) – walnut (*Juglans regia*) forests as well as a great diversity of other species such as wild pear and plum (*Prunus sogdiana*) (Mulongoy and Gidda 2008).

Mascarene Islands

- Wild *Coffea* species (Dulloo *et al.* 1999).

Mexico

- MAB Sierra de Manantlán Biosphere Reserve – perennial and close wild relative of maize endemic to southwest Mexico (*Zea diploperennis*) (UNESCO 2007).

Palestine

- Wadi Sair Genetic Reserve – for forage legumes, fruit trees and vegetable CWR (Al-Atawneh *et al.* 2013).

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; it conserves *Solanum jamesii*, *S. fendleri* and other *Solanum* spp. (Bamberg in Pavek *et al.* 1999, Mulongoy and Gidda 2008).

Portugal

- Madeira archipelago – *Beta patula* (Pinheiro de Carvalho *et al.* 2012).

Syria

- Sale-Rsheida Reserve – *Triticum dicoccoides* and *Hordeum* spp. (Al-Atawneh *et al.* 2008).

Turkey

- Beydaglari Coast National Park (34,425 ha) – contains the rare endemic relative of the faba bean (*Vicia eristalioides*) (Mulongoy and Gidda 2008).
- Bolkar Mountains – five genetic reserves for *Pinus brutia*, *P. nigra* subsp. *pallasiana*, *Cedrus libani*, *Abies equi-trojani*, *Juniperus excelsa* and *Castanea sativa* (Tan 1998, Tan and Tan 2002).
- Ceylanpinar State Farm – seven genetic reserves for wild wheat relatives (*Aegilops* spp., *Triticum* spp.) (Karagöz 1998).
- Kaz Daĝ National Park – ten genetic reserves for wild plum (*Prunus divaricata*), chestnut (*Castanea sativa*), *Pinus brutia*, *P. nigra* and *Abies equi-trojani* (Tan 1998, Tan and Tan 2002).

United States of America

- Central-Southeast USA – *Vitis rupestris*, *V. shuttleworthii*, *V. monticola* (Pavek *et al.* 2003).
- Nevada – *Lathyrus grimesii* (Hannan and Hellier in Pavek *et al*. 1999).
- Organ Pipe Cactus National Monument (133,925 ha) – small populations of wild chilli peppers (*Capsicum annuum*) (Mulongoy and Gidda 2008).
- Southern States of the USA – *Carya floridana* and *C. myristiciformis* (Grauke in Pavek *et al.* 1999).
- Washington State – *Allium columbianum*, *A. geyeri* and *A. fibrillum* (Hannan and Helliern in Pavek *et al*. 1999, Hellier 2000).

Uzbekistan

- Chatkal Biosphere State Reserve – *Amygdalus bucharica*, primary wild relative of *Prunus dulcis* (Hunter and Heywood 2011).
- Nurata Mountain Walnut State Reserve – walnut (*Juglans regia*) (Hunter and Heywood 2011).

Vietnam

- Huu Lien Nature Reserve – litchi, longan, *Oryza*, *Citrus* spp. and rice bean (Hunter and Heywood 2011).
- Ngoc Hoi – *Citrus*, *Oryza* and *Alocasia* spp. (Hunter and Heywood 2011).

BOX 8 CHALLENGES IN NATIONAL CWR CONSERVATION—AGRICULTURE AND BIODIVERSITY COMMUNITIES

The national conservation of CWR 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. CWR conservation is unique in the sense that it is the shared responsibility of multiple stakeholders and it is now widely recognized 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. There is, therefore, 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. In this real sense, the approach to CWR conservation is holistic.

BOX 9 WHY NOT JUST DO *EX SITU* CONSERVATION?

In situ and *ex situ* are different conservation strategies with their own advantages (Table 1).

Table 1 Advantages of *in situ* and *ex situ* conservation strategies.

***IN SITU* ADVANTAGES**	***EX SITU* ADVANTAGES**
Appropriate for all organisms	Efficient and reproducible for many species
Dynamic conservation in relation to environmental changes	Medium and long-term storage is feasible
Permits species/pathogen interactions, so continuing dynamic evolution is possible especially concerning resistance to pests and diseases	Greater diversity of target taxa can be conserved as seeds, ovaries, sperm etc.
Provides easy evolutionary and genetic study	Easy access for evaluation e.g. for resistance to pests and diseases
Best for "recalcitrant" species	Easy access for breeding and other forms of utilization
Possibility of multiple target taxa reserves	Little maintenance required once material is conserved (seed/ovaries/sperm at 5$/year)

Nevertheless, *ex situ* conservation is not enough to effectively conserve the broad diversity and the evolutionary potential of CWR:

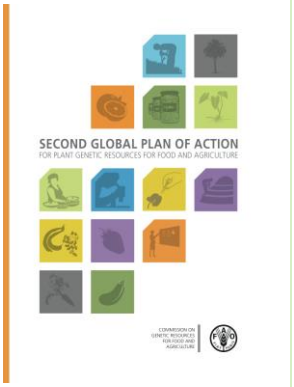
- *In situ* conservation allows continued evolution in the environment, *ex situ* literally freezes evolutionary adaptation (including climate change adaptation).
- *Ex situ* conservation involves collecting samples of populations, but with *in situ* we can conserve whole populations. It is rarely possible to conserve genetically representative population samples *ex situ* because of the sampling process.
- Collections for *ex situ* are often targeted to short-term goals, whereas *in situ* conservation has a long-term conservation ethos.
- Genetic diversity is lost when regenerating *ex situ* accessions and we would need to go back to the wild to collect more.
- If material is only conserved *ex situ* and it is lost or used, we may not be able to recollect if populations are not conserved *in situ*.

In conclusion, complementary conservation is needed as both techniques have advantages and disadvantages.

2.4 POLICY CONTEXT FOR CWR CONSERVATION AND USE

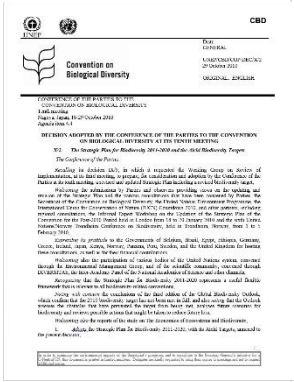
The Convention on Biological Diversity (CBD) (CBD 1992), the International Treaty on Plant Genetic Resources for Food and Agriculture (ITPGRFA 2001), the Second Global Plan of Action for the Conservation and Sustainable Utilization of PGRFA (FAO 2011), and the Global Strategy for Plant Conservation (GSPC) each stress the need to develop and implement national strategies for PGRFA conservation and sustainable use. They also underline the fundamental role of governments to ensure that the conservation and sustainable use of PGRFA continues to be a key element in global efforts to increase food security and nutrition, and to alleviate poverty.

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".

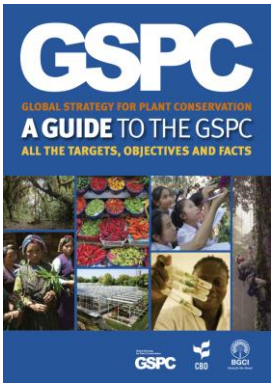


Decision X/2 of the COP 10 (CBD Strategic Plan for Biodiversity 2011–2020) (Nagoya, Japan, October 2010) (CBD 2010b) recognized "the genetic diversity of cultivated plants and farmed and domesticated animals and of wild relatives, including other socio-economically as well as culturally valuable species" 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".

Aichi Target 13 of the CBD Strategic Plan for Biodiversity 2011–2020 (CBD 2010b) highlights more effective CWR conservation as a specific priority, stating that "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".



Target 9 of the GSPC (CBD 2010a) calls for "7O percent 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.



The 2030 Sustainable Development Goals: 16 of the 17 goals can be directly linked with the conservation and use of CWR as a way of eradicating extreme poverty and hunger.

Joint notification of the CBD/ITPGRFA/CGRFA/Bioversity (published in August 2015) called for the "strengthening [of] the *in situ* conservation of PGRFA through incorporation of CWR under areas important for biodiversity in PA networks and other effective area-based conservation measures".

The conservation of CWR at national level should be linked to the implementation of the Global Strategy for Plant Conservation (GSPC) (through the GSPC national focal point), the International Treaty for Plant Genetic Resources for Food and Agriculture (ITPGRFA) as well national instruments related to the conservation of biodiversity such as the National Biodiversity Strategies and Action Plans (NBSAPs)—the principal instruments for implementing the CBD at national level—and National Plant Conservation Strategies, where appropriate.

What are the drivers of policy change with regard to the conservation and use of CWR?

- The intrinsic value of CWR to safeguard food security, especially in a changing climate.
- The indirect use of CWR for the development of crop varieties that are better adapted to changing environments (e.g. pest and disease resistance, temperature resistance, higher and more stable yield) and to meet consumer demands.
- Improving food quality and for medicinal purposes. CWR have been utilized 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 industry development based on the large scale (and possibly international) commercialization of new improved varieties and, (ii) 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 Sustainable Development Goals to eradicate extreme poverty and hunger.

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WWW Agricultural Biodiversity Weblog

WWW Crop Wild Relatives Global Portal

WWW CWRdiversity

WWW *In Situ* Conservation of CWR eLearning Modules

WWW PGR Secure helpdesk: CWR resources

WWW The CWR *In Situ* Strategy Helpdesk

WWW The Importance of Crop Wild Relatives Infographic

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@AgroBioDiverse

@BioversityInt

@CropTrust

@CropWildRelativ

@PGRBham

@SeedCrop

3 NATIONAL STRATEGIC ACTION PLANS

A National Strategic Action Plan for the conservation and sustainable utilization of CWR (NSAP) is 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. It evaluates current conservation actions and establishes future CWR conservation objectives. Equally, the NSAP also addresses the use of CWR, by promoting their value as well as evaluating their use in breeding programmes and the national (and global) demand for CWR in crop improvement. Finally, the NSAP reviews the resources required to implement conservation and sustainable use, it attributes responsibilities and sets CWR conservation action and use in the broader environmental and agricultural policy context.

Why a NSAP is needed for CWR conservation and use?

CWR are unique resources for food security and are increasingly used in crop breeding programmes. However, they are increasingly threatened and are 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. In practice, this is best implemented via a NSAP because each nation is responsible for the conservation of the natural resources within its political boundaries and, as such, conservation is predominantly organized on a national basis. In addition, the NSAP promotes the value and the potential for utilization of a country's CWR diversity. The NSAP should be integrated within other national initiatives (e.g. on biodiversity conservation, agriculture and development strategies) but also with regional and eventually global programmes into a coordinated holistic approach to ensure that the most important CWR resources are conserved and available for use in crop improvement. See presentation available when you click on Figure 13.

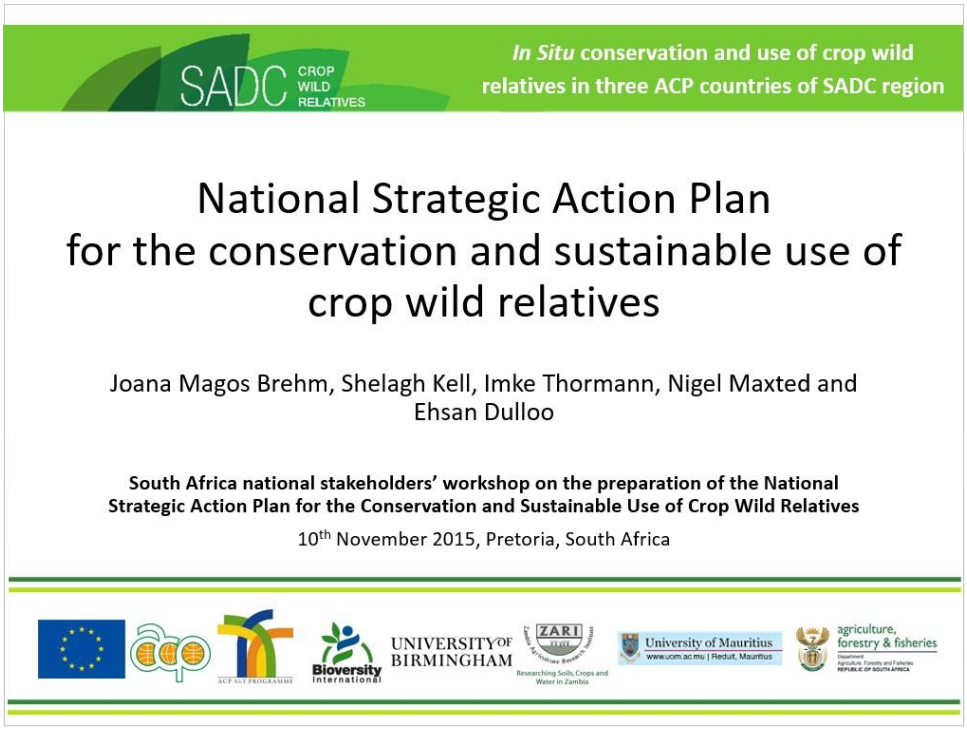

Figure 13 Presentation on the National Strategic Action Plan concept (click on the image).

Which national stakeholders should be involved in the preparation, endorsement and implementation of a NSAP for CWR conservation and use, and how?

Given the dual benefits of CWR as important elements in natural habitats and as gene donors for crop improvement, CWR conservation is best achieved if both national PGR institutes and nature conservation communities work together from the preparation of the NSAP to its implementation. National stakeholders include: farmers' associations, genebank managers, herbarium managers, pre-breeders, public breeding

institutes, private breeding companies, NGOs, academic institutes, ministries of agriculture and environment/conservation of nature etc.

In countries where several ministries share responsibility for PGRFA conservation it is very important that they are all engaged in the preparation of the NSAP and that they then endorse it. Additionally, in countries with a federal structure, where responsibilities for nature conservation are shared between “Länder”, “Cantons” or “Autonomies”, the implementation of conservation actions at national level requires a coordination unit at the federal level.

The table below lists the different stakeholders that were involved in the NSAP for CWR conservation and use in Mauritius (and Rodrigues), South Africa and Zambia, and their level of involvement (preparation, endorsement and implementation of the NSAP).

Table 2 Stakeholders involved in the preparation, endorsement and implementation of the NSAP in the Republic of Mauritius (Mauritius and Rodrigues), South Africa and Zambia.

COUNTRY / AUTONOMOUS REGION	NATIONAL STAKEHOLDERS		PREPARATION *	ENDORSEMENT **	IMPLEMENTATION
REPUBLIC OF MAURITIUS —Mauritius	Governmental	Ministry of Agro Industry and Food Security:			
		• Agricultural Services	X	X	X
		• Deputy Permanent Secretary		X	
		• Forestry Services	X	X	X
		• Mauritius Herbarium	X	X	
		• National Biodiversity Strategic Action Plan project		X	
		• National Plant Protection Office		X	
		• Protected Area Network Expansion project		X	
		• Vallee D'Osterlog Endemic Garden Foundation		X	
	Nature/environment	Mauritian Wildlife Foundation (MWF)			X
		National Parks and Conservation Services (NPCS)	X	X	X (leader)
	Research and breeding institutes/companies	Food and Agricultural Research and Extension Institute (FAREI*)*	X	X	X
		Mauritius Sugar Industry Research Institute (MSIRI)	X	X	X
	Academic institutes	International Sufi School		X	
		University of Birmingham	X		
		University of Mauritius	X	X	
	Farmers	Individual farmers		X	X (1 representative)
	NGOs/others	Bioversity International	X		
		Private forest owners		X	
		Sir Seewoosagur Ramgoolam Botanic Garden		X	

COUNTRY / AUTONOMOUS REGION	NATIONAL STAKEHOLDERS		PREPARATION *	ENDORSEMENT **	IMPLEMENTATION
REPUBLIC OF MAURITIUS — Rodrigues	Governmental	Biodiversity Sub-Committee of the Rodrigues Environment Committee***		X	X (leader)
		Commission for Agriculture	X	X	
		Forestry Services	X	X	X
		Rodrigues Regional Assembly	X	X	
		Rodrigues Regional Assembly (The Commission for Fisheries, 'Increase Capacity Building of the fisher's community of Rodrigues' project)	X		
	Nature/environment	François Leguat Giant Tortoise and Cave Reserve	X	X	X
		Mauritian Wildlife Foundation (MWF)		X	X
		South East Marine Protected Area Rodrigues Island		X	
	Research and breeding institutes/companies	Food and Agricultural Research and Extension Institute (FAREI*)*		X	
	Academic institutes	University of Birmingham	X		
		University of Mauritius	X		
	NGOs/others	Commission de l'Océan Indien		X	
		Bioversity International	X		
		Mauritius Research Council		X	
SOUTH AFRICA	Governmental	Department of Agriculture, Forestry and Fisheries (DAFF)	X	X	X
		Department of Rural Development and Land Reform	X		X
		Gauteng Department of Agriculture and Rural Development (GDARD)	X		X
		Limpopo Department of Agriculture and Rural Development	X		X
		Department of Science and Technology	X		X

COUNTRY / AUTONOMOUS REGION	NATIONAL STAKEHOLDERS		PREPARATION *	ENDORSEMENT **	IMPLEMENTATION
		Department of Environmental Affairs		X	X
	Nature/environment	South Africa Biodiversity Institute (SANBI)	X	X	X
		South African National Parks (SANParks)	X		X
	Research and breeding institutes/companies	Agriculture Research Council – Vegetable and Ornamental Plant Institute (ARC)	X		X
		South African National Seed Organization (SANSOR)	X		
	Academic institutes	Fortcox College	X		X
		Stellenbosch University	X		X
		University of Birmingham	X		
		University of Pretoria	X		X
	Farmers	Southern African Confederation of Agricultural Unions (SACAU)	X		
	NGOs/others	Bioversity International	X		
		BioWatch SA	X		X
		National Agricultural Marketing Council	X		
		SADC Plant Genetic Resource Centre (SPGRC)	X		
		South African Plant Breeders Association	X		
ZAMBIA	Ministries/Governmental departments	Ministry of Agriculture:			
		• Department of Policy and Planning	X	X	
		• National Plant Genetic Resources Centre	X		X
		• Zambia Agriculture Research Institute (ZARI)	X		X (leader)
		• Department of Agriculture (Extension Services)			X
		Ministry of Lands, Natural Resources and Environmental Protection:	X		

COUNTRY / AUTONOMOUS REGION	NATIONAL STAKEHOLDERS		PREPARATION *	ENDORSEMENT **	IMPLEMENTATION
		• Department of Environment and Natural Resources		X	
		• Department of Forestry		X	X
		• Department of National Parks and Wildlife (former Zambia Wildlife Authority)	X	X	X
	Nature/environment	Zambia Environmental Management Agency (ZEMA)	X		
	Research and breeding institutes/companies	Golden Valley Agricultural Research Trust	X		
		Mount Makulu Research Station	X		
		Mongu Research Station	X		
		University of Birmingham	X		
		University of Zambia	X	X	X
		Copperbelt University	X		
		Other Universities			X
	Farmers	Zambia National Farmers Union	X		
	NGOs/others	Agricultural Consultative Forum	X		
		Biodiversity Community Network	X		
		Bioversity International	X		
		Community Technology Development Trust (CTDT)	X		X
		SADC Plant Genetic Resource Centre (SPGRC)	X		
		WorldFish Centre	X		
		Local communities and farmers associations			X
		Traditional leadership			X
		Media (NAIS, ZNBC, ZANIS, private)			X

* The stakeholders involved in the preparation of the NSAP include those that actively contributed to the development and writing of the NSAP, but also those who were invited to attend a first national stakeholders' workshop, where discussions were held regarding the national strategic and concrete conservation actions required to effectively conserve and use CWR.

** National stakeholders endorsed the NSAP either via the organization of national stakeholders' workshops (Mauritius and South Africa) or via individual face-to-face meetings (Zambia).

*** The Biodiversity Sub-Committee of the Rodrigues Environment Committee will be responsible for the implementation of the NSAP. The Biodiversity Sub-Committee is chaired by staff of the Mauritius Research Council (Rodrigues branch) and includes various stakeholders from public and private sectors as well as NGOs (Ministry of Agro-Industry and Food Security 2016).

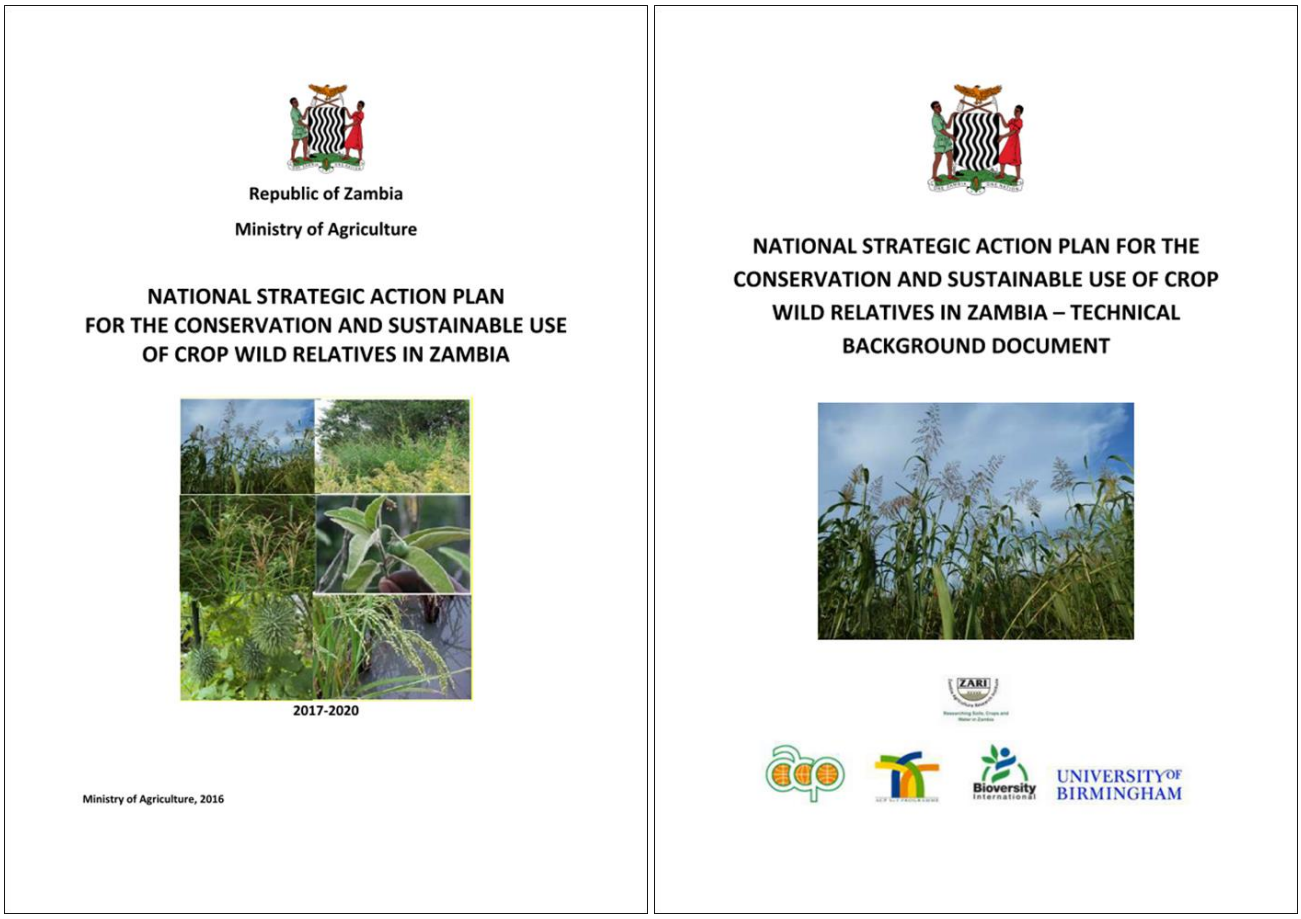

Figure 14 National Strategic Action Plan for the conservation and sustainbale use of CWR in Zambia and accompanying technical background document. Available when clicking over the images.

BOX 10 WHAT DOCUMENTS ARE AVAILABLE TO GUIDE THE DEVELOPMENT OF A NSAP?

In the SADC Crop Wild Relative project two complementary templates were developed to assist countries in preparing their NSAP for the conservation and sustainable use of CWR:

(i) Template for the Preparation of a National Strategic Action Plan for the Conservation and Sustainable Use of Crop Wild Relatives: helps preparing the NSAP (the NSAP mainly targets policy-makers).

(ii) Template for the Technical Background Document of a National Strategic Action Plan for the Conservation and Sustainable Use of Crop Wild Relatives: helps preparing the NSAP technical background document which provides the technical background information and scientific basis of NSAP development to complement the main NSAP document; the scientific information contained here should be reviewed and updated if a future iteration of the NSAP is to be undertaken.

4 TOOLKIT – THE MODULES

National systematic CWR conservation planning

This process involves planning systematic *in situ* and *ex situ* conservation of CWR diversity at the national level. The implementation of which results in the systematic representation of the nation's CWR diversity in an *in situ* network of genetic reserves (within existing protected areas or by establishing novel conservation areas) with back-up *ex situ* collections of genetically representative population samples in national genebanks (i.e. seeds, tissue, DNA, living plants). The conservation recommendations that result from this national CWR conservation planning process can, and should, feed into the National Strategic Action Plan for the conservation and utilization of CWR.

Generation of a CWR checklist

A CWR checklist is a list of all CWR taxa found in a defined geographic unit (region, country etc.), comprising a list of taxon names and authorities.

Prioritization of the CWR checklist

Establishing priorities for CWR conservation is an obvious and essential step in the development of the NSAP. It involves reducing the number of CWR in the checklist to a more manageable and realistic number for active conservation.

Compilation of the CWR inventory

An inventory of CWR is a list of CWR taxa present in a defined geographic unit (region, country etc.) with ancillary information, such as: the applied Gene Pool or Taxon Group concepts, biology, ecogeography, populations, uses, threats and conservation. An inventory is usually created after prioritization of the CWR checklist, for the priority taxa only.

Diversity analyses: distribution and ecogeographic analyses of priority CWR

This is the process of collating ecogeographic and occurrence data for the priority CWR, followed by the analysis of these data to understand the patterns of diversity within and among priority CWR taxa (hotspot analysis, ecogeographic diversity etc.). The results obtained from these analyses then help in formulating, establishing and implementing conservation priorities.

Diversity analyses: genetic data analysis of priority CWR

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

Novel threat assessment of priority CWR

Threat assessment is a process used to evaluate the risk of extinction of a particular taxon. When there is no existing threat assessment information for priority CWR (e.g. national red lists, IUCN Red List of Threatened Species), a novel threat assessment can be undertaken in parallel to conservation planning as the information collated for the diversity analyses can be also used to undertake these assessments. Threat assessements can then be used to further prioritize/enhance CWR conservation.

Gap analysis of priority CWR

A gap analysis of priority CWR is a conservation evaluation technique that identifies 'gaps' in the conservation of these taxa. In practice, gap analysis involves a comparison between the range of natural diversity found in the wild, and the range of diversity already effectively represented by current *in situ* conservation actions (*in situ* gap analysis) and all accessions of the target CWR represented in genebank collections (*ex situ* gap analysis). Gap analysis can be undertaken at both species and infra-specific level (e.g. ecogeographic diversity).

Climate change analysis

Climate change analysis allows (a) the identification of the CWR that are most affected by climate change, (b) the prediction of the impact of climate change on taxon distribution, and (c) the development of recommendations for the *in situ* and *ex situ* conservation of CWR.

Establishment and implementation of* in situ *conservation priorities

A NSAP for the conservation of CWR aims, in part, to recommend 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 are implemented as a contribution to national, regional and global food security. Once appropriate sites for active *in situ* conservation have been identified, the establishment of the network of sites can begin. These sites may be established (a) within existing protected areas, (b) as new conservation areas specific for CWR conservation, or (c) as informal CWR management sites.

Establishment and implementation of* ex situ *conservation priorities

Periodic sampling of CWR populations for *ex situ* conservation should provide, whenever possible, a back-up of populations actively conserved *in situ*. Diversity conserved *ex situ* primarily facilitates the access to these materials for crop improvement and research.

Monitoring CWR diversity

Monitoring of plant populations ensures the systematic collection of data over time to detect changes, to determine the direction of those changes and to measure their magnitude. The monitoring of CWR populations, and the habitats in which they occur, aims (a) to provide data for modelling populations trends, (b) to enable assessment of trends in population size and structure, (c) to provide information on trends in population genetic diversity, and (d) to determine the outcomes of management actions on populations and to guide management decisions.

Promoting the use of conserved CWR diversity

CWR are defined by their potential utilization as gene donors for crop improvement. Conservation of CWR is thus explicitly linked to utilization. This link forms the basis of enduring human food security, highlighting that the promotion of the sustainable use of conserved CWR diversity is as relevant as its effective conservation.

4.1 NATIONAL CWR CONSERVATION PLANNING

This process involves planning systematic *in situ* and *ex situ* conservation of CWR diversity at the national level and can be undertaken using a **floristic** or a **monographic** approach. The implementation of which results in the systematic representation of the nation's CWR diversity in an *in situ* network of genetic reserves (within existing protected areas or by establishing novel conservation areas) with back-up *ex situ* collections of genetically representative population samples in national genebanks (i.e. seeds, tissue, DNA, living plants). The conservation recommendations that result from this national CWR conservation planning process can, and should, feed into the National Strategic Action Plan for the conservation and utilization of CWR (Figure 15).

What are the main steps in the CWR conservation planning process?

Given variations in the CWR diversity present, the availability and quality of data, the financial and human resources allocated to conservation, as well as the different levels of commitment by national agencies and governments, the CWR conservation planning process will differ from country to country. Nevertheless, the following steps are likely to be common among countries:

1. Generation of a national CWR checklist[1]
2. Prioritization of CWR for conservation
3. Compilation of the CWR inventory[1]
4. Diversity analysis of priority CWR (distribution, ecogeographic, genetic diversity analyses)
5. Novel threat assessment of priority CWR
6. Gap analysis of priority CWR
7. Climate change analysis of priority CWR
8. Establishment and implementation of *in situ* conservation priorities
9. Establishment and implementation of *ex situ* conservation priorities
10. Monitoring of CWR diversity
11. Promoting the use of CWR.

The conclusion of this process is the formulation of the NSAP, which includes:

[1] Here 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 complete checklist (all CWR species) and a partial checklist (subset of CWR species).

- Concrete recommendations for the conservation of CWR diversity (including the identification of key sites for active *in situ* conservation of CWR diversity and CWR populations under-represented in *ex situ* collections).
- Provisions for the sustainable utilization of conserved CWR diversity by plant breeders, researchers and other potential users.
- Strategic actions relating to policy interventions that need to be put in place to enable the implementation of the concrete conservation actions and sustainable use recommendations.
- The partnerships and networks that are required to link the regional, national and local stakeholders that contribute to the conservation and sustainable use of CWR diversity and how these partnerships and networks are expected to be established and sustained.
- Details regarding how the implementation of the NSAP is expected to be resourced.

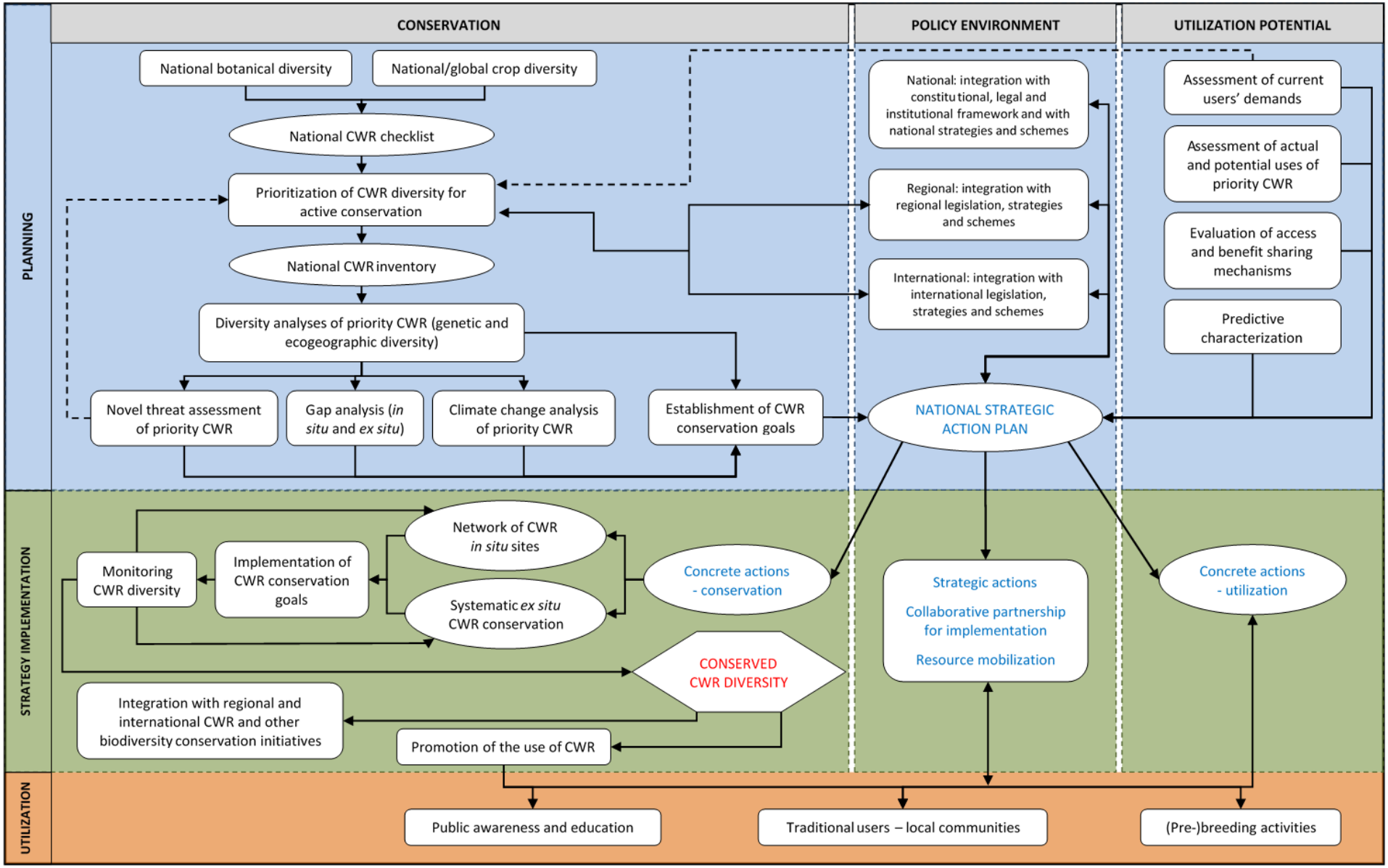

Figure 15 Model for the development of a National Strategic Action Plan for the conservation and sustainable use of CWR.

BOX 11 WHAT DO YOU NEED TO DECIDE BEFORE STARTING CWR CONSERVATION PLANNING?

Prior to start planning CWR conservation [to be integrated into a National Strategic Action Plan for CWR conservation and use (NSAP)], several options regarding the scope and the approach to be undertaken need to be defined.

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 all CWR diversity that occurs in a defined geographic area. This 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 geographic scale.

Both approaches will ultimately conclude with the systematic conservation of priority CWR diversity via a network of *in situ* conservation sites, with back-up 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).

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

CWR 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 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 conservation strategy should link with local, regional and ultimately the global strategy such that nationally designated 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 being 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 conservation strategies to ensure they form a series of local, national, regional and global *in situ* CWR conservation sites.

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 diversity hotspots and implement genetic reserve conservation in a network that maximizes the conserved CWR 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 diversity for millennia and so maintaining a complementary bottom-up approach is equally important. Therefore, just as CWR 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 – Farmer or conservationist based* in situ *conservation

At first it might be thought that farmers 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 that 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.

Option 5* – Status quo *or legislative protection

To promote sustainable *in situ* CWR conservation there is a need to encourage and facilitate stronger legislative protection of sites 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 where the *status quo* without specific protection is unviable. This is particularly important for 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 diversity that we know is threatened and must be conserved if we are to seriously address global food security.

Option 6* – 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 being conserved and then to 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 is the germplasm 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 genebank?
- 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 CWR can then be applied in a pragmatic and balanced manner.

Option 7 – 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.* 1997). This utilitarian concept is fundamental to PGRFA conservation where the goal is to ensure that the maximum possible genetic diversity of CWR diversity is maintained and available for potential utilization.

Source: Maxted *et al.* (2011)

BOX 12 CURRENT STATUS OF CWR CONSERVATION PLANNING

In the past 15 years, knowledge of CWR diversity has significantly increased, particularly through activities undertaken within the context of some notable EU-funded projects (PGR Forum, AEGRO, PGR Secure and the SADC CWR project) and the GEF-funded project, *In situ* Conservation of Crop Wild Relatives through Enhanced Information Management and Field Application; there have also been recent advances under the auspices of the Crop Trust.

Fundamental to this increase in knowledge has been the development of an agreed definition of a CWR (Maxted *et al*. 2006), which has enabled the identification of the breadth of taxonomic CWR diversity at national, regional and global levels, as well as providing the foundation for prioritizing CWR taxa for conservation action. However, initial studies have shown that CWR diversity found in nature is seriously threatened, with significant taxonomic and genetic diversity loss currently occurring.

At the taxon level, Red List assessments of CWR have increased our understanding of the main pressures threatening CWR populations (Bilz *et al*. 2011, Kell *et al*. 2012), and indirectly—at the genetic level—it is recognized that the loss of taxonomic diversity is an under-representation of the loss of genetic diversity (Maxted *et al.* 1997). Techniques for identifying diversity within taxa, both within and among populations, as well as techniques for conservation gap analysis, have diversified and are being enhanced through targeted research on CWR, and are greatly facilitating the production of national CWR and crop gene pool conservation strategies (for examples, see here as well as Maxted and Kell 2009; also see Iriondo *et al.* (2016) and Labokas (2016) for a review on progress in national CWR conservation planning in the European region). Furthermore, recent investigations have highlighted the global centres of CWR diversity (Castañeda-Álvarez *et al.* 2016) and for the first time have identified where CWR *in situ* conservation actions should be focused in a global context (Vincent *et al.* 2017). These recent advances have provided a solid foundation for the development of a strategic approach to CWR conservation planning at the national, regional and global levels, that is based on a range of commonly agreed and widely tested scientific concepts and techniques.

4.1.1 Floristic approach

A floristic approach encompasses all CWR that occur 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. The geographical area may contain all, or part of, the ranges of the plant taxa that occur. This approach is commonly associated with the development of a NSAP for CWR conservation.

At national level: CWR NSAPs for the Republic of Mauritius

In the Republic of Mauritius, NSAPs for CWR conservation and sustainable use were developed independently for the islands of Mauritius and Rodrigues. This means that two separate CWR checklists were developed, one for each island. Both CWR checklists were obtained through a process of data harmonization and cross-checking of the national flora of both Mauritius and Rodrigues with the Mansfeld's World Database of Agricultural and Horticultural Crops (Hanelt and IPK 2001, available here), taking into account the broad range of crop types (food, forage and fodder, ornamental, medicinal, and forestry), as well as a broad definition of a CWR which is any species in the same genus as a crop. 528 and 142 CWR were identified in Mauritius and Rodrigues, respectively. Based on the socio-economic value of the related crop, utilization potential for crop improvement, relative distribution and the IUCN Red List Categories (as an indication of relative threat), CWR on each of the islands were prioritized for conservation. Eighteen and nine CWR taxa were prioritized for Mauritius and Rodrigues, respectively. An ecogeographic survey, including a field prospection, was carried out to support the identification of priority CWR hotspots on each of the islands separately and to identify the main threats affecting priority CWR. Additionally, a gap analysis helped identify the gaps in *in situ* and *ex situ* conservation of priority CWR. Conservation recommendations were then based on the results obtained and included in the *NSAP for the Conservation and Sustainable Use of CWR for the Republic of Mauritius*.

Figure 16 *Coffea macrocarpa* A. Rich., a tertiary wild relative of Arabic coffee, Vulnerable (according to the 2001 IUCN Categories and Criteria) and endemic to Mauritius. (Photo: Mukesh Rughoo)

Source: Ministry of Agro-Industry and Food Security (2016)

At national level: checklist of Portuguese CWR

Figure 17 *Vicia bithynica* (L.) L., a tertiary wild relative of faba beans with potential for conferring resistance to rust and Ascochyta Blight, in Mafra, Portugal. (Photo: Joana Magos Brehm)

The Portuguese CWR checklist, which includes 2262 taxa, was developed from a geographically filtered list from the CWR Catalogue for Europe and the Mediterranean (Kell *et al.* 2005). To ensure that all globally important crop genera as well as nationally grown crops were considered, several documents were used for validation: the complete list of agricultural, vegetable, fruit and ornamental species produced by the Portuguese National Catalogue of Varieties (DGPC 2003), the Temperate and Boreal Forest Resources Assessment 2000 (TBFRA-2000) for the forestry crops (UNECE/FAO 2000), a priority list of ornamental genera representing the recommendations from the Herbaceous Ornamental Crop Germplasm Committee (HOCGC) (OPGC 2002) and a report by Pimenta (2004) on an updated list of ornamental plant species grown in Portugal. Twenty-two species were identified as conservation priorities based on eight criteria (native status, economic value, threatened status, *in situ* and

ex situ conservation status, global and national distribution and legislation) and by combining different prioritization schemes. 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 (2009), Magos Brehm *et al.* (2008, 2010)

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 2001, available here), the 'Enumeration of cultivated forest plant species' (Schultze-Motel 1966) for forestry species, the Community Plant Variety Office list of plant varieties for ornamental plants and the Medicinal and Aromatic Plant Resources of the World (MAPROW) (U. Schippmann, pers. comm. 2004). This was then 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 for Europe and the Mediterranean was generated by extracting the taxa within the relevant genera in Euro+Med PlantBase that matched the identified crop genera.Source: Ministry of Agro-Industry and Food Security (2016)

Source: Kell *et al.* (2008)

4.1.2 Monographic approach

A monographic approach is restricted to certain crop gene pools (usually prioritized). It is monographic because the methodology is comprehensive for individual target taxa throughout their full geographic range, or their full range within a geographically defined unit at any geographical scale.

At national level: CWR NSAP for South Africa

Figure 18 *Asparagus densiflorus* (Kunth) Jessop, a gene pool tertiary relative of asparagus with confirmed uses in increase of fertility and a potential source of resistance to several diseases (e.g. rust, fusarium crown and root rot), pictured here in South Africa. (Photo: SANBI)

In South Africa, a NSAP for CWR conservation and sustainable use was produced based on a partial CWR checklist of food (including beverages) and fodder crops. Such an approach was justified by the extremely high number of taxa in the flora (about 22,616) (Germishuizen *et al.* 2006) and given the national interest in focusing on food security. A food and fodder CWR checklist for South Africa was developed by matching the South African National Plant Checklist (SANPC) (Germishuizen *et al.* 2006) and the Red List of South African Plants online database with a list of crop genera that was compiled using various resources including crop genera of crops cultivated worldwide (Kell, unpublished) and minor and under-utilized crops from Africa (see more details here). A total of 1609 native and introduced taxa (species, subspecies and varieties) within 145 genera were included in the food and fodder CWR checklist for South Africa and further prioritized for conservation action based on the socio-economic value of the related crop at global, continental and regional (SADC) scales, utilization potential for crop improvement, relative

distribution/occurrence and conservation status (see more details here). A total of 258 priority CWR were identified for which occurrence data (including field surveying of some of them) were collated. Systematic conservation planning of priority CWR resulted in the identification of priority areas for active *in situ* conservation and for further ex situ collecting. Concrete conservation recommendations that resulted from this analysis were then incorporated into the *NSAP for the Conservation and Sustainable Use of CWR in South Africa*.

Source: DAFF (2016), Hamer *et al.* (2016)

At national level: CWR NSAP for Zambia

Figure 19 Wild sorghum pictured here on the margins of a cultivated field in Chilanga, Zambia. (Photo: Dickson Ng'uni)

Conservation planning for priority CWR was undertaken in Zambia with the purpose of informing the *NSAP for the Conservation and Sustainable Use of CWR in Zambia*. The Zambia partial CWR checklist was developed based on a total of 59 crops (from 29 genera) cultivated nationally which were prioritized by the SADC Crop Wild Relative project (that funded this study) national committee (see more details here). The Zambia partial CWR checklist includes 459 taxa out of which 31 were further prioritized based on their relative geographical distribution, utilization potential for crop improvement, threat status, and economic use value of the related crops (see more details here). Collation of occurrence data from various sources was undertaken, diversity and gap analyses were carried out, and existing protected areas where priority CWR occur were identified for their active conservation. In addition, *ex situ* conservation gaps were identified and conservation recommendations were made.

Source: ZARI (2016a,b)

At regional level: collection of wild rice in eastern and southern Africa

A collecting programme targeting wild rice in eastern and southern Africa took place between 1997 and 1998. The collecting strategy was developed from an initial ecogeographic study based on data from several African and international herbaria and available literature on occurrence and distribution of the target species within the region, as well as 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 reported.

Source: Kiambi *et al.* (2005)

Figure 20 A population of *Oryza longistaminata* A.Chev. & Roehr., a primary relative of both Asian and African rice, which has been used to improve yield and to confer drought tolerance and resistance to a number of diseases, pictured here Zambia. (Photo: ZARI)

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 9,866 unique geo-referenced records were collected from between 1932 and 2004. Predicted distribution maps were obtained for the *Aegilops* taxa and compared through 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 the establishment of a novel protected area were also made.

Figure 21 *Aegilops cylindrica* Host, a wild relative of wheat (*Triticum* spp.), in the Erebuni State Reserve (Armenia), a genetic reserve dedicated to the conservation of wild wheat, including *Triticum urartu* Tumannian ex Gandilyan, *T. boeoticum* Boiss., *T. araraticum* Jakubz and *Aegilops* spp. (Photo: René Hauptvogel)

Source: Maxted *et al.* (2008)

At global level: *ex situ* conservation priorities for global priority CWR

Castañeda-Álvarez *et al.* (2016) have model the global distribution of 1,076 taxa related to 81 crops of global importance using occurrence information from biodiversity, herbarium and gene bank databases. They then compared the potential geographic and ecological diversity for each of these taxon with what is currently conserved ex situ in order to detect gaps in conservation. Main results showed that CWR diversity is generally poorly represented in gene banks as about 29% of the taxa (313 wild relatives of 63 crops) were not represented in gene banks and a further 24% (257 taxa) were represented by fewer than ten accessions. More than 70% of taxa were thus identified as high priority for further collecting in order to improve their representation in gene banks, and over 95% were insufficiently represented in terms geographic and ecogeographic diversity across their native distributions. Main ex situ collecting gaps occur in the Mediterranean and the Near East, western and southern Europe, Southeast and East Asia, and South America.

Source: Castañeda-Álvarez *et al.* (2016)

4.1.3 Integrating national CWR conservation planning at global, regional, and local levels

4.1.4 References

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WWW Crop Wild Relatives Global Portal

WWW CWR *In Situ* Strategy Helpdesk. An Integrated European *In Situ* Management Work Plan: Implementing Genetic Reserves and On-farm Concepts (AEGRO)

WWW *In Situ* Conservation of CWR eLearning Modules

WWW PGR Secure Crop Wild Relative and Landrace Conservation Helpdesk

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WWW Crop Wild Relatives Global Portal

WWW CWRdiversity

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4.2 GENERATION OF A CWR CHECKLIST

What is a checklist of crop wild relatives?

A CWR checklist is a list of CWR taxa found in a defined geographic unit (region, country etc.), comprising a list of taxon names and authorities. A national CWR checklist is a list of all CWR taxa present in a country.[2]

Figure 22 *Imperata cylindrica* (L.) P.Beauv., a tertiary gene pool wild relative of sugar cane, pictured here in South Africa. (Photo: SANBI)

We need to identify the CWR that exist, where they occur and their conservation status in order to conserve and use them effectively. CWR checklists provide policy-makers, conservation practitioners, plant breeders and other user groups with basic information about which CWR taxa occur in a particular geographic unit, and they are essentially the starting point for formulating strategies for *in situ* and *ex situ* CWR conservation. They also serve to highlight the breadth of CWR diversity available in the target area, which may include resources for CWR conservation and use that are important to 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 reporting of CWR diversity has been largely neglected. However, in recent years there has been a substantial increase in the number of CWR checklists. A few of these checklists comprise the entire national CWR diversity—using the floristic approach, e.g. Portugal (Magos Brehm *et al.* 2008) and the United Kingdom (Maxted *et al.* 2007)—but most of them are limited to single crop gene pools or small groups of species, or to certain regions within the countries. See examples here. The importance of creating a checklist of CWR at national instead of sub-national level or for selected crop gene pools should be emphasized; it provides the best foundation for developing a National Strategic Action Plan for the conservation and sustainable use of CWR.

4.2.1 Methodology

The preparation of a CWR checklist can be seen as an eight stage process: (i) determine the geographic scope (if not national), (ii) establish whether a regional CWR checklist already exists, (iii) determine the scope of the CWR checklist, (iv) produce a digitized list of crops, (v) produce a digitized list of the national flora, (vi) match the crop genera against the floristic checklist and generate the CWR checklist, (vii) annotate the CWR checklist, and (viii) make the checklist available to users (Flowchart 1).

(i) Determine the geographic scope

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

(ii) Establish whether a regional CWR checklist exists

Where a regional[3] CWR checklist exists, as in Europe (Kell *et al.* 2005, 2008) and the SADC region (see here for more examples), it may be filtered for a specific country to generate the national CWR checklist. If

[2] Note that we deliberately distinguish between a checklist and an inventory. See here for more information on the definition of a CWR inventory.

[3] Region is defined here as a geographic area comprising different countries (e.g. Europe, Mediterranean region, SADC region, Sub-Saharan Africa) rather than a sub-unit within a country.

using this approach, it is important to harmonize the species names obtained from the regional inventory with the existing national flora checklist using the following methods: (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 taxon 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). Online taxonomy checkers can be used for this purpose (e.g. Taxonomic Name Resolution Service v3.2).

(iii) Determine the scope of the CWR checklist

The scope of the CWR checklist should be discussed and agreed with the various stakeholders in order to decide which wild relatives of which crops and crop gene pools to include. The choices may be partially dependent on the availability of crop data and digitized flora, along with financial resources and human capacity.

- Nationally cultivated crops *versus* crops cultivated elsewhere but with CWR that occur in the target geographic area – Given the high level of interdependence among countries with respect to the conservation and use of PGRFA (see Khoury *et al.* 2016), it is highly advisable that all crops (nationally and globally grown) are considered when preparing the checklist, as all countries depend on CWR diversity that occurs in other countries for the improvement of their crops.
- Major food crops *versus* minor and underutilized crops, forage and fodder crops, or even forestry, industrial, ornamental and medicinal crops – A step of prioritization or selection of crops/crop groups prior to the development of the CWR checklist may be undertaken. A floristic approach to the development of the CWR checklist will comprise all CWR that occur in a geographically defined area, whereas a monographic approach will produce a checklist of CWR of one, or several selected or priority, crop gene pools.
- Native CWR *versus* native and introduced CWR – This is a pragmatic decision based on these species' importance in crop breeding programmes. Note that an introduced CWR may have adapted to particular environments hence developing adaptive traits that might be of interest for crop improvement.

In general, the more inclusive the checklist, the greater its use. Therefore, a broad geographic and crop scope is recommended where possible. This will result in a large number of CWR listed in the checklist. Subsequently, the checklist will be prioritized to identify CWR requiring the most immediate conservation action, reducing it to a manageable number of taxa. Nevertheless, the monographic approach may be practical, though inevitably its less inclusive scope may mean that the exercise will need to be repeated when sufficient resources are available for a more comprehensive approach.

(iv) Produce a digitized list of crops

Several sources may need to be consulted when compiling a list of crops, if that list is not already available. Key sources include:

- Globally cultivated species resources (e.g. Mansfeld's World Database of Agricultural and Horticultural Crops; Kell, unpublished results).
- Regional or national crop checklists.
- Underutilized/neglected crop lists.
- Individual crop studies.
- National, regional or international agricultural statistics (e.g. EuroStat; FAOSTAT).
- Crop genebank accessions.
- Expert consultation.

Any non-digitized source of crop data can be scanned and converted to a digital file. There are several freely available optical character recognition (OCR) softwares online (e.g. Microsoft Office OneNote) and they also come with most scanners. As 100% recognition accuracy is difficult to achieve, the scanned information will have to be confirmed manually. The resulting digitized list of the crops/crop genera should then be made available.

(v) Produce a digitized list of the national flora

Countries usually have some form of national floristic checklist or Flora. When either of these is unavailable it may be possible to: (a) use the Flora of a neighbouring region (e.g. the Flora of Turkey lists many of the species found in Syria)—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), (b) use regional or global plant checklists to extract wild species lists for the country (e.g. GBIF and see more resources here)http://www.gbif.org/ -), or (c) undertake a herbaria and genebank survey of those specimens and accessions recorded in the country to produce a national flora checklist.

Any non-digitized Flora checklist can be scanned and converted to a digital file. There are several freely available optical character recognition (OCR) softwares online (e.g. Microsoft Office OneNote) and they also come with most scanners. As 100% recognition accuracy is difficult to achieve, the scanned information will have to be confirmed manually.

(vi) Match the crop genera against the floristic checklist and generate the CWR checklist

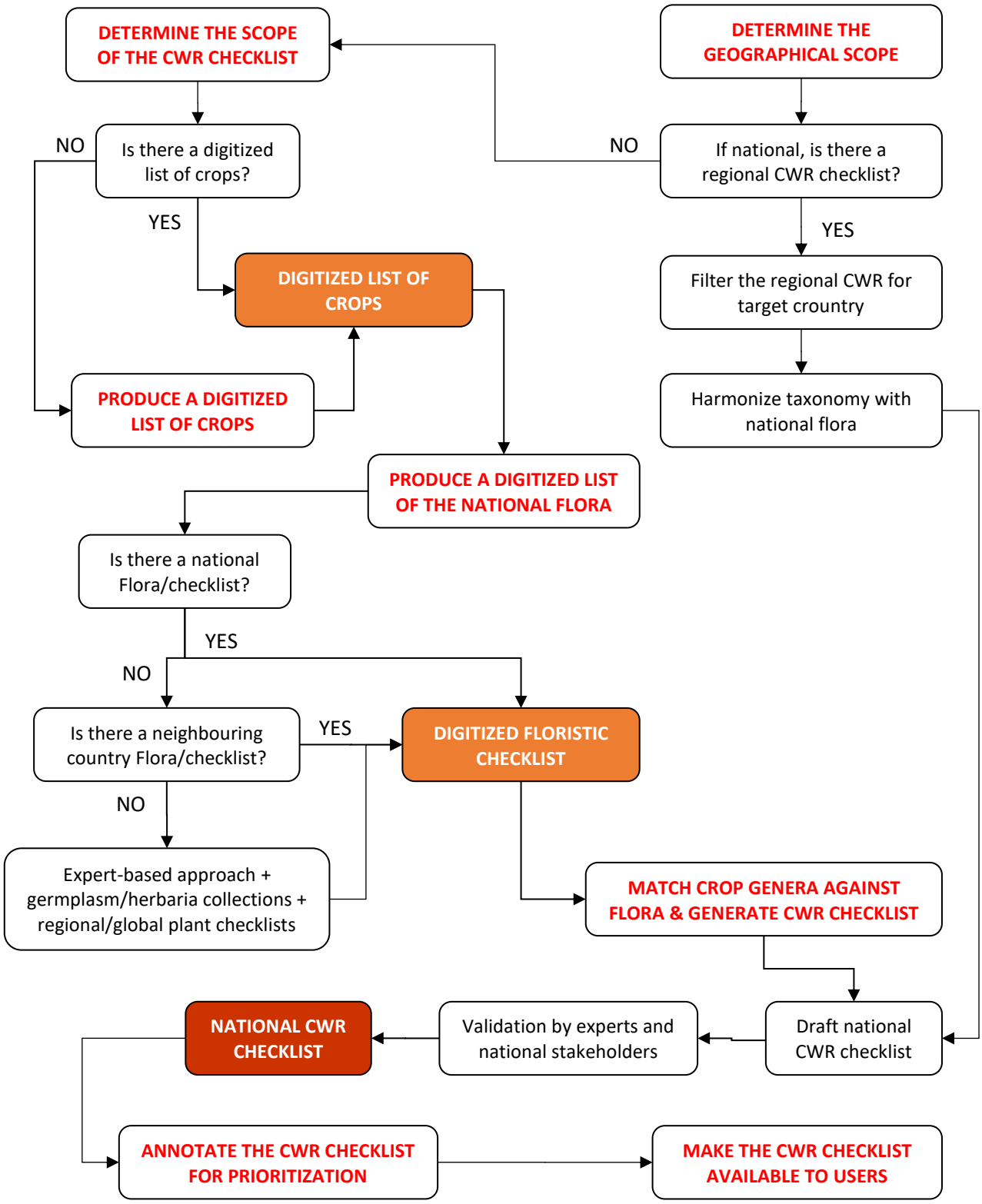
Once the digitized list of crops and Flora checklist are available, the crop genera are matched digitally with the Flora genera and all the matching taxa are, by applying the generic definition of CWR, the CWR. Once the draft CWR checklist has been generated it should be validated through consultation with appropriate floristic and monographic experts as well as national stakeholders in order to resolve minor errors and to engender stakeholder buy-in to the project. A checklist and inventory template for compiling the CWR checklist is currently being developed.

(vii) Annotate the CWR checklist for prioritization

If, in order to prioritize CWR for active conservation, there is a need to collate additional information for all CWR in the checklist, then the resulting checklist is called an annotated CWR checklist. See here for criteria to be used to prioritize CWR taxa.

(viii) Make the CWR checklist available to users

The CWR checklist should be made public and available to users, either via a web-enabled database, a pdf file or a publication. The CWR portal includes a repository of, among other information, CWR checklists from all around the world.



Flowchart 1 Overview of the creation of a CWR checklist.

4.2.2 Examples and applied use

Creating a national flora plant checklist using web-based resources

A flora checklist was successfully compiled for Angola from exclusively free web-based resources. These included online 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 online herbaria databases such as that of Royal Botanic Gardens, Kew. The project involved a one-year full time researcher and 30 collaborators, who provided expertise on specific plant families. It resulted in two products: a hard copy of the checklist of the Angolan plants, with additional information on collectors, synonyms and literature references, and a website (Flora of Angola Online) containing the information included in the hard copy.

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

Germplasm survey-based CWR checklist – 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:

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

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

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

Using a regional botanical checklist and digitized matching of flora against crops to obtain the CWR Catalogue for Europe and the Mediterranean

The creation of the CWR Catalogue for Europe and the Mediterranean is a successful example of how 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 2001, available here), the 'Enumeration of cultivated forest plant species' for forest species (Schultze-Motel 1966), the Community Plant Variety Office list of plant varieties for ornamental plants and the Medicinal and Aromatic Plant Resources of the World (MAPROW) (U. Schippmann, pers. comm. 2004). This list of crop genera was then 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. Finally, the CWR Catalogue was generated by extracting the taxa within the genera in Euro+Med PlantBase that matched the crop genera.

Source: Kell *et al.* (2005, 2008)

Using a regional CWR checklist to extract a national CWR checklist

When developing a national CWR checklist, a regional CWR checklist may be filtered to obtain a list of taxa for that specific country. The CWR Catalogue for Europe and the Mediterranean has been used to extract a list of CWR for Portugal and a number of other countries. See examples of the floristic approach to CWR conservation for more details.

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

Using a botanical checklist and agricultural statistics to create a CWR checklist and inventory

Examples of manual matching to generate a national CWR checklist 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:

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 create CWR checklist.
4. Define the criteria for prioritizing 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 taxa already included in national legislation. In the Seychelles the criteria were: national importance of crops (human food, animal food, industrial and ornamental), relative threat of genetic erosion, rarity, native status, existing priorities of the national conservation agency, potential for use of taxon 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; plans may include:
    - Assessment of current *in situ*/*ex situ* conservation activities for the priority CWR.
    - Current monitoring activities.
    - Assessment of current threats to priority taxa.
    - Assessment of current and potential exploitation of priority taxa.
    - Gap analysis of priority taxa.
    - Immediate and future conservation priorities.
    - Research priorities.

Subsequently, in both cases the national CWR checklists, 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)

Generation of a food and fodder CWR checklist for South Africa

A food and fodder CWR checklist for South Africa was developed using the *Crop and Crop Genus Lists for National CWR Checklists and Checklist Prioritization* (Kell, unpublished) (which lists genera of crops cultivated worldwide), the *Assessment of Activities on Underutilized Crops* (Williams and Haq 2002), Appendix 4 of the *World Programme for the Census of Agriculture 2010* (FAO 2005), and a draft, unpublished list of indigenous and alternative food crops in South Africa prepared by the the Agricultural Research Council (ARC). The crop genera from the first resource includes those from the *Mansfeld's World Database of Agricultural and Horticultural Crops* (Hanelt and IPK Gatersleben 2001, available here) and Annex 1 of the International Treaty on Plant Genetic Resources for Food and Agriculture (ITPGRFA) (FAO 2001). The combined list includes 6,020 crop genera not limited to food and fodder crops. Food and fodder crop genera were extracted and duplicate genera and wild harvested plants removed, which left a total of 420 genera. This food and fodder crop genus list was then matched to the South African National Plant Checklist (SANPC) (Germishuizen *et al.* 2006) and the Red List of South African Plants online database to extract their wild relatives that occur in South Africa. A total of 1609 native and introduced taxa (species, subspecies and varieties) within 145 genera were included in the food and fodder CWR checklist for South Africa which has a focus on major crops, but also includes wild relatives of less established but potentially important crops.

Figure 23 *Ipomoea robertsiana* Rendle, wild relative of sweet potato, here pictured in Bergville, KwaZulu-Natal, South Africa. (Photo: Percy Moila)

Source: Hamer *et al.* (2016)

Generation of a partial CWR checklist for Zambia

The Zambia partial CWR checklist was developed following various steps:

- A list of crops that are cultivated in Zambia was compiled from: the *Zambia Seed Technology Handbook* developed by the Ministry of Agriculture, Food and Fisheries (MAFF 1995), the database of Zambian National Plant Genetic Resources Centre and the Central Statistics Office (CSO)/Ministry of Agriculture and Livestock (MAL), crop survey reports for the period from 2009–2014. The list comprised a total of 107 crop taxa in 64 genera that are known to be cultivated in Zambia.
- The initial list of 107 crops was then subjected to the national stakeholders representing key national institutions for endorsement. Key institutions that endorsed this list were: Biodiversity Community Network (BCN), Community Technology Development Trust (CTDT), Department of National Parks and Wildlife of the Ministry of Tourism and Arts (former Zambia Wildlife Authority, ZAWA), University of Zambia (UNZA), and the Zambia Agriculture Research Institute (ZARI).
- The 107 crops were then prioritized by these stakeholders at a national stakeholders' meeting based on (by order of importance): (i) national socio-economic importance of the crops based on crop production and marketing statistics from the

Figure 24 *Pennisetum polystachion* (L.) Schult., a wild relative of pearl millet, here pictured in Zambia. (Photo: Graybill Munkombwe)

CSO/MAL Crop Survey Reports (2009–2014) and their importance for food security and industrial use, (ii) knowledge of occurrence of CWR in the country, and (iii) the local cultural and use value of a particular crop including food and medicinal use values. Although some of the crops could not qualify based on the first criterion, they were included on the priority list because of their high cultural and use values in particular local communities and their potential to become of national socio-economic importance in future. The agreement on the priority crops was reached upon by consensus among the experts involved in the stakeholders' meeting.

- A list of 59 crops (from 29 genera) nationally cultivated (both native and introduced) resulted from the process described above which includes cereals, food legumes, vegetables, root and tuber, oil, fibre, pasture and forage, and green manure crops.
- The taxonomic backbone for the development of the national checklist of CWR was *A Checklist of Zambia Vascular Plants* (Phiri 2005) which includes a total of 6305 taxa. This flora checklist was then digitized using an OCR type of software in order to be able to manipulate it and subsequently enable the matching of the digitized list with the crop genera.
- The prioritized list of crop genera (29) was subsequently matched with the digitized version of the national flora checklist in Microsoft Excel, generating a total of 459 wild relatives.
- The generated partial CWR checklist was finally validated by national stakeholders in a national stakeholders' consultation meeting. National stakeholders included: Agriculture Consultative Forum, National Agricultural Information Services, Biodiversity Community Network, Community Technology Development Trust, Department of National Parks and Wildlife of the Ministry of Tourism and Arts, Department of Policy and Planning of the Ministry of Agriculture, Environmental Protection and Natural Resources, Ministry of Lands, University of Zambia, WorldFish Centre and Zambia Agriculture Research Institute, representing policy-makers, researchers, breeders and advocacy. The Zambia partial CWR checklist is available here.

Sources: Muliokela (1995), Phiri (2005), Ng'uni *et al.* (2017)

Generation of a partial CWR checklist for the SADC region

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Vincent H, Wiersema J, Kell S, Fielder H, Dobbie S, Castañeda-Álvarez N, Guarino L, Eastwood R, Leon B and Maxted N (2013) A prioritized crop wild relative inventory to help underpin global food security. Biological Conservation 167: 265–275.

Williams JT and Haq N (2002) Global Research on Underutilized Crops. An Assessment of Current Activities and Proposals for Enhanced Cooperation. ICUC, Southampton, UK.

4.2.4 Additional materials and resources

Lists of global or regional crop diversity:

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

EC (European Commission) (2016) Plant variety catalogues and databases.

FAO (2001) International Treaty on Plant Genetic Resources for Food and Agriculture. Food and Agriculture Organization of the United Nations. (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. Springer, Berlin, Heidelberg, New York.

Rehm S and Espig GE (1996) Die Kulturpflanzen der Tropen und Subtropen. Anbau, wirtschaftliche Bedeutung, Verwertung.

Sanchez-Monge E (1991) Flora Agricola. Vol 1 and 2. Ministerio de Agricultura, Madrid.

Schultze-Motel J (1966) Verzeichnis Forstlich Kultivierter Pflanzenarten [Enumeration of Cultivated Forest Plant Species]. Kulturpflanze Beiheft 4.

Vul'F EV and Maleeva OF (1969) Mirovye Resursy Polezznych 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.

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, Gatersleben, Germany.

WWW World Agroforestry Centre (2011a) Agroforestry Database. (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. (This tool enables the selection of useful tree species for planting anywhere in Africa using Google Earth).

Underutilized crops/neglected species lists:

Batlle 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). 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). 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). 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). 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.

Williams JT and Haq N (2002) Global research on underutilized crops. An assessment of current activities and proposals for enhanced cooperation. ICUC, Southampton, UK.

WWW Freedman B (2011) Famine Foods Database. (List of plants that are not normally considered as crops but that are consumed in times of famine).

WWW Plants for a Future (1996–2012) Plants for a Future Database. (A resource for information on edible and medicinal plants and those with other uses).

International agricultural statistics:

WWW FAOSTAT (Data on global production and value for crops that can be queried at a national level).

WWW EUROSTAT (Provides crop production information for European Union countries).

Flora checklists:

WWW Catalogue of Life

WWW eFloras.org (Links to flora information from various geographic units: Andes of Ecuador, Chile, China, Madagascar, Nepal, North America, Pakistan)

WWW Euro+Med PlantBase – the information resource for Euro-Mediterranean plant diversity

WWW Plants of Southern Africa (Online information about plants native to southern Africa and related topics)

WWW NEW Plants of Southern Africa (POSA) (Access to plant names and floristic details for southern African plant species)

WWW The Plant List – a working list of all plant species

WWW Tropicos.org – Missouri Tropical GardenTropicos

WWW USDA, ARS, National Genetic Resources Program. Germplasm Resources Information Network – (GRIN)

Global/regional checklists/inventories of CWR:

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. CAB International, Wallingford, UK, pp. 69–109.

Lala S, Amri A and Maxted A (2017) Towards the conservation of crop wild relative diversity in North Africa: checklist, prioritization and inventory. Genetic Resources and Crop Evolution, doi:10.1007/s10722-017-0513-5.

WWF and IUCN (1994) Centres of plant diversity. A guide and strategy for their conservation. 1st volume. IUCN Publications Unit, Cambridge.

WWW Harlan and de Wet Crop Wild Relative Inventory

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 on CD-ROM.

WWW USDA, ARS, National Genetic Resources Program. Germplasm Resources Information Network – (GRIN)

National CWR checklists:

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. (Available in English and French)

Hovhannisyan M (unknown date) State of national inventories on *in situ*/on farm in Armenia.

Bolivia:

Hunter D and Heywood V (eds) (2011) Crop Wild Relatives, A Manual of *In Situ* Conservation. Issues in Agricultural Biodiversity. Earthscan, London. (Available in English and French)

Bhutan:

Tamang A (2004) Crop wild relative inventory of Bhutan. MSc thesis, University of Birmingham, UK.

China:

Kell S, Qin H, Chen B, Ford-Lloyd B, Wei W, Kang D and Maxted N (2015) China's crop wild relatives: diversity for agriculture and food security. Agriculture, Ecosystems and Environment 209: 138–154.

Denmark:

Poulsen G (2009) Conservation of CWR in Denmark. Crop Wild Relative 7: 13–14.

Finland:

Fitzgerald H (2013) The National Crop Wild Relative Strategy Report for Finland. MTT Report 121, Jokioinen, 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 Utilization of Plant Genetic Resources for Food and Agriculture. Proceedings of the European Symposium, 30 June to 3 July 1998, Braunschwig, Germany. International Plant Genetic Resources Institute, Rome, Italy, pp. 38–43.

WWW Germany:

PGRDEU – Germany online CWR inventory

Guatemala:

WWW USDA, ARS. Atlas of Guatemalan Crop Wild Relatives (Atlas Guatemalteco de Parientes Silvestres de las Plantas Cultivadas)

WWW Ireland:

National Crop Wild Relative Database

Italy:

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

Panella L, Landicci S, Torricelli R, Gigante D, Donnini D, Venanzoni R and Negri V (2014) The National Crop Wild Relative Strategy for Italy: First Steps to be Taken.

WWW Madagascar:

Madagascar CWR inventory (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. CAB International, Wallingford, UK, 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.

Seychelles:

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

South Africa:

Hamer M, Adebola PO, Gerrano AS, Jansen van Rensburg WS, Kell S, Klopper RR, Magos Brehm J, Maluleke NL, Maxted N, Nkuna L, Raimondo DC, Thormann I, Tjikana TT, van Wyk E, Venter SL and Dulloo ME (2016) Identification of crop wild relatives in South Africa. 11th Southern African Plant Breeders Association Symposium. 8–10 March, Stellenbosch, South Africa.

Raimondo DC, Hamer M, Nkuna L, Mogale M, Ramashwe F, Ramavhunga M, Leballo G, Mantjane P and Khatieb S (2016) Identifying conservation priorities for crop wild relatives in South Africa. SADC Crop Wild Relatives Final Dissemination Meeting. 23–25 November, Pretoria, South Africa.

WWW South African National Biodiversity Institute (SANBI), Agricultural Research Council (ARC) and Department of Agriculture, Forestry and Fisheries (DAFF) (2017) CWR checklist and priority taxa of South Africa, doi:10.7910/DVN/LJWKBN, Harvard Dataverse, V1.

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.

Rubio Teso ML, Iriondo JM, Parra-Quijano M and Torres E (2014) National Strategy for the Conservation of Crop Wild Relatives of Spain.

Sri Lanka:

Hunter D and Heywood V (eds) (2011) Crop Wild Relatives, A Manual of *In Situ* Conservation. Issues in Agricultural Biodiversity. Earthscan, London. (Available in English and French)

WWW Sri Lanka CWR

Switzerland:

Häner R and Schierscher B (2009) First step towards CWR conservation in Switzerland. Crop Wild Relative 7: 14–16.

Häner R, Schierscher B, Kleijer G, Rometsch S and Holderegger R (2009) Crop wild relatives conservation. Agrarforschung Schweiz 16(6): 204–209. (German) (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. CAB International, Wallingford, UK, 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)

WWW UK CWR inventory

United States of America:

Khoury CK, Greene S, Wiersema J, Maxted N, Jarvis A, Struik P (2013) An inventory of crop wild relatives of the United States. Crop Science 53(4): 1496–1508.

Greene S and Khoury C (2011) What's in our back yard? Developing an inventory of US native and naturalized crop germplasm. Presentation on initial stages of US CWR project for C-8 symposium, ASA conference. October 2011.

WWW Crop wild relatives of the United States

Uzbekistan:

Hunter D and Heywood V (eds) (2011) Crop Wild Relatives, A Manual of *In Situ* Conservation. Issues in Agricultural Biodiversity. Earthscan, London. (Available in English and French)

Venezuela:

Berlingeri C and Crespo MB (2012) Inventory of related wild species of priority crops in Venezuela. Genetic Resources and Crop Evolution 59(5): 655–681.

Zambia:

WWW Ng'uni D and Munkombwe G (2017) CWR checklist and priority CWR of Zambia, doi:10.7910/DVN/8YXCFR, Harvard Dataverse, V1.

Several countries:

FAO Country Reports (2009). Albania, Benin, Brazil, Japan, Jordan, Kenya, Lao People's Democratic Republic, Malaysia, Mali, Pakistan, Senegal, Tanzania, Zambia, Zimbabwe. (Inventories of the wild relatives of major and minor crops, monographic approach)

Data standards and schema:

Cook FEM (1995) Economic Botany Data Collection Standard. Prepared for the International Working Group on Taxonomic Databases for Plant Sciences (TDWG). Royal Botanic Gardens, Kew.

Moore JD, Kell SP, Maxted N, Iriondo JM and Ford-Lloyd BV (2008) CWRML: representing crop wild relative conservation and use data in XML. BMC Bioinformatics 9: 116.

WWW Moore JD, Kell SP, Maxted N, Iriondo JM and Ford-Lloyd BV (2005–2008) Crop Wild Relative Information Schema

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).

4.3 PRIORITIZING THE CWR CHECKLIST

Why do we need to prioritize CWR for active conservation?

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 CWR conservation planning.

Figure 25 *Beta macrocarpa* Guss, a primary wild relative of and potential gene donor to cultivated beets namely of salt tolerant genes; it is Endangered (EN) at European level; here it is pictured in Quinta de Marim (Ria Formosa Natural Park, Portugal). (Photo: Maria Cristina Duarte)

There has been considerable debate about how species, in general, should be prioritized for conservation and about which criteria should be used (e.g. Fitter and Fitter 1997, Maxted *et al.* 1997). Possible criteria include: threat of genetic erosion, endemicity, rarity and population decline (Whitten 1990, Department of Environment 1996, Sapir *et al.* 2003), quality of habitat and intrinsic biological vulnerability (Tambutii *et al.* 2001), species abundance in relation to their geographical range size (Hoffmann and Welk 1999), "responsibility for the conservation of a species" (estimate of the geographic proportion of a species distribution in a certain country against the worldwide distribution) (Schnittler and Günther 1999), recovery potential, feasibility and sustainability of conservation (Whitten 1990), taxonomic uniqueness (Vane-Wright *et al.* 1991, Faith 1992) and genetic distinctiveness, phylogenetic criteria and the ability of a species to speciate within "new" environments (Linder 1995), cultural importance (Norton 1994, Dhar *et al.* 2000), economic factors (Bishop 1978) 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 CWR conservation priorities, several different criteria and numerous methods (see BOX 13) have been used depending on the needs and available resources of individual countries and/or the conservation agencies within the countries that are undertaking the prioritization exercise. Relatively recent studies have shown how CWR can be prioritized globally (Maxted and Kell 2009, Vincent *et al.* 2013), regionally (e.g. Ford-Lloyd *et al.* 2008) and nationally (e.g. Maxted *et al.* 2007, Magos Brehm *et al.* 2010, Kell *et al.* 2015). At each scale, the economic value of the related crop (hence breeder demand), the potential utilization for crop improvement (i.e. degree of relatedness of the wild relative to the crop/ease of crossing with the crop), and relative level of threat are the most commonly used criteria (Barazani *et al.* 2008, Ford-Lloyd *et al.* 2008)—prioritization methods usually use a combination of all three of these criteria.

An alternative, and more flexible, approach is to assign different levels of conservation priority to CWR—still based on the selected prioritization criteria—rather than identifying a list of equally important priority CWR. The top priority CWR are thus a number of taxa for which it is reasonable to consider implementing active conservation. In this way, a more extensive list can be more easily and objectively justified, maintained and updated, and taxa that are not of immediate priority may be given conservation attention at a later date. In addition, by using this approach, some of the taxa that are of less immediate conservation priority 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 taxa for *ex situ* conservation.

However, whichever prioritization methodology and criteria are used, the total number of target CWR should be adjusted to a number that can be actively conserved using available financial and human resources. There

is no precise way of estimating the most appropriate number of target CWR and so any estimate will be subjective.

BOX 13 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). This method consists of a series of rules that a species has to meet in order to fit in to a certain category, and can have two variants: it can be used to select those species that simultaneously fulfil ALL criteria (e.g. GP1B AND threatened), or to select those species that fulfil SOME of the criteria and so allowing some flexibility (e.g. ALL CWR THAT ARE EITHER GP1B OR GP2 OR threatened).

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 plant taxa worldwide (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). Scoring systems have also been complemented with multivariate analyses in order to identify groups of species with similar profiles (e.g. Given and Norton 1993), determine 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 to develop 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". 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 all 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). Primarily, this priority-ranking system has been applied to vertebrates and plants (Master 1991), where the species' ranks were based on a series of criteria relating to species' rarity (number of individuals, number of populations or occurrences, rarity of habitat and size of geographic range), as well as 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/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 was 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)

4.3.1 Methodology

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 or complex and time-consuming depending on a number of factors such as the scale, methodology, and criteria used, the number of taxa in the CWR checklist and the available resources. Both criteria and methodology should be defined by the national agency or researcher that is prioritizing CWR and should, ideally, involve major stakeholders that play a role in CWR conservation and use (see Magos Brehm *et al.* 2016).

In terms of the method, the starting point for prioritization is the CWR checklist. Whatever the approach, floristic or monographic, prioritization essentially consists of three main steps: (i) define the prioritization criteria to be applied, (ii) define the prioritization methodology and (iii) apply both the criteria and

prioritization methodology to the CWR checklist (Flowchart 2). Associated with these steps there will also be a need to consider how many priority CWR will be flagged for immediate conservation action.

(i) Define the prioritization criteria. There are three main criteria that are generally used in CWR prioritization:

- **Socio-economic value of the related crop**: the primary application of a CWR is in the genetic improvement of existing crop varieties or the creation of new ones. The economic importance of the related crop species is thus a good indicator of the value of their wild relatives. The selection of priority crops will vary according to the 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 food security and nutrition), crops with high economic value and crops with multiple use values. It should be noted that a single genus may contain more than one crop (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: production value, quantity produced and/or surface area cultivated over a specific time period, number of varieties grown at national level, value to local populations or regions of the target country and the importance of the crop as an energy source e.g. average annual contribution of dietary energy (kilocalories) per capita per day. In addition, these sub-criteria can be considered at national, regional, continental and/or global scales, and by considering some or all of these different levels it will help to build a clearer picture of the relative importance of crop wild relatives at these different scales. See how this criterion has been used in China and South Africa.
- **Utilization potential for crop improvement**: wild taxa belonging to a single crop gene pool are genetically related to one another, and some are more closely related to the crop than others. To determine the degree of relatedness between a crop and its CWR and therefore the utilization potential of the wild relatives, where genetic information is available, CWR taxa can be classified using the Gene Pool concept. For some crops, the Gene Pool concept has already been defined (see here and here), however, if genetic data are not available and the Gene Pool concept has not been previously defined, the Taxon Group concept, 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. In addition, wild relatives in GP3 or TG3 and TG4, that have already been used as gene donors or have shown promise for crop improvement, should also be assigned high priority. If neither the Gene Pool nor the Taxon Group concept can be applied, then the available information on genetic and/or taxonomic distance should be analyzed to make reasoned assumptions about the most closely related taxa. 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 classifications are available to establish new Taxon Group concepts and determine the degree of relatedness of each wild relative to its associated crop (see here for more materials on this subject).
- **Threat status**: relative threat is commonly used to prioritize taxa for conservation, i.e. the more threatened—for example with an increased likelihood of genetic erosion or actual extinction of the species—the greater the conservation priority. Using this criterion involves the collation of existing threat assessments in a three stage process: (i) identify potential sources of CWR threat assessments, (ii) identify whether CWR have been Red List assessed and (iii) collate threat assessments (at national, regional and global levels). For CWR lacking threat assessments, the following steps can be taken: (i) gather the necessary data and undertake a novel Red List assessment, (ii) use an indicator to determine threat (e.g. endemism, distribution, inferences from known threats to taxa/loss of habitats/land use types) or (iii) consider not using threat status as a prioritization criterion. Existing threat assessments can be gathered from national Red Lists and Red Books published based on the IUCN Red List Categories and Criteria (IUCN 2001)—the most commonly applied means of assessing threat to wild taxa—or from other national threat assessment systems, the IUCN Red List of Threatened Species (for global Red List assessments), or peer-reviewed papers and reports and expert knowledge. Threat assessments can be carried out at different geographical scales (i.e. global, regional, national), and all scales should be taken into account in the prioritization process. However, as the implications of threat

status depend on the scale of the assessment, this should also be taken into account when applying the criterion of relative threat.

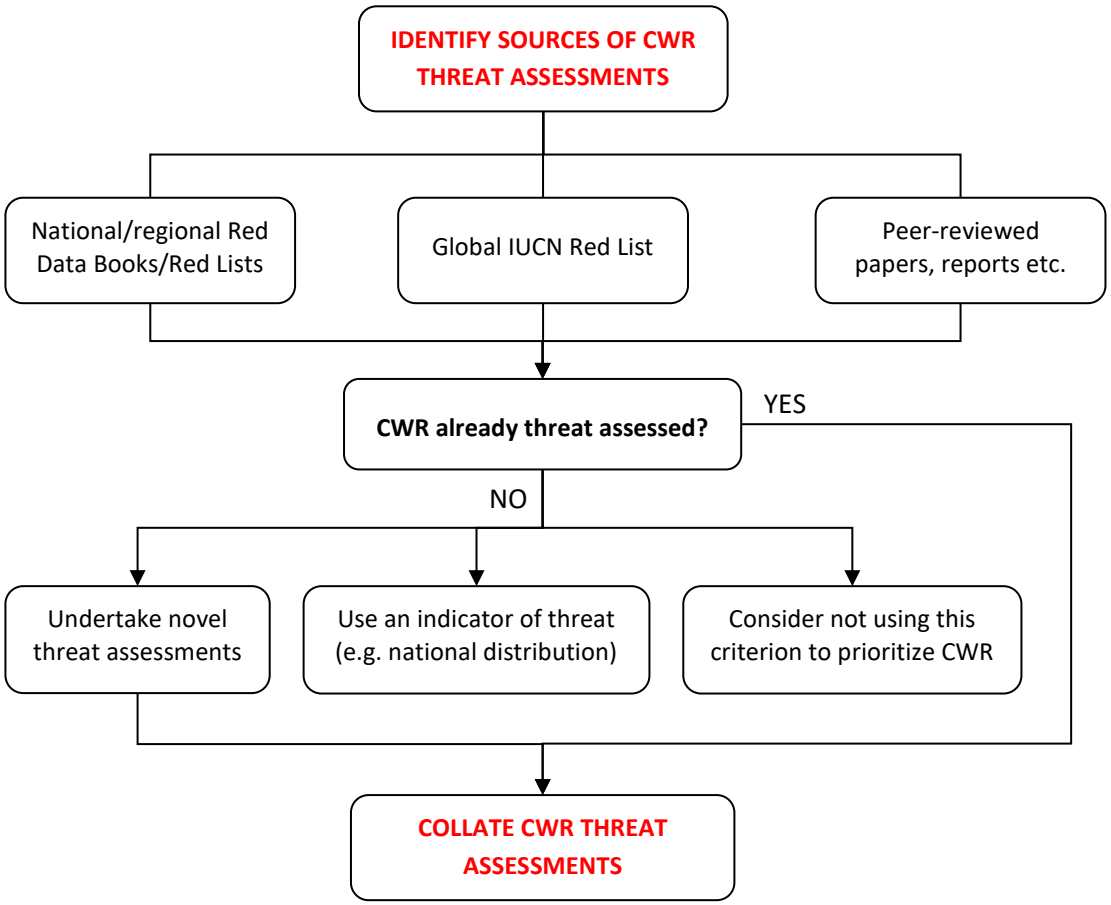
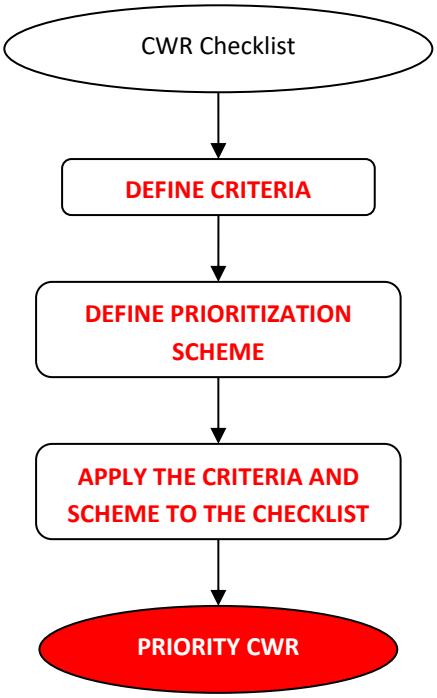


Figure 26 Collation of CWR threat assessments.

(ii) Define the prioritization methodology. Prioritization schemes often include rule-based and scoring systems, with or without weighting of the criteria, and using different combinations of criteria (see BOX 13). Prioritization may be carried out either in parallel or in series. Prioritization in parallel (i.e. scoring systems) is where the selected criteria are scored against all taxa first, then the scores are summed and the taxa with the higher scores are the prioritized taxa. Prioritization in series is where the criteria are scored in a sequence using one criterion at a time and only the high scoring taxa for the first criterion is scored for the second criterion and so on, until finally the remaining taxa at the end of the process are the prioritized taxa. While the prioritization in parallel may include some irrelevant/distantly related CWR, the prioritization in series may miss important CWR. The choice of the method is up to the researcher/country' stakeholders doing the prioritization and care should be taken in making this decision.

(iii) Apply both the criteria and prioritization methodology to the CWR checklist. Once the criteria and the method have been defined, they will need to be applied to the CWR checklist. If a scoring system has been defined as the prioritization method, then scores for each criterion need to be assigned to each CWR in the checklist. The scores are then summed, and the taxa with the highest total scores are prioritized. The minimum total score required for prioritization is subjective and may depend on the financial resources available to conserve priority CWR. If a serial prioritization is to be carried out, then CWR may be filtered based on the first prioritization criterion, then the second criterion, and so on. After applying all criteria, the prioritized taxa are those that remain. Regardless of the method used, it will culminate in a list of priority CWR.



Flowchart 2 Process of prioritizing the CWR checklist.

BOX 14 OTHER PRIORITIZATION CRITERIA

Three criteria are generally used when prioritizing CWR: economic value of the related crop, utilization potential for crop improvement and threat status. Nevertheless, there are many other criteria that have been used and can be considered when prioritizing CWR:

- **Status of occurrence**: whether the CWR is native to the country, introduced*, and if it is known to be invasive.
- **Conservation status**: whether sufficient genetic diversity is already conserved *in situ* and/or *ex situ*. Additional conservation efforts may not be justified for those CWR already efficiently conserved, and resources should focus on those species that are not conserved.
    - *Ex situ*: careful attention to the information obtained from current *ex situ* conservation holdings should be paid because: the material held in genebanks might be incorrectly determined, dead, in poor condition 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.
    - *In situ*: two types of *in situ* conservation can be distinguished: passive, when a species occurs within a protected area but it is not being monitored and managed, and active conservation, when species and genetic diversity is afforded long-term monitoring and management. Therefore, a species that is found in a protected area is not necessarily adequately conserved. Higher conservation priority can then be assigned to CWR that do not occur within existing protected areas, then to those that are passively protected and lastly to those that are actively protected in at least part of its native range.
- **Legislation:** if the taxon is under any kind of regional, national or local legislative protection 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.
- **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 that 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. When deciding priorities on the basis of the geographical range of taxa, a degree of objectivity is required since there is no clear dividing line between a taxon with a limited, and therefore threatened, range and one with a limited range but not in immediate need of conservation action.
    - *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 (see Ford-Lloyd *et al.* 2008, 2009). 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 extent of the species' distribution within those countries.
    - *National distribution:* the distribution of the taxon within the country (e.g. the number of provinces/districts/states where each taxon occurs, extent of occurrence). It may be considered as an indicator of rarity or threat; a species occurring in few regions within the country is considered rarer than a species occurring throughout the country.
- **Other criteria**: these may include population data, genetic diversity information, relative costs of conservation, selection of wild relatives of crops in centres of crop origin when prioritization is being carried out in countries located in centres of crop origin etc.

* 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).

BOX 15 HOW TO DEAL WITH MISSING INFORMATION WHEN PRIORITIZING CWR FOR CONSERVATION

When gathering information to prioritize CWR for conservation action, we often face the problem of missing information—for example, not all CWR have been Red Listed and the genetic relationships between crops and their wild relatives are not known for all crop gene pools. Missing information is a general problem in all steps of conservation planning and we need to make use of the available information in the best way possible, as well as taking into account that some information is missing.

Regarding the three main prioritization criteria: economic value of the related crop, utilization potential for crop improvement and threat status, missing information may include:

- Socio-economic value data for all relevant crops.
- Known or potential uses of the wild relative in crop improvement.
- Gene Pool or Taxon Group concepts for the wild relative.
- Threat status of the wild relative.

Options to help compensate or nullify the impact of the different types of missing information when prioritizing CWR:

- Socio-economic value data missing for all relevant crops. This situation is very common as only major crops or crop groups usually have this type of information. Rather than using socio-economic data, any indicator of economic value can be used instead, e.g. knowledge of the local, national or regional socio-economic value of crops (e.g. for particular nutritional qualities, local market value or cultural importance), the number of varieties of a crop cultivated in a country or region, the number of accessions of crops held in national or regional genebanks to give an indication of how important those crops are for the country/region. However, not only do these indicators introduce a degree of subjectivity to the analysis, practitioners should be careful when ranking their importance with respect to other crops since direct comparisons cannot be made using different indicators (Kell *et al.* submitted). For instance, socio-economic data are often combined into crop groups (e.g. FAOSTAT presents data for millets, a crop group that includes *Echinochloa*, *Eleusine*, *Eragrostis*, *Panicum*, *Pennisetum*, *Setaria* crops). In this particular case, all crop genera within the crop group can be given the same socio-economic value.
- Known or potential uses of the wild relative in crop improvement. When the uses of a wild relative are unknown, the Gene Pool concept can be used as a proxy for the potential of the wild relative for crop improvement, as it reflects its genetic proximity to the crop. If the Gene Pool concept is also missing, the Taxon Group concept can be applied instead to determine the taxonomic proximity of the wild relative to the crop.
- Gene Pool or Taxon Group concepts for the wild relative. If these data is not readily available in the current main sources (the Harlan and de Wet inventory and GRIN Taxonomy for Plants), ideally literature searches should be undertaken. If this information is still missing and if you are using a scoring system, the score for missing information should distinguish between situations where there is no information on the potential utilization for crop improvement and cases where the wild relative is not of potential use for crop improvement, i.e. rather than scoring a '0', a 'not applicable' would be more suitable. On the other hand, if you are using a serial system then you might consider either prioritizing only those species which have potential utilization for crop improvement information (Gene Pool or Taxon Group concepts and known and potential uses in crop improvement) or using the generic concept (or the TG4 definition, i.e. that all wild species in the same genus as the crop are CWR) and prioritize all species within the same genus of a crop.
- Threat status of the wild relative. If the extinction risk of a particular CWR has not been assessed either using the IUCN Categories and Criteria (IUCN 2001) or another (national) threat assessment system, then we can categorize these taxa as NE (Not Evaluated). If you are using a scoring system the score for NE should take into account that the species is a priority for Red List assessment and not necessarily a low priority for conservation action. In this way, there is no implication in terms of conservation planning. If you are using a serial system you could prioritize first based on the criteria for which you have data and then add to the prioritized list those CWR that have information on threat status and that are threatened (as suggested by Kell *et al.* submitted).

Other suggestions include:

- If a scoring system is being applied to prioritize the CWR checklist, calculate an 'index of scoring precision' per species in order to estimate the number of criteria that contributed to the score obtained for that particular CWR. It can be estimated by counting the number of criteria used in the scoring of that species, divided by the total number of criteria (Magos Brehm *et al*. 2012). This is only applicable when a scoring system with more than five criteria is used for prioritizing CWR, and it implies that all criteria are equally valuable, which is unlikely to be the case. How to use this information to obtain the final list of priority species or to assign different levels of conservation priority is the responsibility of the researcher undertaking the task.
- To decide not to use the criteria for which information for the majority of the CWR is missing in a scoring system. For instance, if only four species out of a few hundred have been Red Listed, it is not advisable to use 'threat status' as a prioritization criterion. It is suggested that for any prioritization criterion, if more than two thirds of the data for the taxa being prioritized is missing then that criterion should not be used.

Finally, it should be highlighted that CWR taxa that lack any of the data listed above should be tagged as 'high priority to obtain the missing information'.

4.3.2 Examples and applied use

Collation of existing 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. Existing threat assessments were collated and, where 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).

Given that a national Red List did not exist; a large-scale literature search was conducted to identify all relevant threat assessment information. Sources included: (i) 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, (ii) assessments undertaken using the 2001 version of the IUCN Categories and Criteria (IUCN 2001) (e.g. Aguiar *et al.* 2001a,b; Mitchell 2004), (iii) other assessments that used the threat assessment vulnerability index by Maxted *et al.* (2004) (e.g. Magos Brehm 2004), and (iv) information on species endangered by overexploitation (e.g. Ramos Lopes and Carvalho 1991). Threat assessment information was then used, together with other criteria, to establish conservation priorities among the Portuguese CWR (see Magos Brehm *et al.* 2010). When multiple assessments for the same taxon were collated, prioritization was based on the most recent.

CWR prioritization at national level: China

Priority CWR were selected in China based on three main criteria: (i) socio-economic value of the related crop, (ii) threat status, (iii) value of CWR in crop improvement programmes.

(i) Socio-economic value of the related crop. FAO crop production statistics (FAO 2014) were used to obtain annual production values of human food crops cultivated in China over the ten year period 2002–2011. Human food crops with an average annual production value of >US$500 million over this period with native CWR in China were selected from the CWR China checklist. Additionally, the global values of human food crops in terms of average annual energy supply per capita over the ten year period 2000–2009 were calculated from FAO food supply statistics (FAO 2014) for the major sub-regions of the world to highlight the crops of particular global value for food security. Wild relatives of these crops that were not already included in the list based on national economic importance were added to the priority list of taxa.

(ii) Threat status. Threatened and Near Threatened taxa in the list obtained in (i) as well as those endemic to China were identified using the China Red List of Biodiversity – Higher Plants Volume (MEP and CAS 2013).

(iii) Value of CWR in crop improvement programs. Taxa that are likely to have greater use value for crop improvement were identified by consulting data on the degree of relationship between the crop species and the wild relatives in the crop gene pool and/or the known use of the CWR in breeding programs (Vincent *et al.* 2013).

The final priority CWR list comprised the wild relatives identified by each of the three criteria above.

Source: Kell *et al.* (2015)

CWR prioritization at national level: India

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

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

A first prioritization shortlisted those taxa that (i) were morphologically and genetically closest to their related crops, (ii) have a limited distributional range, (iii) are rare and/or endemic, (iv) are threatened due to overexploitation, (v) are taxa of high socio-economic significance and (vi) are lacking adequate information.

Final priorities were assigned to taxa that met at least one of the following criteria:

- Endemic to a particular region.
- Distribution restricted to one to two biogeographic zones.
- Critically Endangered due to overexploitation or habitat destruction.
- Contributed genes of resistances to modern cultivars and facing threats due to anthropogenic factors.
- Potential source of useful traits.
- 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 prioritized.

Source: Rana *et al.* (2000)

CWR prioritization at national level: South Africa

The South Africa food and fodder CWR checklist was prioritized based on five main criteria: (i) socio-economic value of the related crop, (ii) potential for use of the wild relative in crop improvement, (iii) threat status, (iv) distribution status and (v) occurrence status.

- Socio-economic value of the related crop. Socio-economic value was considered at regional (SADC region), continental (Africa) and global scales allowing wild relatives of a range of food crops to be considered. The 10–year average production value (in million US$) (2003–2012), with countries averaged, for the SADC region was obtained from FAOSTAT and provided by the *Crop and Crop Genus Lists for National CWR Checklists and Checklist Prioritization* spreadsheet (Kell, unpublished). In addition, the importance of human food crops or crop groups as an energy source in Africa was assessed as those with an average annual contribution of dietary energy (kilocalories) per capita per day of ≥1.5% over the period 2000–2009 (extracted from Kell *et al.* 2015). Finally, crops of particular global value for food security were identified on the basis that they provide ≥3% of plant derived dietary energy supply in one or more sub-regions of the world.
- Potential for use of the wild relative in crop improvement. The gene pool concept and the taxon group concept were used as an indication of their relatedness to the crop, hence their potential utilization value in crop improvement. In addition, confirmed used in crop improvement were also considered. Both the Harlan and de Wet inventory and GRIN Taxonomy for Plants were used to obtain such information. Where a taxon has potential for breeding for more than one crop, the score for the genepool level for each crop was allocated and then the scores were totaled. This meant that a higher priority was assigned to such taxa than taxa that only have breeding potential for a single crop.
- Threat status. The *Red List of South African Plants* (Raimondo *et al.* 2009) was consulted in order to obtain the threat status of all CWR in the checklist.
- Distribution status. Each taxon in the CWR checklist was categorized into either South Africa endemic or no endemic.
- Occurrence status. Each taxon in the CWR checklist was categorized into either indigenous to South Africa or naturalized, i.e. alien species that form populations that maintain a reproductive population for at least 10 years without direct intervention by people[4].

Each taxon in the food and fodder CWR checklist for South Africa was scored for each criterion using the scoring system presented in the Table below. The scores were then summed for each taxon; the scores ranged from 1 to 26. Those taxa that scored ≥11 were included in the priority list. In addition, all GP1b, and GP2 taxa that did not score ≥11 were further added to the priority list because these are indigenous taxa that have been studied and found to have potential for gene transfer to crops and so they are important in the context of crop improvement. Finally, those taxa in GP3 that have either conrfirmed or potential uses in crop improvement have been also added to the priority list. The final priority list of CWR included a total of 258 taxa (234 species, from 32 genera and 15 families).

CRITERIA	SCORES					
	5	4	3	2	1	0
Economic value of related crop: SADC region (average production value for 2003-2012, with	>2 billion US$/year	1-1.9 billion US$/year	0.5-0.999 billion US$/year	0.2-0.499 billion US$/year	0.001-0.199 billion US$/year	<0.001 billion US$/year

[4] Definition of naturalized species from USDA Natural Resources Conservation Service.

countries averaged)						
Socio-economic value of related crop: Africa (daily energy contribution averaged between 2000-2009)	>10% of daily energy supply (Kcal/capita/day)	= 7–9.9% (Kcal/capita/day)	4–6.9% (Kcal/capita/day)	2–3.9% (Kcal/capita/day)	0.1–1.99% (Kcal/capita/day)	
Socio-economic value of related crop: global importance			Provide ≥3% of plant derived dietary energy supply in one or more sub-regions			Provide <3% of plant derived dietary energy supply in one or more sub-regions
Potential for crop improvement: Gene Pool (GP) concept (totalled if GP for >1 crop) OR Taxon Group concept (TG)	GP1b OR TG1a	GP2 OR TG1b	GP3 OR TG2	TG3	TG4	
Threat status according to IUCN categories OR Categories for taxa not meeting IUCN threat criteria but of conservation concern[5]	Critically Endangered/ Critically Endangered-Possibly Extinct	Endangered	Vulnerable Critically Rare	Data Deficient/ Near Threatened Rare/Declining	Least Concern	Extinct Not Evaluated Not Critically Rare/Rare or Declining
Distribution status			Endemic			Not endemic
Occurrence status			Indigenous			Naturalised

Source: Hamer *et al.* (2016)

[5] Both the the 2001 IUCN Red List Categories and Criteria Version 3 and national Red List categories.

CWR prioritization at national level: 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 (MAGRAMA 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 experts and revised. Given the large number of taxa from 202 genera, priority genera were 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 with registered crop varieties in Spain. Additional genera were also prioritized due to their national socio-economic importance. Fifty genera were then prioritized 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, 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 further prioritized using the following criteria:

- Taxon belonging to Gene Pools 1B and 2, or classified into Taxon Groups 1B, 2 or 3, or
- Threatened (or Near Threatened according to IUCN Red List Categories), or
- Endemic to Spain.

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

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

Figure 27 *Lupinus angustifolius* L. (blue lupin), one of the priority CWR in Spain. Wild populations occur in Spain and it belongs to the primary Gene Pool of the cultivated forms of blue lupin. It is also a secondary wild relative of the cultivated yellow lupin (*L. luteus* L.) (Photo: Rubén Milla).

CWR prioritization at regional level: SADC region

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4.3.4 Additional materials and resources

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WWW CWR *In Situ* Strategy Helpdesk

National/regional CWR prioritization:

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Economic value data:

WWW EUROSTAT (Provides information for European Union countries)

WWW FAOSTAT (Data on global production and value for crops that may be queried at a national level)

Gene Pool and Taxon Group information:

WWW Harlan and de Wet Crop Wild Relative Inventory

WWW USDA, ARS, National Genetic Resources Program. Germplasm Resources Information Network – (GRIN)

Global/regional Red Lists and global/regional CWR Red Lists:

WWW Global:
IUCN Red List of Threatened Species

Europe:

Bilz M, Kell SP, Maxted N and Lansdown RV (2011) European Red List of Vascular Plants. Publications Office of the European Union, Luxembourg.

National Red Lists and national CWR Red Lists:

WWW National Red Lists Portal. (Searchable for regional and national red listed species)

Bolivia:

Mora A, Zapata Ferrufino B, Hunter D, Navarro G, Galeano G, Apaza KS, Baudoin MJ, Dulloo ME, Cuellar S, Beck SG, Ferreira W and Scheldeman XA (2009). Libro Rojo de Parientes Silvestres de Cultivos de Bolivia. VMABCC-Bioversity International, Rome, Italy.

Databases of invasive species:

WWW CABI Invasive Species Compendium

WWW European and Mediterranean Plant Protection Organization: EPPO Global Database (includes invasive plant species)

WWW ISSG Invasive Species Specialist Group: Global Invasive Species Database

4.4 COMPILATION OF THE CWR INVENTORY

Why do we need to prioritize CWR for active conservation?

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 CWR conservation planning.

Alongside checklists, CWR inventories provide the essential foundations for the formulation of *in situ* and *ex situ* conservation strategies. CWR inventories usually include information on priority CWR relevant to conservation planning and they provide policy-makers, conservation practitioners, plant breeders and other user groups with a view of current CWR priorities. As CWR priorities change over time, so should CWR inventories.

Figure 28 *Brassica barrelieri* (L.) Janka, a secondary wild relative of turnip (*B. rapa* L.), here pictured in Spain. (Photo: Julia Chacón-Labella)

Figure 29 A wild population of *Lupinus angustifolius* L. (blue lupin) in Spain. Wild populations of L. angustifolius belong to the primary gene pool of their cultivated counterparts. It is also a secondary wild relative of the cultivated yellow lupin (*L. luteus* L.). (Photo: José Iriondo)

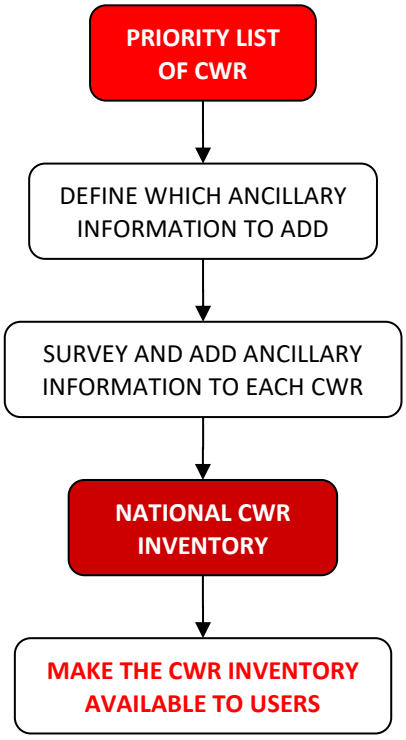
4.4.1 Methodology

The preparation of a CWR inventory involves three steps: (i) define which ancillary information should be added to each prioritized CWR, (ii) survey and add that information to the information system and (iii) make the CWR inventory available to users (Flowchart 3).

(i) Define which ancillary information should be added to each prioritized CWR. Types of information for each priority CWR include: nomenclature, related crop(s), Gene Pool or Taxon Group relationship to each related crop, actual and potential utilization of the CWR for crop improvement, biology, habitats, ecogeography, direct uses, threats and threat status, current conservation actions and legislation. It should be emphasized that some of these data might have already been collated in the annotated CWR checklist to prioritize it (e.g. potential utilization for crop improvement, threat data).

(ii) Survey and add that information to the information system. Various sources of information will need to be surveyed in order to be able to collate the ancillary information defined in the previous point. A checklist and inventory template to compile the CWR inventory is currently being developed.

(iii) Make the CWR inventory available to users. This can be achieved via a scientific publication, grey publication, a website or a research data repository (e.g. Dataverse).



Flowchart 3 Overview of the creation of a national inventory of CWR.

4.4.2 Examples and applied use

Inventory of priority CWR of the SADC region

Inventory of global priority CWR

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, called the Harlan and de Wet Crop Wild Relative inventory. It is referred to as the Harlan and de Wet Crop Wild Relative inventory 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 inventory contains background information on 173 food and agricultural crop gene pools and 1,667 priority CWR taxa from 37 families, 109 genera, 1392 species and 299 sub-specific taxa. The taxa included were deemed priority CWR based on their inclusion in GP1B or GP2, or Taxon Groups (TG)1B, 2 or 3 (see here for more information on the Gene Pool and Taxon Group concepts). There are also a limited number of GP3 and TG4 taxa included if they have previously been shown to be useful in breeding. Taxa are organized by genus in alphabetical order and according to the GP or TG 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 facilitates global and national conservation planning as, for the first time, a comprehensive and systematic list of global priority CWR taxa of the major and minor crops of the world is available.

Source: Vincent *et al.* (2013)

4.4.3 References

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4.4.4 Additional materials and resources

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4.5 DIVERSITY ANALYSES: DISTRIBUTION AND ECOGEOGRAPHIC DIVERSITY OF PRIORITY CWR

What is an ecogeographic study and why it is needed?

It involves the collation of occurrence data for the priority CWR, followed by the analysis of these data in order to understand the patterns of diversity within and among priority CWR taxa (hotspot analysis, ecogeographic diversity etc.). An ecogeographic survey 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" (Maxted *et al.* 1995). The results obtained from these analyses will assist the formulation, establishment and implementation of conservation priorities through: (i) production of (predicted) species distribution maps, (ii) assessment of sampling biases, (iii) characterization of the priority CWR at ecogeographic level, (iv) identification of areas for *in situ* conservation of priority CWR (hotspots, complementarity areas etc.) and (v) 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 genebanks.

Ecogeographic analyses are generally based on the collation of information from herbarium specimens, genebank accessions, databases, literature and all other possible data sources. If possible, they should be complemented by the collection of novel occurrence data, particularly if the taxon is poorly known.

This method has become routine and is now commonly applied to conservation planning, it is also becoming increasingly sophisticated and detailed due to the development of tools such as Geographic Information Systems (GIS) (see BOX 16). However, it should be stressed that using ecogeographic analysis is always sub-optimal, wherever possible it is better to use genetic diversity analyses rather than using ecogeography as a proxy for genetic diversity.

BOX 16 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.
- Establishment of genetic reserves.
- Predict the impact of climate change on natural populations, etc.

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

4.5.1 Methodology

An ecogeographic study comprises three main phases: project design, data collection/analysis and the ecogeographic products. The project design includes: (i) identification of target taxa expertise, (ii) selection of target taxa taxonomy, (iii) delimitation of target area and (iv) design and creation of the database structure (optional). The data collection and analysis phase includes: (v) survey of occurrence data, as well as passport, site and environment, and existing characterization and evaluation data, (vi) collation of occurrence data into the database, (vii) data verification and (viii) data analysis. The ecogeographic products include: (ix) a CWR occurrence database (which contains raw data), (x) a conspectus (that summarizes the taxonomic, geographical and ecological data for the target taxa) and (xi) a report (which interprets the data and results obtained) (Flowchart 4).

(i) Identification of taxa expertise. Taxon experts and experts in the flora of a target area may provide accurate species location and ecological information and may be able to recommend relevant grey literature, Floras, monographs, taxonomic databases, the appropriate herbaria and genebanks to visit. They could 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 genebank curators.
- NGOs working in conservation in the target region or on target crops.

(ii) Selection of target taxa taxonomy. The most widely accepted taxonomic classification can be determined with the aid of:

- Target taxon experts.
- National or global Floras.
- Taxonomic monographs.
- Recent taxonomic revisions.
- Taxonomic databases etc.

It is important to detect existing synonyms 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 Strategic Action Plan for CWR Conservation (NSAP), this step would already have been undertaken as part of the creation of the CWR checklist.

(iii) Delimitation of the target area. Normally an ecogeographic study should include the whole range of a species' distribution so as to avoid the problem of non-compatible datasets that can be inherent in multiple surveys of the same taxon. However, given that conservation planning included in a NSAP is undertaken at national level, the whole country should be the target area.

(iv) (Design and creation of the occurrence database structure.) This step is optional as the use of the existing Occurrence data collation template is recommended (see step vi for more details).

(v) Survey of occurrence data. Sources of data are likely to include:

- Herbaria and genebanks (as well as online sources). See BOX 17 on 'Factors to take into consideration when using *ex situ* passport data in conservation planning'.
- Scientific and 'grey' literature: Floras, monographs, recent taxon studies, reports of Environmental Impact Assessment studies[6], databases, gazetteers, scientific papers, soil maps, vegetation maps, atlases etc., available both in paper form and as digital files.
- Existing GIS layers illustrating species distribution.
- 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 observations of the target taxa.
- For examples of data sources, click here.

[6] Environmental Impact Assessments (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 are a means of assessing the possible negative and positive natural, social and/or economic impacts that a project (e.g. highway, dam, building etc.) may have. EIA reports generally provide species lists of flora (and fauna) that occur in the area where the project is to be undertaken, and so they are important sources of species distributional data.

In addition, have a careful look at the recommendations listed in Annex A of Castañeda *et al.* (2011), which aims to facilitate the recording of passport data.

Ideally, occurrence data should be available for every CWR included in the study, though it should be stressed that georeferencing is often required to ensure the necessary data is complete. The broader the sampling of occurrence data the more geographically and ecologically representative the data, and ultimately the results, will be.

(vi) Collation of occurrence data into database. The use of the existing Occurrence data collation template is recommended. The template caters for different types of data (genebank accessions, herbarium specimens, bibliographic references, internet references, biodiversity or botanical databases (e.g. GBIF), personal communications from experts and field observations) and, if the data is to be used for ecogeographic diversity analyses, the template also helps the user to prepare the data for use in the CAPFITOGEN tools (Parra-Quijano *et al.* 2016)http://www.capfitogen.net/en/).

(vii) Data verification (Figure 30).

- Check for duplicates. There are several types of duplicates:
  - **Duplicate records**: occurrence records that refer to the exact same record but the information came from different sources or was reported twice from the same source. These should be removed from the dataset.
  - **Duplicate accessions/herbarium vouchers**: genebank accessions or herbarium vouchers that were collected in the same locality, by the same collectors on the same date but held in different institutions. Usually these refer to collections that were divided by the collectors to be distributed among different institutions. These should not be removed from the dataset but should be tagged as duplicates. They may be useful, for example, to give an idea of the amount of seed available, however they are not relevant for the diversity, gap or climate change analyses.
  - **Duplicate populations:** populations (with the exact same coordinates) that have been sampled more than once at different dates by the same, or different, collectors. These are not duplicate records nor duplicate accessions/vouchers and should not be removed from the dataset. They will give an indication of how intensively that particular species is being collected, but they are also not relevant for diversity, gap or climate change analyses.
- Check for spelling errors and standardize data format.
- Georeference all the entries, if possible. All data should also be georeferenced by using (online) gazetteers, maps, Google Earth etc. (see here for georeferencing resources).
- Assign a level of geographic precision (Table 3). Different levels of precision can be assigned to each record. The appropriate level of precision to be considered for each type of data analysis can then be decided upon. For example, to locate areas for active *in situ* conservation, only very accurate data (levels 1, 2 and 3) might be used, but to map hotspots, both accurate data and coarser scale data might be used (levels 1, 2, 3 and 4).
- Check for outlier locations. Distribution maps should be created (using GIS if possible) to look for outlier collection sites. All outlying individual records should then be corrected or, if correction is not possible, tagged and not used in the analysis.

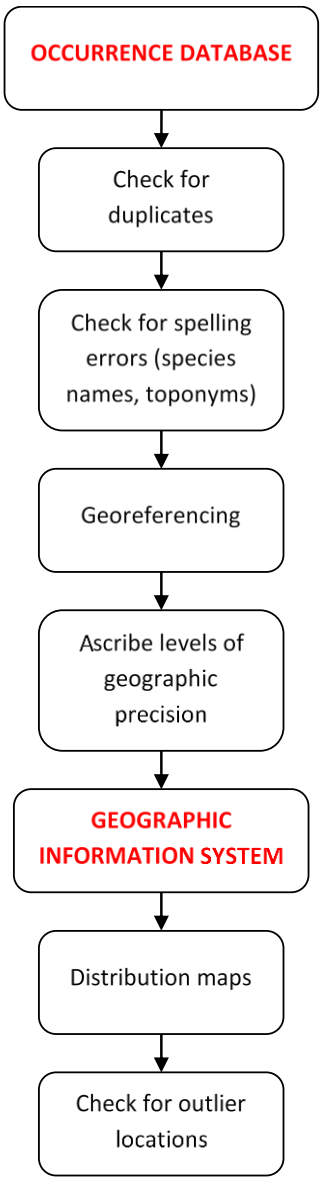


Figure 30 Schematic representation of occurrence data verification.

Table 3 Examples of location data and their corresponding level of geographic precision (from Maxted *et al.* 2013).

LEVEL OF GEOGRAPHIC PRECISON	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

(viii) Diversity analyses of collated occurrence data. Data analyses may include:

- Distribution maps and assessment of sampling bias: these analyses will provide an understanding how CWR taxa are distributed throughout the target region as well as revealing any bias in the occurrence data.
    - **Species distribution maps**. These may include observed distribution maps (generally a point map based on occurrence data) and predicted distribution maps (which require species distribution modelling). Predicted distribution maps are often used when the occurrence dataset is incomplete for a particular species. Incomplete datasets are often due to a lack of survey work having been carried out for a species whose distribution is largely unknown. Species distribution maps are generally created using a Geographic Information System (GIS). There are several softwares that can be used (click here for examples) but we recommend DIVA-GIS which is freely available online, or a more sophisticated software (e.g. ArcGIS) for more options for analysis and map presentation. Predicted distribution maps can be produced using a species distribution modelling software. We recommend the use of MaxEnt (Phillips *et al.* 2006) due to its performance when compared with other modelling approaches and its widespread use in conservation analyses (Elith *et al.* 2006).
    - **Assessment of sampling bias**. Analysis of bias determines whether species or certain geographic areas are over- or under-represented in an occurrence dataset. The results of this analysis will provide an understanding of how the collation of data has impacted the results of an ecogeographic analysis. In addition, it will reveal under-represented taxa and/or areas that have not been sampled and where the taxon is likely to occur, therefore highlighting the need of further field survey work to obtain a more balanced occurrence dataset (for more information, refer to Hijmans *et al.* 2001). Regarding geographic sampling bias in particular, Scheldeman and van Zonneveld (2010) present methods—including species accumulation curves and the rarefaction method—that can be undertaken using DIVA-GIS.
- Ecogeographic diversity analysis: this analysis will provide an understanding of the patterns of ecogeographic diversity across the distribution of each priority CWR taxon. The results can then be used to identify appropriate areas for active *in situ* conservation or populations suitable for collection and *ex situ* conservation. An ecogeographic diversity study may involve the production of ecogeographic land characterization maps (ELC maps) (Parra-Quijano *et al.* 2008, 2012b). These maps identify various ecogeographic scenarios in which a species occurs, which—assuming they are a good proxy for genetic diversity—reflect the adaptations of the studied species that enable it to thrive in that particular set of ecological conditions. As a result, ELC maps help to identify important diversity within a taxon, which links to the potential utilization of intra-CWR diversity for crop improvement. Ecogeographic diversity analysis can be undertaken using the CAPFITOGEN tools (Parra-Quijano *et al.* 2016) and in general it involves:
    - Deciding whether a species-specific or a generalist ELC map is to be produced. A species-specific ELC map is produced based on the selection of appropriate geophysical/bioclimatic/edaphic

variables that are most likely to determine the shape of the geographical distribution of that particular species. The map should reflect the ecogeographical diversity within one species across the target geographic area. It is a more complex and time-consuming approach than a generalist ELC map but is also more biologically meaningful from the species point of view as it is a better reflection of the potential adaptive scenarios for that species.

In contrast, a generalist map characterizes the target geographic area from an ecogeographic perspective rather than reflecting the potential adaptive scenarios of a specific CWR. Therefore, the selection of variables must be derived from an analysis of the environmental factors that are most likely to limit or condition plant life in that area, rather than those that are likely to be relevant in shaping the distribution of a single species. It is a simple approach and less time-consuming than the former, but it must be acknowledged that different CWR taxa are likely to respond differently to the range of environments in the geographic area, and that the ELC map is a general approximation to the selective pressures that may be generating local adaptation (Iriondo pers. comm. 2016).

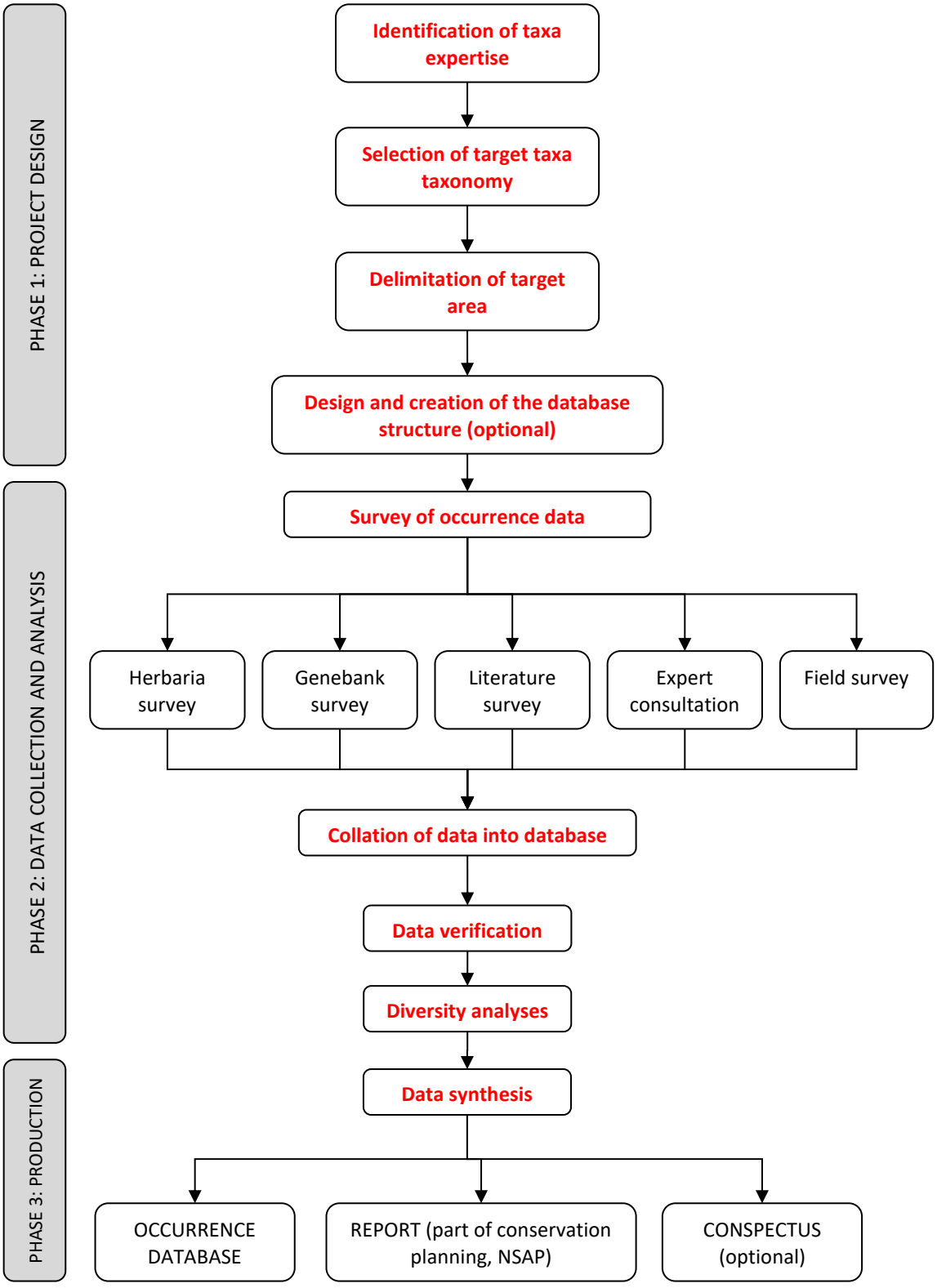
- Selecting ecogeographic variables. If a species-specific ELC map is to be created, then the variables selected must be those that are most likely to define the species' distribution/adaptive scenarios in a geographic area (Parra-Quijano *et al.* 2016). On the other hand, if a generalist approach is undertaken, then variables that limit plant life in general across the target geographic area are preferred (Iriondo pers. comm. 2016). Appropriate ecogeographic variables can be selected based on knowledge gained though bibliographic surveys, expert knowledge and statistical analyses. Parra-Quijano *et al.* (2016) provide some guidelines on how to select the ecogeographic variables, including a detailed explanation of the SelecVar tool from the CAPFITOGEN tool set (Parra-Quijano *et al.* 2016) that can be used to select appropriate variables. It includes a total of 105 variables (67 bioclimatic, 31 edaphic and 7 geophysical).
- Creating the ELC map using the selected ecogeographic variables. ELCmapas from the CAPFITOGEN tool set (Parra-Quijano *et al.* 2016) can be used to create an ELC map.

- Hotspot and complementarity analyses: these analyses provide an understanding of the patterns of diversity within and among priority CWR taxa. They can be undertaken at species level and at ecogeographic diversity level (and even at genetic level; click here to find how you can obtain CWR genetic data).
  - **Hotspot analysis**. A 'hotspot' refers to an area with a high concentration of CWR or high concentration of ecogeographic/genetic diversity. At species level, a hotspot map based on an occurrence dataset can easily be produced using DIVA-GIS. To produce hotspot maps based on predicted species distribution models, a more sophisticated software will need to be used (e.g. Arc-GIS) (see here for examples). DIVA-GIS can also be used to produce hotspot maps at the ecogeographical level. This involves overlaying the species' distribution onto an ELC map and extracting the ecogeographic category for each species occurrence data point. The binomial species-ecogeographic categories produced using this method are then used to produce the hotspot map, rather than using the species itself as the unit.
  - **Complementarity analysis**. This analysis uses an iterative process of grid square—or another defined geographic unit—selection to identify the minimum number of sites in the target geographic area that are needed to conserve all priority CWR (Rebelo and Sigfried 1992; 1994a,b). The analysis can be based on a grid (i.e. the target area is divided into grid squares and the grid square size is manually set) or based on an existing network of protected areas (to assess the representativeness of CWR in the network). The first selected grid square/area is the grid/area that contains the highest concentration of the target CWR, and the second selected grid/area is the one with the highest concentration of CWR excluding the taxa already in the first selected grid/area. This selection process is repeated until the selection of further grid squares/areas would only duplicate taxa already included in the previously selected ones (Rebelo 1992; 1994a,b). The complementarity analysis approach is generally preferred to the hotspot approach because it identifies a network of *in situ* conservation sites that covers most (if not all) target CWR.

Like the hotspot analysis, the complementarity analysis can be undertaken at species, ecogeographic or genetic diversity level, but rather than using the species name as the unit, the binomial species-ecogeographic category should be used instead. This involves overlaying the species distribution onto the ELC map and extracting the ecogeographic category for each occurrence data point. Complementarity analysis can be carried out using the tool Complementa from the CAPFITOGEN tool set (Parra-Quijano *et al.* 2016) for both grid and protected area analysis, or DIVA-GIS can be used for grid analysis only. More information on the establishment of genetic reserves to actively conserve CWR based on these analyses is provided here.

- Other data analyses:
  - Ecogeographic characterization of the CWR taxon (e.g. using the ecogeographic categories in which the taxon occurs) or of *ex situ* collections or *in situ* populations. ECOGEO from the CAPFITOGEN tool set (Parra-Quijano *et al.* 2016) can be used for this purpose.
  - Mapping and detection of ecogeographic patterns (e.g. identifying whether a CWR occurs on a particular soil type, or whether the frequency of a character state changes along an environmental gradient).
  - Gap analysis, an important step in any conservation planning process (click here for details on how undertake a gap analysis).

(ix) Data synthesis. After the data has been collated and analyzed, the following products should be produced: an occurrence database (which contains raw data after verification and standardization), an (optional) conspectus (which summarizes all of the data collated for each CWR) and a final report (which interprets the data obtained and is usually a part of a conservation planning report or a CWR National Strategic Action Plan/National Strategy).



Flowchart 4 Ecogeographic study model for CWR (modified from Maxted *et al.* 1995).

BOX 17 USING *EX SITU* PASSPORT DATA IN CONSERVATION PLANNING

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 genebank 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 genebanks.

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

BOX 18 CHALLENGES ACCESSING CWR OCCURRENCE DATA

Information on CWR occurrence is available from a wide range of sources, from herbarium and germplasm collections of the target taxon from the target area to relevant literature (monographs, revisions, field guides, floras, articles, papers). However, retrieving it presents a number of challenges:

- Herbarium and germplasm CWR occurrence data often involves visiting the herbarium or genebank to collect the data, which might not always be possible due to financial resources or time constraints.
- In recent years there has been an exponential growth of web-enabled ecogeographic datasets, helping researchers to survey herbaria and genebanks more easily. Most notably the Global Biodiversity Information Facility (GBIF), established in 2001, provides extensive access to global taxon nomenclature, taxon and accession distribution and conservation and environmental data. However, CWR themselves are not tagged in this resource and so searching for CWR occurrence data must be done through querying by country of origin and/or by CWR taxon name.
- In other existing databases, such as those managed by plant genebanks, the problem presented above also applies: 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. 2 used by many genebanks, the SAMPSTAT descriptor allows for designation of wild species samples but does not make a distinction between CWR and other wild species.
- The Crop Wild Relative Global Occurrence Dataset has been developed under the project Adapting Agriculture to Climate Change: Collecting, Protecting, and Preparing Crop Wild Relatives and includes a total of 5,647,442 georeferenced occurrence records from 80 crops gene pools (both crops and their wild relatives) (Castañeda-Álvarez *et al.* 2014). The data included in this database was gathered from more than 100 data providers (including GBIF). Although a great source of CWR occurrence data, care should be taken if using this database alongside further surveying of individual herbaria and genebanks, as it is likely that duplicate records (as well as duplicate accessions/herbarium vouchers) will be gathered. It is important that these are identified during the data verification stage of the ecogeographic study.
- While information on CWR *per se* is very specific to the PGR conservation and use community, because they are wild species they are also collected, conserved and studied by a broad community of taxonomists, ecologists, geneticists and physiologists etc. Therefore, these communities should be consulted when collating CWR occurrence data as they often have significantly larger datasets than the PGR community itself.

These challenges are not insurmountable but they do demand a carefully considered approach (particularly with regard to obtaining information from non-PGR communities) and a considerable amount of time. Nonetheless, it should be emphasized that the more occurrence data that is available, the more reliable and relevant the results of the analysis in formulating effective conservation plans.

BOX 19 STANDARDS AND DESCRIPTORS—WHAT ARE THEY?

Occurrence data should be collated using standard descriptors. 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 utilize. Standard descriptors for occurrence data have been compiled and reviewed in the Occurrence data collation template, while formal characterization and evaluation descriptors are associated with various standardized Crop descriptor lists published by FAO, Bioversity, UPOV – however, these may or may not be suitable for describing the crop's associated CWR. 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. This ensures uniformity, while reducing errors and problems associated with text synonyms and saves a considerable amount of time and effort associated with data entry.

4.5.2 Examples and applied use

CWR diversity and *in situ* and *ex situ* gap analyses in Norway

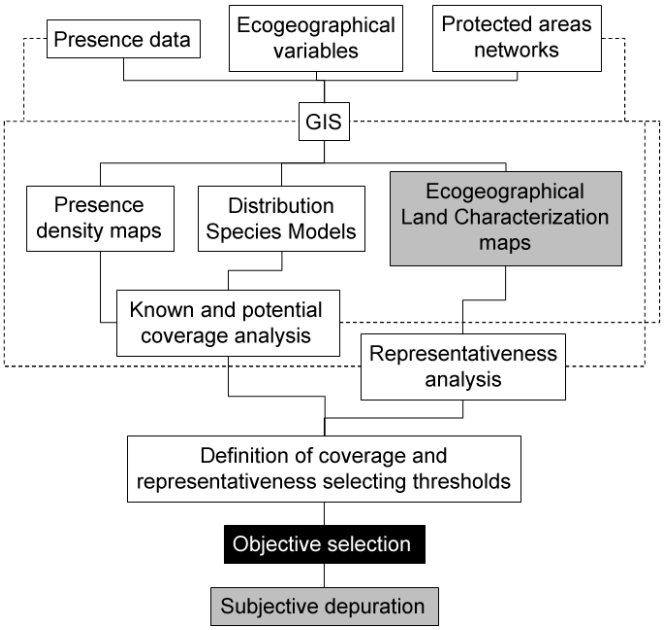
Diversity and *in situ* and *ex situ* gap analyses were carried out for priority CWR in Norway. Species occurrence data were gathered from GBIF. Observed distribution maps for individual taxa were created and predictive species distribution models were obtained in MaxEnt to undertake a gap analysis that determined how many taxa were predicted to be conserved *in situ* within the current protected areas (PA) network in Norway. The CAPFITOGEN tools were used to create an ecogeographic land characterization (ELC) map and to identify complementary *in situ* genetic reserves and *ex situ* collecting priorities which target the full range of ecogeographic diversity of priority taxa. The areas with the highest taxa richness were found to be around Oslo and the south-east coast of Norway, with up to 131 different priority CWR. The most taxa rich PAs were those in the Oslo and Østfold region, Kristiansand and the islands in Vestfold. A network of 19 complementary grids (≈ 10 Km^2) contain 201 priority CWR, and a separate analysis identified a network of 23 complementary existing protected areas that contain 181 priority taxa. *Ex situ* gap analysis identified 177 taxa not conserved *ex situ* and of the 24 with accessions, 15 had the minimum of five populations conserved throughout their ecogeographic range.

Source: Phillips *et al.* 2016

Figure 31 Large population of *Trifolium pratense* and *T. repens*, found in the Arctic Circle, northern Norway. (Photo: Jade Phillips)

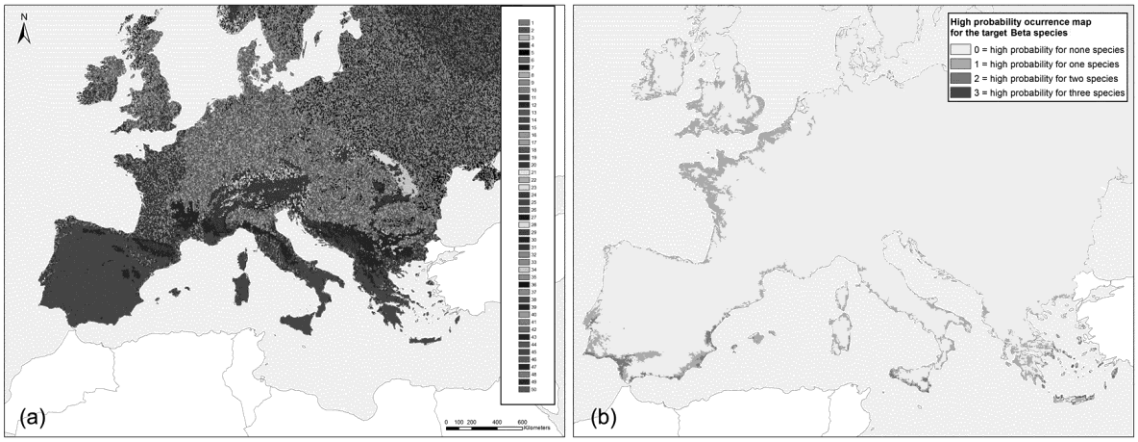
Ecogeographic land characterization mapping to identify genetic reserves

Ecogeographic land characterization (ELC) maps are based on bioclimatic, geophysical and edaphic variables, which are combined to form a map that categorizes the target geographic area of study into various environmental adaptive scenarios. This approach has been used to identify genetic reserves for beet CWR in Europe by combining population density maps, ecogeographic data and species distribution models. The process is summarized in the following model:



1. A map of population density of the selected species was developed as a starting point.
2. Locations with a richness of at least two species were selected.
3. Areas representating the most ecogeographic units for a group of species were selected.
4. Sites located within existing protected areas, with the greatest number of populations of the target species and representing both common and marginal ecogeographic units were identified.

The premise of this approach is that the conservation of species across sites with the greatest ecogeographic variability implies that the maximum range of genetic diversity of adaptive importance within and among these species is conserved and, possibly, also the most interesting allelic variation in the genes of interest for crop improvement. Below (a) shows an ELC 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, 2012b)

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 on the Iberian Peninsula 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 by grouping according to ELC maps 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 strategies such as CEM, and this method is easy to apply and update.

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

Ecogeographic characterization of *Lupinus luteus*

Spanish populations of *Lupinus luteus* were characterized ecogeographically as follows:

1. Selection of good quality georeferenced presence data.
2. Collation of ecogeographical GIS layers/variables (from passport data and by extracting information from georeferencing collecting sites).
3. Selection of the most relevant ecogeographic variables both through consultation with experts and by analyzing their relative statistical significance.
4. Performing a Principal Component Analysis (PCA) in order to reduce the number of variables.
5. Creation of tables with accessions and their corresponding ecological descriptors.
6. Estimation of ecogeographical distances between all pairs of accessions (by using the Gower similarity coefficient).
7. Performing a cluster analysis on the distance matrix and UPGMA agglomerative method to create dendrograms that represented ecogeographic similarities between accessions.
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)

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WWW Climatic Research Unit

WWW CGIAR Consortium for Spatial Information (CGIAR-CSI) (CRU-TS v3.10.01 Historic Climate Database for GIS, Global Aridity and PET Database, STRM 90m Digital Elevation Database, Global High-Resolution Soil-Water Balance)

WWW EUNIS – European Nature Information System

WWW FAO Soils Portal

WWW GeoNetwork

WWW Global Land Cover Characterization

WWW WorldClim – Global Climate Data (1 km resolution grids of climate and derived bioclimatic datasets)

WWW World Database on Protected Areas (WDPA) Protected Planet

WWW World Soil Database: Harmonized World Soil Database v1.2

Plant/CWR occurrence data:

WWW BioCASE – Biological Collection Access Service for Europe

WWW Bioversity International's Collecting Missions Database

WWW CIP (International Potato Center) Biomart Portal (potato and sweetpotato databases)

WWW Consortium of Pacific Northwest Herbaria (CPNWH) (portal to the regional herbaria of the Pacific Northwest North America)

WWW Crop Wild Relative Global Occurrence Database

WWW EUNIS – European Nature Information System

WWW EURISCO (European search catalogue of *ex situ* PGR accessions)

WWW European Native Seed Conservation Network (ENSCOBASE) (European database of major *ex situ* botanic garden genebank holdings)

WWW GBIF (Global Biodiversity Information Facility)

WWW GENESYS – the Global Gateway to Genetic Resources (global database of major *ex situ* gene bank holdings)

WWW Inter-American Biodiversity Information Network (IABIN)

WWW JSTOR (herbaria resources)

WWW Kew Bibliographic Databases (provides links to the Kew Record of Taxonomic Literature, Economic Botany and Plant Micromorphology)

WWW Kew Herbarium Catalogue (herbarium database)

WWW Mediterranean Germplasm Database [reference database for the agro-food plant germplasm stored at the Istitute of Biosciences and Bioresources (IBBR) of the Italian National Research Council (CNR) in Bari, Italy; with >56,000 accessions from all over the world]

WWW Natural History Museum, UK (herbarium database)

WWW PlantSearch, Botanical Garden Conservation International (botanic garden holdings information)

WWW Royal Botanic Garden Edinburgh (herbarium database)

WWW SADC region: Magos Brehm J, Gaisberger H, Kell S and Thormann I (2017) Occurrence data for priority CWR of the SADC region, doi:10.7910/DVN/QUOPCB, Harvard Dataverse, V2.

WWW Solanaceae Source (a global taxonomic resource for the nightshade family)

WWW Sotelo H and Helpdesk G N (2017) A global database for the distributions of crop wild relatives. Version 1.3. Centro Internacional de Agricultura Tropical (CIAT). Occurrence Dataset http://doi.org/10.15468/jyrthk accessed via GBIF.org on 2017-05-02.

WWW speciesLink (Brazilian database of biodiversity collections)

WWW The Harold and Adele Lieberman Germplasm Bank (cereals)

WWW Tropicos (Missouri Botanical Gardens, USA) (herbarium resources)

WWW US Genetic Resources Information Network (GRIN) (database of USDA *ex situ* genebank holdings)

Plant/CWR occurrence data – national datasets:

WWW Australia: Virtual Australian Herbarium

WWW Guatemala: Atlas of Guatemalan Crop Wild Relatives

WWW Japan: Genebank Project, NARO

WWW Mexico: Biodiversidad Mexicana – Proyecto global de maíces nativos

WWW Russia: AgroAtlas

WWW South Africa: BGIS Biodiversity GIS (search for spatial biodiversity information from South Africa)

WWW United States: US Virtual Herbarium

WWW Zambia: Ng'uni D, Munkombwe G and Masiye T (2016) Occurrence data for priority CWR of Zambia, doi:10.7910/DVN/Z5XN1F, Harvard Dataverse, V1.

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, 10th edition. Times Books, London.

WWW GeoNames

WWW Getty Thesaurus of Geographic Names® Online

WWW Global Gazetteer Version 2.3, Falling Rain Software, 1996–2016

WWW Google Maps

Google Earth

GEOLocate – A Platform for Georeferencing Natural History Collections Data

GIS software:

Arc-GIS/Arc Info

DIVA-GIS (geographic information system software, tutorials, documentation, spatial data, discussion forum) (freely available)

- GRASS GIS (freely available)
- gvSIG (freely available)
- Marxan (conservation planning) (freely available)
- R (with some GIS functionalities)

4.6 DIVERSITY ANALYSES: GENETIC DATA ANALYSIS OF PRIORITY CWR

Why should we consider the genetic diversity of priority CWR in conservation planning?

The ultimate aim of plant genetic resources conservation is to ensure that its diversity is efficiently conserved over time. Diversity includes both species diversity and the genetic diversity within species. The intrinsic value of CWR, being a source of adaptive genes for crop improvement, emphasizes the importance of conserving their genetic breadth so this is available for utilization in crop breeding programmes. Genetic diversity information can be used for: (i) assessing genetic diversity across the geographic breadth of the species, (ii) obtaining genetic baseline information against which to detect changes in diversity and identify genetic erosion, (iii) targeting CWR populations for *in situ* and *ex situ* conservation and (iv) identifying traits of interest for crop improvement. Therefore, considering either existing CWR genetic diversity data or undertaking novel genetic diversity studies in order to aid conservation planning is of utmost importance. Note that often these data are not available or there are no (economic or human) resources to undertake novel genetic diversity studies. In these cases, 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 maximize the overall genetic diversity of the species conserved.

- *Assess the genetic diversity within the target taxon*. Typically, conservation biology aims to conserve the maximum number of species and numbers of individuals within a species. However, the conservation of intrinsic genetic diversity within a taxon has been identified as equally important. The genetic diversity 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, it 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. Nevertheless, it should be emphasized that what we should really consider in CWR conservation planning is the adaptive diversity rather than neutral genetic diversity (see BOX 20). However, adaptive studies are time consuming and expensive and the alternative approaches are either to use neutral genetic diversity or ecogeographic diversity as a proxy for adaptive genetic diversity.

Figure 32 Wild barley (*Hordeum spontaneum* K. Koch) collected in Jordan and germinated for leaf tissue collection needed for DNA extraction and genetic diversity analysis. (Photo: Imke Thormann)

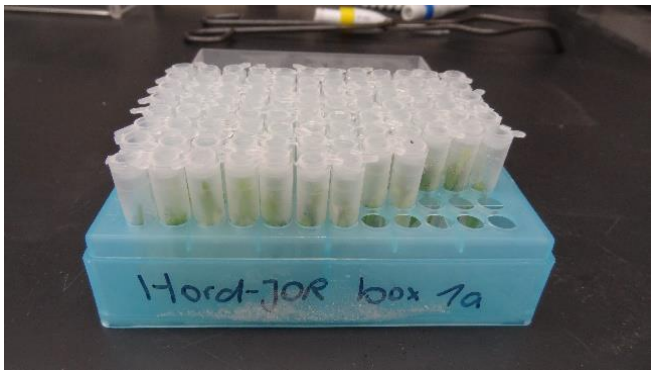


Figure 33 Leaf tissue obtained from germinated seeds of wild barley (*Hordeum spontaneum* K. Koch) collected in Jordan, needed for DNA extraction and genetic diversity analysis. (Photo: Imke Thormann)

- *Establish genetic baseline information*. 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. Like demographic changes in population number, changes in allelic richness and evenness over time can occur naturally. By monitoring genetic change, natural changes can be distinguished from those associated with adverse population management that result in genetic erosion and would ultimately lead to population extinction. Establishing the genetic baseline and assessing genetic diversity regularly over time enables these

deleterious changes to be detected early and population management changes to be implemented before there is significant genetic erosion.

- *Target CWR populations for conservation*. The selection of priority populations for *in situ* and *ex situ* conservation based on genetic criteria has been debated for a long time (e.g. Marshall and Brown 1975, Lynch 1996, Petit *et al.* 1998, Delgado *et al.* 2008). The amount and patterns of genetic diversity both within and among populations of a species, genetic population structure, and common and localized alleles (see BOX 21) are some of the data that can be useful when prioritizing 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 among, populations, then a limited number or even a single genetic reserve may be enough to efficiently conserve the species (for example, the population with higher genetic diversity and with the highest number of common and localized alleles). However, if different populations of the same CWR are genetically distinct, or if the partitioning of genetic diversity among populations 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 also important to take into account that, even in cases where there is only a small fraction of genetic differentiation among 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 is particularly important when considering the conservation of populations in the margins of a species' range, due to the need for species to adapt to changing environmental conditions brought about by climate change.
- *Identify traits of interest for crop improvement*. CWR adaptive traits form the functional component of genetic variation relevant for crop improvement. Ultimately, the identification and utilization of these traits justifies the conservation of CWR.

BOX 20 ADAPTIVE GENETIC DIVERSITY *VERSUS* NEUTRAL GENETIC DIVERSITY

Two distinct but complementary components of genetic variation can be distinguished. 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 years (e.g. Bowen 1999, Fraser and Bernatchez 2001, Merilä and Crnokrak 2001, Reed and Frankham 2001, McKay and Latta 2002, Holderegger *et al.* 2006). 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 environments (e.g. Falconer and Mackay 1996, McKay and Latta 2002, van Tienderen *et al.* 2002). Adaptive genetic variation is evaluated in quantitative genetic experiments under controlled and uniform environmental conditions. Nevertheless, the assessment of adaptive variation is very time consuming and quantitative traits involved in adaptation are sometimes difficult to find. Moreover, since 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. Relatively recent developments in high-throughput sequencing now provide an opportunity to discover the genetic signatures of selection at a genome-wide level (Brieuc and Naish 2011). Although finding individual genes under selection based on patterns of genetic variation 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, including microsatellites and AFLPs (Amplified Fragment Length Polymorphisms). The assessment of neutral genetic variation has been used frequently as a shortcut to infer global genetic diversity and to support strategies for the conservation of threatened taxa (e.g. Palacios and González-Candelas 1999, Rottenberg and Parker 2003, Eckstein *et al.* 2006, Watson-Jones *et al.* 2006, Magos Brehm *et al.* 2012). The use of molecular markers is a fast and relatively cheap technique which allows the study of gene flow, migration and dispersal.

Whether or not a correlation between neutral and adaptive variation exists has been widely debated and conclusions are not always in agreement. Some authors have found that neutral and adaptive genetic diversity and differentiation are positively correlated (e.g. Merilä and Crnokrak 2001, Pearman 2001), whereas other studies indicate that measurements of neutral diversity have a very limited prediction ability of quantitative variation (e.g. Reed and Frankham 2001, 2002) and thus cannot be used as a surrogate for adaptive genetic data. 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 diversity (Ahuja 2011). 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 the 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 disperse (Lefèvre 2007). 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 21 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 ≥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≥0.05) or rare (P<0.05). They defined four classes of alleles: (i) common and widespread (population frequency P≥0.05, and occurring in ≥25% of populations), (ii) common and local (population frequency P≥0.05, and occurring in <25% of populations), (iii) rare and widespread (population frequency P<0.05, and occurring in ≥25% of populations) and (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. The conservation of "rare and widespread" alleles will depend on the total number of sampled plants collected and stored as *ex situ* accessions or, using an *in situ* approach, it will depend on the proportion of the population included in the conservation area. The "rare and local" class includes very rare variants and recent or deleterious mutants which are extremely difficult to collect but a fraction of which will always be included in any conservation strategy.

4.6.1 Methodology

Taking target CWR genetic data into account when planning for conservation involves the following seven steps: (i) survey for existing genetic studies on target CWR, (ii) formulate the genetic questions to be answered and design the experiment, (iii) evaluate whether there are financial resources to undertake (further) genetic studies, (iv) assess whether there is a sufficiently large population sample to carry out the genetic study, (v) determine whether there are skilled staff to carry out the genetic study, or alternatively, (vi) perform an ecogeographic diversity study for target CWR that can be used as a proxy of genetic diversity, and (vii) incorporate genetic information into conservation planning (Flowchart 5). Finally, a genetic erosion monitoring scheme should be implemented in order to detect changes in the genetic diversity of the CWR.

(i) Survey for existing genetic studies on target CWR. Existing information should be collated and its use for conservation planning will depend on the type of information obtained (e.g. neutral genetic diversity across geographic breadth, genetic erosion assessment). Information on a plant's life history traits, including its breeding system and seed dispersal mechanism, should be gathered as they are crucial in determining the patterns of genetic diversity within and among populations (see BOX 22). Ideally, if no genetic information is available, novel genetic studies (on adaptive or neutral diversity) should be carried out.

(ii) Formulate the questions to be answered using genetic techniques and design the experiment. CWR genetic information can be used in several steps of conservation planning, from identifying processes of genetic erosion to establishing population priorities for active *in situ* and *ex situ* conservation and identifying traits for crop improvement. An experiment should be designed appropriately to answer the biological question/s to be addressed. Where possible, experts should be consulted to help with experiment design.

(iii) Evaluate whether there are sufficient financial resources to undertake a genetic study. The design of the genetic experiment will determine the necessary costs of the work and will enable the investigator to evaluate whether or not there are sufficient financial resources available to undertake the study.

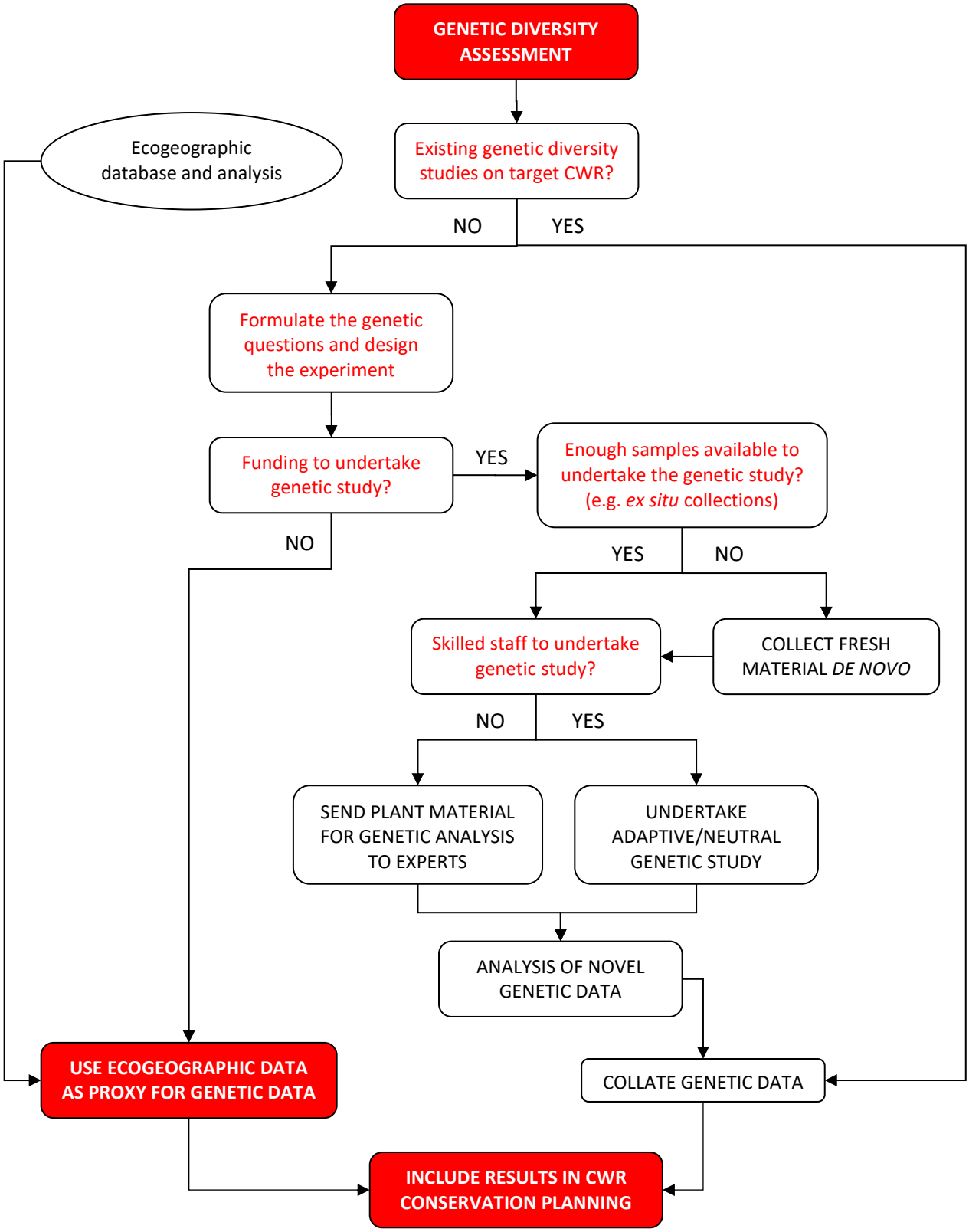
(iv) Assess whether there are enough population samples available to undertake the genetic study. Samples may either be plant material already present in available *ex situ* collections or material obtained through fresh collection from across the geographic range of the species.

(v) Determine whether there are skilled staff able to undertake the genetic study. If financial resources and expertise are available, a genetic study is desirable. If financial resources are available but no skilled staff, plant samples should be collected and then sent to skilled experts for analysis.

(vi) Perform an ecogeographic diversity study. This is an alternative approach that can be carried out when current financial and human resources are insufficient for a genetic study. Ecogeographic diversity (together with information on reproduction and dispersal systems) can be used as a proxy for genetic diversity. In other words, across the geographic distribution of a priority CWR species 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.

(vii) Incorporate the genetic information (either from existing genetic data or from a novel study) into conservation planning. The genetic diversity data that results from these analyses may then be incorporated into conservation planning through:

- The production of hotspot maps of genetic diversity (see here for more details about mapping hotspots).
- A complementarity analysis to detect the minimum number of sites that could conserve all genetic diversity (see here for more details about complementarity analysis).
- Analysis of genetic diversity gaps in existing conservation efforts of priority CWR, both *in situ* and *ex situ* (see here for more details about gap analyses).



Flowchart 5 Using genetic diversity data in CWR conservation planning.

BOX 22 NEUTRAL 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 neutral 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/density and population spatial distribution may affect the genetic variation within populations—as well as the genetic structure within and among populations—see a literature review of several case studies undertaken by Loveless and Hamrick (1984).

In addition, Hamrick and Godt (1996) performed two-trait combination analyses on five different life history characteristics (breeding system, seed dispersal mechanism, life form, geographic range and taxonomic status) in order to study how genetic diversity varies in seed plants. They analyzed inter-specific variation of allozyme genetic diversity to determine the percentage of polymorphic loci within the species (*P*), the 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 life history traits studied were:

- Breeding system: outcrossing, selfing, mixed mating.
- Seed dispersal mechanism: attached, gravity, animal, wind.
- Life form: annual, short-lived and long-lived perennial taxa.
- Geographic range: endemic, regional, narrow, 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 differentiation among populations and more genetic diversity than non-woody species with similar life history traits.
- Species in 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.

BOX 23 ECOLOGICAL FACTORS, GENETIC VARIATION AND POPULATION STRUCTURE

How ecological factors affect genetic variation and population structure (adapted from Loveless and Hamrick 1984). N_e = effective population size, NA = neighbourhood area.

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 NA; 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 NA
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 variability	Homogeneous clones; population highly subdivided
Facultative apomixis	Moderate; depends on breeding system and other factors	Founder effect may limit number of genets and 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

ECOLOGICAL FACTOR	GENETIC VARIATION WITHIN POPULATIONS	GENETIC STRUCTURE AMONG POPULATIONS	GENETIC STRUCTURE WITHIN POPULATIONS
Pollination mechanism			
Small and large 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 and will result in moderate to large N_e and large NA
General entomophily			
Butterfly/moth			
Bird/bat			
Wind	High		Wind pollination results in large N_e and NA and reduces subdivision
Seed dispersal			
Gravity	Intermediate	Limited dispersal promotes differentiation	Limited seed movement reduces N_e and 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 and decreases subdivision
Animal-attached	Low		Dispersal by wind and animals may reduce clumping and family structure
Seed dormancy			
Absent	Determined by other factors	Determined by other factors	Determined by other factors
Present	Increases potential genetic variation	Reduces divergence; slows loss of alleles by drift and isolation	Slows loss of alleles; increases generation time of genotypes; increases N_e; inhibits subdivision; may be countered by differential fecundities or other factors
Phenology			

ECOLOGICAL FACTOR	GENETIC VARIATION WITHIN POPULATIONS	GENETIC STRUCTURE AMONG POPULATIONS	GENETIC STRUCTURE WITHIN POPULATIONS
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 NA; 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 hinders divergence	Slows loss of variation; increases N_e; increases mating opportunities; slows subdivision
Timing of reproduction			
Monocarpic	No prediction	Promotes drift and divergence among populations	Restricts mating possibilities; shortens effective generation time; reduces N_e, which promotes differentiation in time and space but reduces flowering 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/drift effects and a short population lifespan promote 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		

ECOLOGICAL FACTOR	GENETIC VARIATION WITHIN POPULATIONS	GENETIC STRUCTURE AMONG POPULATIONS	GENETIC STRUCTURE WITHIN POPULATIONS
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 likely to result in high 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 NA) or may reduce pollinator visits (decrease NA 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 increases genetic patchiness and subdivision
Uniform	No prediction	Promotes migration and homogeneity	Promotes gene flow and reduces subdivision
Linear	No prediction	Divergence enhanced in linear arrays of populations	Subdivision is increased in linear habitats

4.6.2 Examples and applied use

A CWR genetic reserve on The Lizard Peninsula in the United Kingdom

A recent study of CWR diversity across England demonstrated that The Lizard Peninsula, the most southerly point of mainland UK, is a hotspot of CWR taxon diversity (Fielder *et al*. 2015). The Lizard Peninsula is ecogeographically diverse in terms of its geology, soil types, topography and range of microclimates, which could give rise to a similarly diverse range of genetic diversity in the flora of the area. As a result, a genetic diversity study of eight CWR that occur on The Lizard was carried out to investigate whether it is also a hotspot of CWR genetic diversity and therefore a suitable site for the first genetic reserve with active management and monitoring of CWR in the UK.

Figure 34 Wild chives, *Allium schoenoprasum* L., a wild relative of cultivated chives, flowering on The Lizard Peninsula, Cornwall, UK. (Photo: Hannah Fielder)

AFLP molecular markers were used for this study, and populations of eight CWR were sampled from sites on The Lizard and also outside of The Lizard, in the southwest of the UK, to make a comparison. AFLPs measure genome-wide, neutral genetic diversity. Although the value of CWR lies in their adaptive diversity, methods to directly measure this diversity remain prohibitively expensive and time-consuming. However, by sampling diversity across the genome, the range of diversity conserved can be maximized and so too, the likelihood of conserving valuable adaptive traits.

Results showed that there was no significant difference between the amount of genetic diversity found in CWR populations on The Lizard compared to populations sampled from other parts of southwest UK, for any of the eight taxa studied. However, the diversity on The Lizard was found to be largely distinct from southwest populations for many of the study taxa.

It was concluded that, due to the diversity of CWR taxa and ecogeography on The Lizard and the differentiation of CWR populations at this site from other sites across the southwest, that it is a suitable location for the first UK CWR genetic reserve. A large area of the peninsula is already subject to formal and active conservation management and through discussion with local reserve managers, CWR have now been acknowledged in the management plan of The Lizard National Nature Reserve. It is hoped that this will help to establish long-term management of CWR in this area and that the genetic diversity data obtained through this study will provide a baseline for ongoing monitoring of CWR populations. In addition, it should be noted that although The Lizard is a suitable site for a genetic reserve, these results suggest that The Lizard is not, on its own, sufficient to conserve all of the genetic diversity for these CWR in the UK. Therefore, a recommendation is made that a network of complementary genetic reserves is established across the country.

Source: Fielder *et al*. (in prep)

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

A genetic diversity study using AFLP molecular markers 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. *barbatus* has low but significant genetic differentiation among populations (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 a high number of private alleles. Additionally, no significant pattern of isolation by distance was observed between the populations of *D. cintranus* subsp. *barbatus* (*P*=0.267), indicating no geographic restriction to gene flow. Given these results, a Bayesian clustering analysis was also performed, and the results obtained on population genetic structure complemented the analyses. Two genetic clusters were identified for *D. cintranus* subsp. *barbatus*.

Figure 35 *Dianthus cintranus* Boiss. & Reut. subsp. *barbatus* R. Fern. & Franco, a wild relative of ornamental carnations (*D. caryophyllus* L.), endemic to Portugal, pictured here in Caramulo. (Photo: Joana Magos Brehm)

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 combined in order to prioritize populations of the studied species for *in situ* and *ex situ* conservation. Each of these criteria were standardized to "1", giving the highest priority to species with the largest expected heterozygosity, number of polymorphic loci and to those whose populations had higher genetic differentiation as well as to those with the smallest populations and the highest number of threats. These standardized scores were then summed per population and transformed into percentages using the highest score as the reference value of 100%, as suggested by Delgado *et al.* (2008) based on the Vane-Wright *et al.* (1991) principles. The populations with higher percentages were prioritized for active conservation.

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

Figure 36 Site in Condeixa-a-Nova where a genetic reserve should be established for *Dianthus cintranus* Boiss. & Reut. subsp. *barbatus* R. Fern. & Franco, based on genetic, population size and threat data. (Photo: Joana Magos Brehm)

Islands as refugia of *Trifolium repens* genetic diversity

A genetic diversity study using AFLP molecular markers was carried out to compare mainland wild and landrace populations of *Trifolium repens* 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 genetic 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 homogenization. It was concluded that islands, such as St Kilda, can act as refugia of genetic diversity and can, therefore, provide an opportunity to conserve populations from the threats that endanger their diversity and, at the same time, allow populations to diverge from their mainland counterparts.

Source: Hargreaves (2010) and Hargreaves *et al.* (2010)

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WWW CWR Portal – publications on genetic studies of CWR.

Technical documents on genetic diversity analysis:

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WWW Bioversity International training modules on molecular analysis of diversity.

4.7 PRIORITY CWR: NOVEL THREAT ASSESSMENT

Why is threat assessment important in CWR conservation planning?

CWR, like any other wild plant species, are increasingly subject to anthropogenic threats. As a result, they experience genetic erosion and are increasingly at risk of extinction. Moreover, these threats have a direct economic and social impact on humankind; if the genetic diversity within CWR is unavailable for exploitation, food insecurity is then a threat to humankind itself. Assessing the risk of extinction of CWR taxa is therefore an important stage in conservation planning. This will help to identify the taxa in greatest need of immediate conservation action, it will improve our understanding of the specific conservation requirements of CWR and will establish a baseline for monitoring their threat status over time.

Novel threat assessment is particularly important for those CWR that have not yet been assessed at all and for those with outdated assessments. For the remaining taxa, existing threat assessments may already have been collated at the CWR prioritization step. Nevertheless, it should be highlighted that sufficient resources are rarely available to undertake novel threat assessment of all the CWR in a checklist. CWR conservation planning requires the collation of large and complex datasets that enables the implementation of conservation actions, and these datasets may also be used in the threat assessment process. Novel threat assessment can then be undertaken in parallel to conservation planning and implementation, and can be used to further prioritize/enhance CWR conservation.

The assessment of threats facing CWR diversity can be carried out at two levels: (i) the individual taxon level (commonly species but also at infra-specific level) and (ii) the genetic level:

1. Assessing the threat status of individual taxa can inform CWR species prioritization for conservation—the most threatened species having higher conservation priority. Further, threats to a specific region may be assessed to aid conservation planning (i.e. to identify areas with high numbers of threatened CWR). However, in this case, it would require the completion of a large number of individual species assessments and a comparison of the threats in different regions.
2. At the genetic level, the threats of genetic erosion and pollution to CWR should be examined and understood as they can eventually lead to population—or even taxon— extinction. A decrease in genetic diversity results in the loss of genes and alleles that then will not be available for future exploitation for crop improvement. This will ultimately have a negative impact on future food security. Additionally, the loss of genetic diversity implies a reduced capacity for taxa to adapt to the rapid changes in environmental conditions the planet is experiencing, and therefore a lack of availability of particular adaptive elements in crop gene pools for the development of new crop varieties able to withstand these new conditions.

The *IUCN Red List Categories and Criteria* (IUCN 2012a) have been widely used for assessing species extinction risk (or threat status). They were developed to improve objectivity and transparency in the threat assessment process, and therefore to improve consistency and understanding among users. These categories and criteria can be used to assess the risk of extinction of a species at the global level.

However, when the threat status of a species is being assessed at national (or regional) level—as in the context of a National Strategic Action Plan for the conservation of CWR—then the regional criteria, *Guidelines for Application of IUCN Red List Criteria at Regional Levels* (IUCN 2012b), should be used to determine the appropriate Red List category for a taxon. This is particularly relevant for species that also occur outside of the target region[7] of the study, as wild populations are not delimited by national boundaries. When the distribution of 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 that will affect the stability, and therefore the extinction risk, of the species. For example, a taxon classified as Least Concern globally might be Critically Endangered within a particular region where numbers are very small or declining. Conversely, a taxon

[7] 'Region' is defined by the IUCN (2012b) as any sub-global geographically defined area (e.g. continent, country or province).

classified as Vulnerable on the basis of a global decline in numbers or range might be Least Concern within a particular region where its population is stable (IUCN 2012a). As a result, the *Guidelines for Application of IUCN Red List Criteria at Regional Levels* (IUCN 2012b) were developed to re-assess the risk of extinction of species in a particular region within the light of its overall distribution. However, when the regional population is isolated from conspecific populations, global criteria can be used without modification.

BOX 24 ALTERNATIVE METHODS FOR THREAT ASSESSMENT

The fact that the IUCN Red List threat assessment method is so widely applied indicates its success. However, 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. For species found in areas where the flora is less well known, applying the IUCN Red List criteria is challenging or impossible. Furthermore, 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* (IUCN 2012a), alternative methods may be used.

An alternative approach was outlined by Burgman *et al*. (1995, 2000), who used the quantification of the number of observations (both herbarium specimens and germplasm accessions) to give an approximation of taxon vulnerability. However, their work was based on the assumption that threat and rates of material collection were directly related, which might not be an accurate reflection of the actual threat situation. Salem (2003) scored different attributes (status, commonness, life form and use) in order to calculate the conservation values of species. The author then assigned a relative conservation rank to each taxon and calculated an average conservation value for all species within particular protected areas in order to establish priorities and allocate conservation efforts. In addition, 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).

More recently, Miller *et al.* (2012) compared two alternative methods to the IUCN Red List assessment method. The first method used available georeferenced data to calculate the Extent of Occurrence (EOO) for all plant species in Puerto Rico, excluding unsuitable habitats such as lakes, then all species with an EOO greater than 20,000 km^2 (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 km^2 threshold all specimens then were georeferenced, so time was not spent georeferencing common species. After georeferencing, EOO values were recalculated, and those species with EOO values above 20,000 km^2 were considered ''Not At Risk'' and if EOO's were still less than 20,000 km^2, species were categorized as ''At Risk.'' Therefore, the ''At Risk'' species would be considered threatened under IUCN's criterion B1.

The second method included four steps. Step one analyzes the age of collections and occurrence data, if a species has not been collected since 1900 it is considered to be "At Risk". Step two assesses geographic distribution by determining if species are known from six or more provinces or municipalities with an area greater than 9,000 km^2, or smaller individual islands. Those known from six or more locations are considered to be ''Not At Risk'', and remaining species occurring in five or fewer locations continue on to step three. Step three assesses rarity from the abundance of herbarium specimens. If a given species is represented by less than or equal to the median number of 28 specimens per species, then it is ''At Risk,'' and if known from more than 28 specimens, it is analyzed in step four. Step four assesses species decline by determining whether the species is known from less than or equal to the median number of seven specimens collected since 1st January 1960. Those species with less than seven specimens may be in decline and are considered ''At Risk''.

The authors conclude that both methods are likely to over-estimate threat but, while they do not replace the IUCN Red List assessment, they do provide a quick methodology that is easy to apply and do not rely of full assessment datasets that are—and are likely to remain—unavailable.

BOX 25 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 the following taxon-specific biological traits that are believed to be related to climate change vulnerability:

1. *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.
2. *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.
3. *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.
4. *Dependence on interspecific interactions that are likely to be disrupted by climate change*: many species interact with symbionts, pollinators, seed dispersers and competitors. The more specific these interactions, the more susceptible they will be to change.
5. *Poor ability to disperse to or to colonize 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 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)

4.7.1 Methodology

Before undertaking Red List assessments using the *IUCN Red List Categories and Criteria* (IUCN 2012a, available in several languages), users are advised to consult the IUCN Red List website for detailed information about the assessment process. An online IUCN Red List training course is also freely available.

Assessment of the threatened status of species using the *IUCN Red List Categories and Criteria* (IUCN 2012a) is essentially a four to five-step process: (i) collate and document data for each taxon, (ii) [undertake remedial studies], (iii) evaluate the taxon against the IUCN Red List criteria, (iv) collate relevant information about populations of the species in neighbouring countries and apply the IUCN Red List regional criteria, if the taxon is being assessed at regional level (e.g. national assessments of non-endemic species), and (v) submit global assessments to IUCN for publication (Flowchart 6).

(i) Collate and document data for each taxon. Seven data types should be collated for each taxon (see BOX 26): (i) taxonomy, (ii) distribution, (iii) population, (iv) habitat and ecology, (v) use and trade, (vi) threats and (vii) conservation actions. These data are gathered from a number of sources, including taxon experts, published and grey literature, databases, websites, herbaria and genebanks. If needed, and if possible, field data should also be obtained. To know more about the limitations of using herbarium data in the Red List assessment process (see BOX 27).

(ii) [Undertake remedial studies]. If there is not enough data to assess target taxa, further remedial studies in demography, reproductive biology, chorology, genetics etc., could be carried out.

(iii) Evaluate the taxon against the IUCN Red List criteria. Each taxon is evaluated against the IUCN Red List criteria (IUCN 2012a) and a Red List category is then selected (Figure 37). There are five main Red List criteria: (A) population reduction, (B) geographic range (see BOX 28), (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 (see Table 4). Use this Red List summary sheet (also available in French and Spanish), outlining all five criteria, to evaluate if a taxon belongs in an IUCN Red List threatened category. If the species meets the criteria in at least one of the main classes, it is assigned one of the following threatened categories: Critically

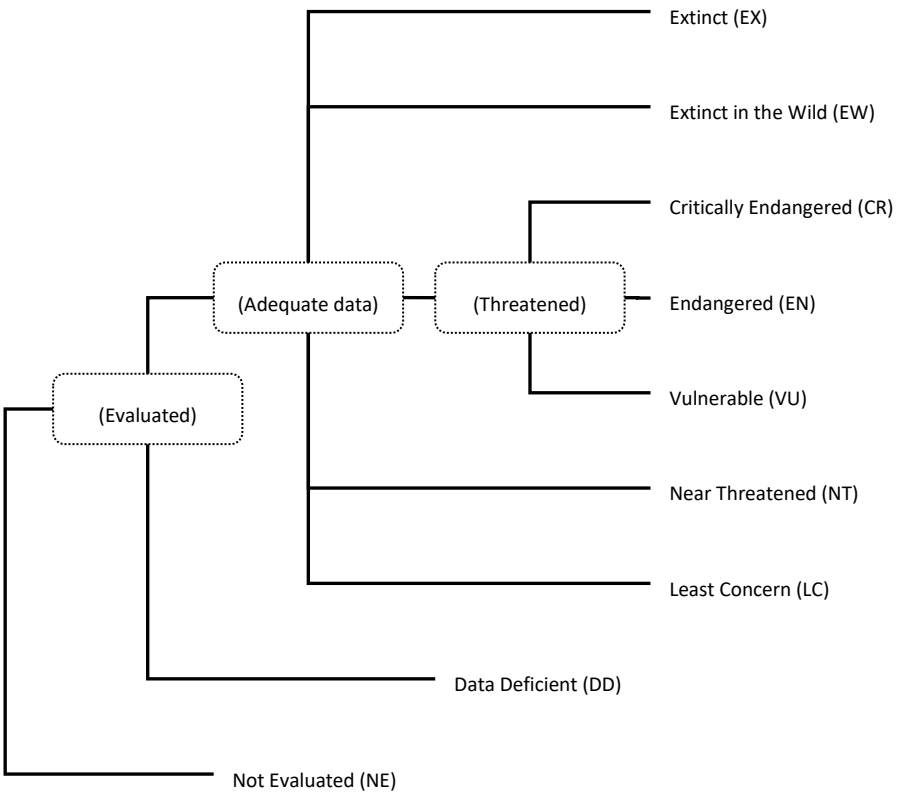


Figure 37 Structure of the IUCN Red List categories (IUCN 2012a).

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 any other threat categories and criteria that are met are 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 categories 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). Before proceeding with the Red List assessment please read the *Guidelines for Using the IUCN Red List Categories and Criteria* (IUCN Standards and Petitions Subcommittee 2016). 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 prioritized for further study in order to gather the required data. Look here for tools that can be used to estimate some of the parameters needed to carry out Red List assessments.

Table 4 Parameters of the sub-criteria against which species are evaluated (*requires data from at least two time points) (Source: Magos Brehm *et al.* 2008b) [for more on the measurements of extent of occurrence (EOO) and area of occupancy (AOO) see BOX 28].

POPULATION REDUCTION (% reduction over time)	GEOGRAPHIC RANGE	LOCATIONS	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)

(iv) Collate relevant information about populations of the species in neighbouring countries and apply the IUCN Red List regional criteria, if the taxon is being assessed at regional level. If the taxon is being assessed

at regional—not global—level (e.g. national assessments of non-endemic species), the next step is to collate relevant information about populations of the species in neighbouring countries and assess whether it is necessary to downgrade (or rarely to upgrade) the taxon's global Red List category. Information may be sourced from Red List assessments and conservation status data from the neighbouring countries, from expert knowledge and available literature and knowledge of the taxon's breeding and dispersal system, combined with its distribution in the region. For a regional Red List assessment, the taxon is subjected to a series of questions which aim to determine whether the taxon's regional Red List category should remain the same, be downgraded or upgraded from the global assessment (see Figure 38). 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 *Guidelines for Application of IUCN Red List Criteria at Regional Levels* (IUCN 2012b). The regional categories are the same as the global ones, but there are two additional categories: Regionally Extinct (RE) and Not Applicable (NA). The category NA is applied for species with marginal populations in the region or when a species is not 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.

(v) Submit global assessments to IUCN for publication. Global Red List assessments (i.e. species assessed at global level as well as national/regional endemics) can be submitted for publication in the IUCN Red List of Threatened Species (see here how the assessment process is generally carried out). The IUCN has developed the Species Information Service (SIS), which is a 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 the the use of SIS facilitates the Red List assessment procedure. For further information about using SIS, users should consult the IUCN Red List website.

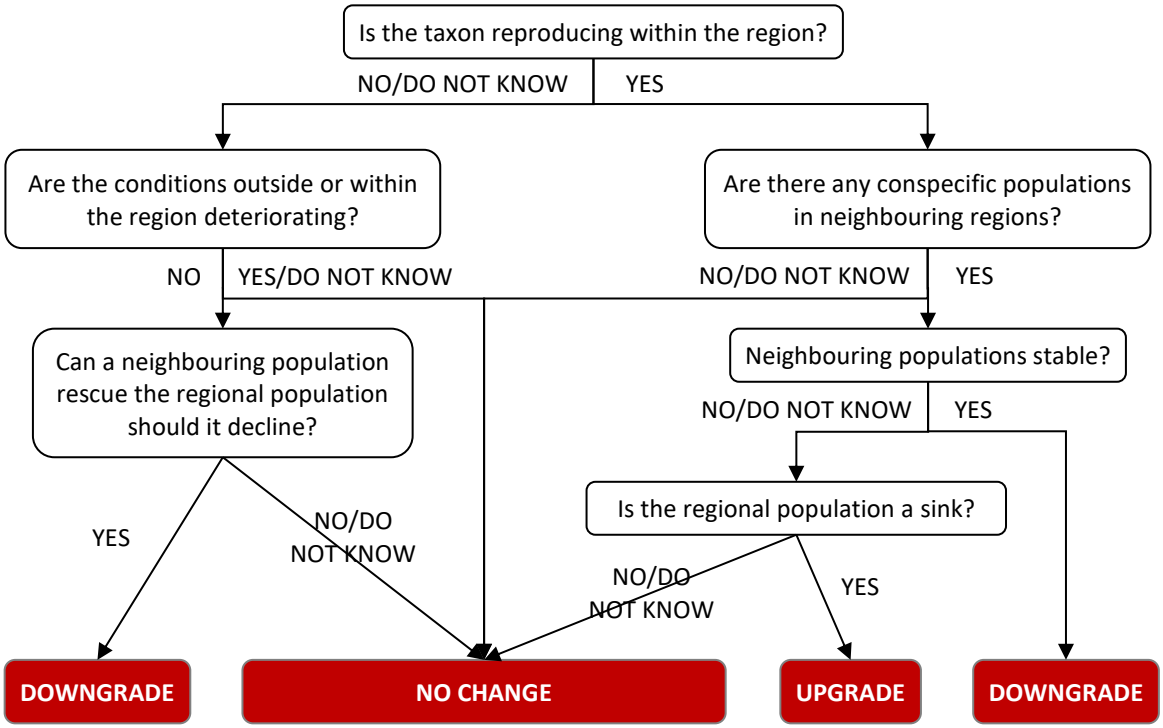
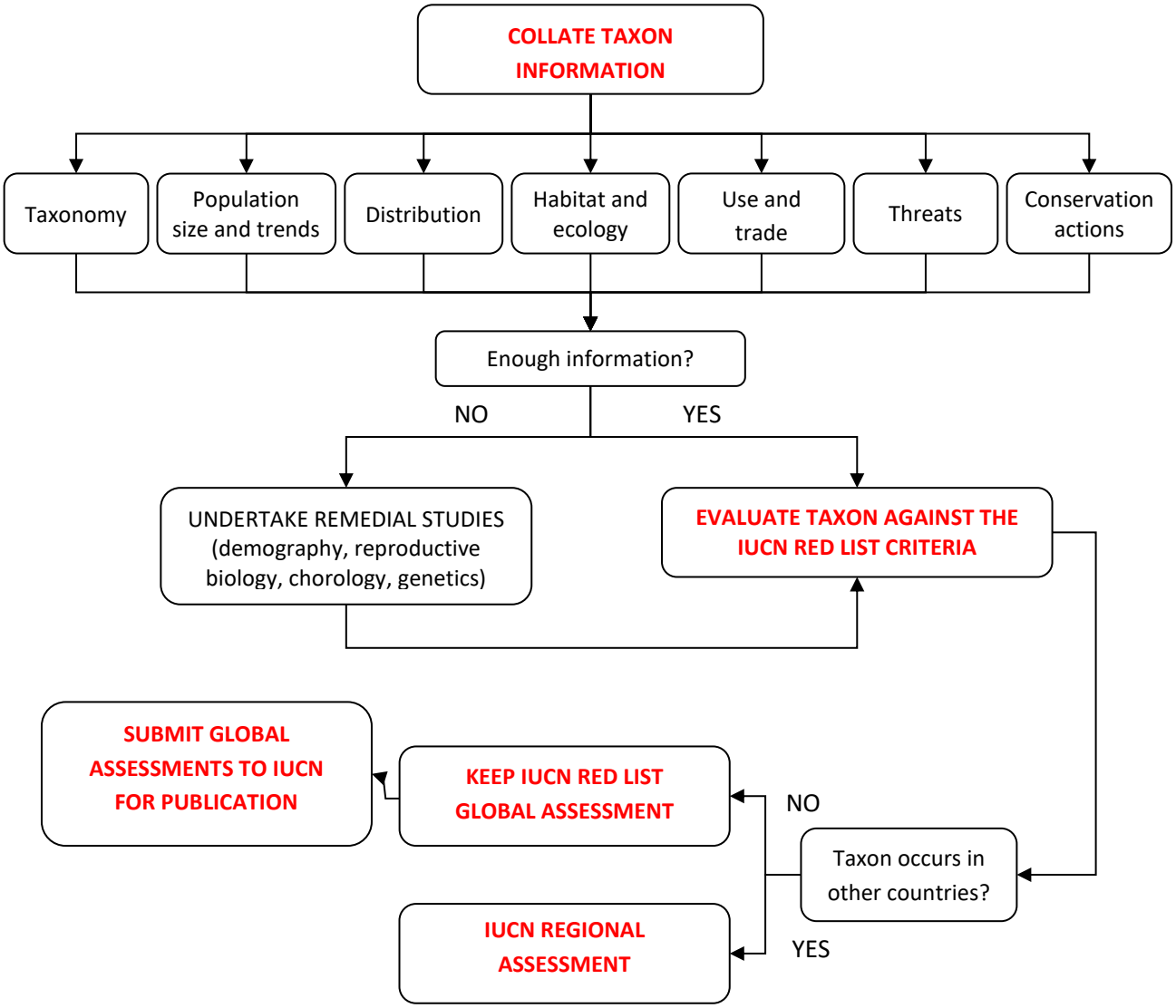


Figure 38 Basic scheme of how to undertake a regional Red List assessment (from Magos Brehm *et al.* 2008b and adapted from IUCN 2003).



Flowchart 6 Novel threat assessment of CWR taxa.

BOX 26 SUMMARY OF DATA TYPES USED IN RED LISTING

Taxonomy:

1. Nomenclature (taxon name, authority, synonyms etc.).
2. Recent taxonomic changes, any current taxonomic doubts or debates about the validity or identity of the species, or issues of synonymy.
3. Note any subspecific taxa.
4. Crop(s) the species is related to (common and scientific names) and information on the degree of relatedness between the wild relative and 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:

1. Summary of the current information available regarding the geographic range of the species.
2. Countries of occurrence (and sub-national unit(s), where applicable) recorded using built-in descriptors in IUCN's Species Information Service (SIS).
3. Extent of occurrence and/or area of occupancy (See the Box on 'Geographic range measurements used in criterion B' LINK TO BOX).
4. A map showing the distribution of the species.

Population:

1. Summary of the size and trend information available (i.e. increasing, decreasing or stable) of the overall population of the species. If the population is severely fragmented, this is also recorded.
2. 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.
3. Where no quantitative information on population sizes or trends is available, an indication of whether the species is common, abundant, or rare etc. should be noted where possible. If there really is no information about the population, this should be noted.

Habitats and ecology:

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

Use and trade:

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

Threats:

1. 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.
2. 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.
3. Threats are documented using IUCN's Threats Classification Scheme.

Conservation:

1. Any conservation actions currently in place and any realistic actions needed to mitigate threats causing declines, including information on both *in situ* and *ex situ* conservation measures.
2. Conservation actions are documented using IUCN's Conservation Actions Classification Scheme.

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

BOX 27 USE OF HERBARIUM DATA IN RED LISTING

Application of the *IUCN Red List Categories and Criteria* (IUCN 2012a) requires the use of 'the best available evidence'. For plants, herbarium and genebank collections usually 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, 2012a).

Often, information used in Red List assessments is interpreted from locality and habitat information contained on specimen labels and inferences and projections are made regarding distribution ranges, 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 regarding scientific name, locality, habitat, ecology, date of collection, collector name and collector number—the historical specimens (before or from 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, the use of specimen passport information from a single population sample 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). However, despite the uncertainty, herbarium specimens can be a good start when assessing species extinction risk.

BOX 28 GEOGRAPHIC RANGE MEASUREMENTS USED IN 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."

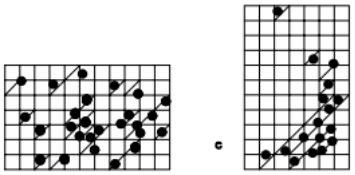
Extent of occurrence (EOO): "Extent of occurrence is defined as the area contained within the shortest continuous imaginary boundary which can be drawn to encompass all the known, inferred or projected sites of present occurrence of a taxon, excluding cases of vagrancy. This measure may exclude discontinuities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

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."

A) Known spatial distribution

B) Extent of occurrence (EOO)

C) Are of occupancy (AOO)



Source: IUCN (2012a)

4.7.2 Examples and applied use

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 had good knowledge of the national flora of their countries 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 via email correspondence and the completion and editing of the assessments was undertaken primarily by three members of staff from 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 threatened, with 3.3% (19) of them 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 is the threat that has by far the greatest impact on CWR in Europe, followed by arable farming, which is 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 growing in agricultural areas—this includes grazing in semi-natural habitats such as Mediterranean maquis (Kell *et al.* 2012). 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 yet to be accurately quantified.

Figure 39 *Crambe feuillei* A.Santos, an European Critically Endangered (CR) wild relative of the oil producing and fodder crop, *C. abyssinica* R.E.Fr. (Arnoldo Santos Guerra)

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

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 an herbarium survey following the model proposed by Maxted *et al.* (1995), with an aim to draft the preliminary distribution of the target taxa and 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 2012b) were then used. Area of occupancy (AOO) was generally calculated using a grid size of 4 km^2 except for those species known to have very small populations and limited range distribution in the country, in such cases a grid size of 1 km^2 was used. The results 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: Haruntyunyan *et al.* (2010)

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4.7.4 Additional materials and resources

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WWW IUCN Red List of Threatened Species – Assessment Process

WWW IUCN Red List of Threatened Species – Red List Training

WWW IUCN Red List of Threatened Species – References

WWW IUCN Red List of Threatened Species – Classification Schemes

National/regional Red Lists:

WWW BGCI ThreatSearch! (comprehensive database of conservation assessments of plants)

WWW National Red List – Research papers

Technical documents and tools for threat assessment:

(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.

Bachman S, Moat J, Hill A, de la Torre J and Scott B (2011) Supporting Red List threat assessments with GeoCAT: Geospatial Conservation Assessment Tool. Zookeys 150: 117–126.

Analysis Tool for Geospatial Red List Species Assessment (GeoCAT) [calculates the Extent of Occurrence (EOO) and Area of Occupancy (AOO)]

GeoCAT Screencasts (shows how to use GeoCAT step by step)

Threat assessment – other papers:

Sapir Y, Shmida A and Fragman O (2003) Constructing Red Numbers for setting conservation priorities of endangered plant species: Israeli flora as a test case. Journal for Nature Conservation 11: 91–107.

4.8 GAP ANALYSIS OF PRIORITY CWR

What is 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 elements (Noss and Cooperrider 1999, Eken *et al.* 2004, Rodrigues *et al.* 2004, Langhammer *et al.* 2007). Practically, all gap analyses, including those for CWR, involve a comparison between the range of natural diversity and the diversity already effectively represented by current *in situ* conservation actions (*in situ* gap analysis) and all accessions of the target CWR represented in genebank collections (*ex situ* gap analysis).

There is extensive literature associated with gap analysis, a method which essentially identifies areas in which selected elements of biodiversity are under-represented (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). However, these examples

are 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, was first cited by Ingram and Williams (1993). Since then, a systematic gap analysis methodology for identifying gaps in species or genetic diversity conservation has been developed and illustrated with a case study for African *Vigna* wild relatives. This case study aimed to evaluate the effectiveness of current *in situ* and *ex situ* conservation, to identify the 'gaps', and therefore assisting the development of conservation strategies for African *Vigna* genetic resources (Maxted *et al.* 2008a). More recently, a methodology for collecting crop gene pools for *ex situ* conservation based on GIS tools has been developed (e.g. Ramírez-Villegas *et al.* 2010, Castañeda-Álvarez *et al.* 2015, Khoury *et al.* 2015a,b, Castañeda-Álvarez *et al.* 2016).

The results of the diversity analyses (distribution and ecogeographic diversity, genetic diversity) and novel threat assessment provide the information needed to identify gaps in current *in situ* and *ex situ* conservation actions for CWR. The Figure 40 summarises how these analyses feed into a gap analysis study.

Conservation gaps (both *in situ* and *ex situ*) can be detected at different levels (Figure 41): (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 hold a particular trait of interest that are not conserved *versus* populations with that same trait that are) and (iv) genetic diversity level (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 is often 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 that are required.

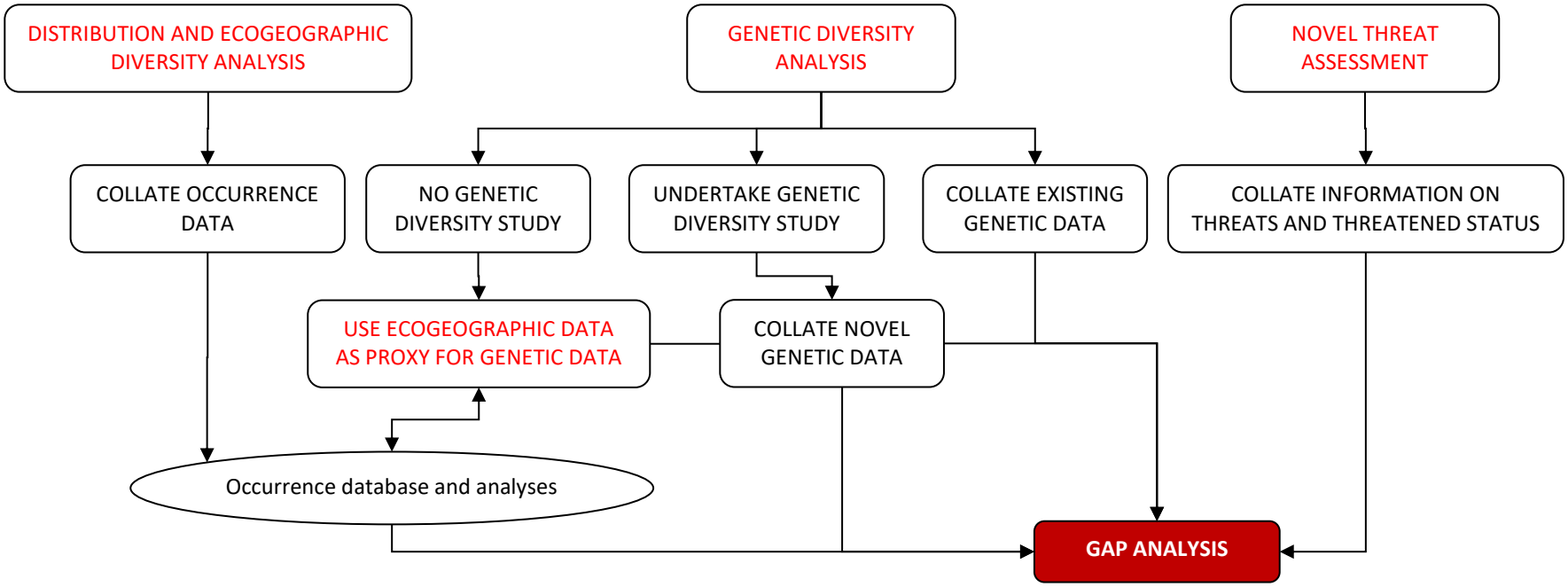


Figure 40 Using distribution and ecogeographic diversity analyses, genetic diversity analysis and threat assessment to aid gap analysis.

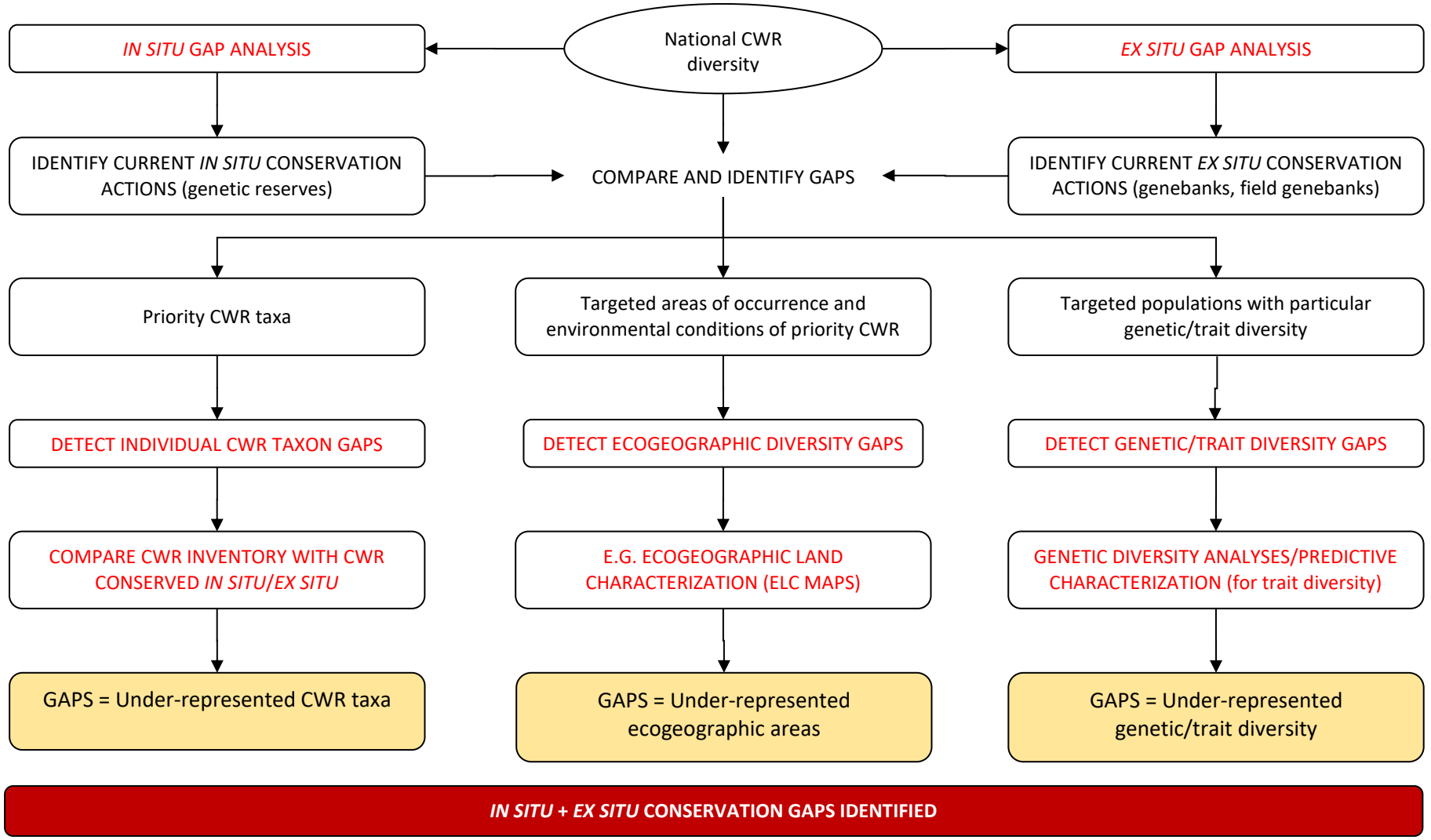


Figure 41 *In situ* and *ex situ* gap analysis methodologies for CWR diversity.

4.8.1 Methodology

4.8.1.1 **In situ *gap analysis***

In situ gap analysis can be carried out at different levels:

(i) *Individual CWR level*: whether the target CWR taxa are adequately represented by active *in situ* conservation.

(ii) *Ecogeographic level*: whether the whole ecogeographic range of the CWR is represented *in 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.

(iii) *Genetic level*: whether specific CWR populations that contain genetic diversity of interest (e.g. high genetic diversity) are conserved *in situ*.

(iv) *Trait level*: whether specific CWR populations that contain a particular trait of interest (e.g. resistance to drought etc.) are adequately conserved *in situ*.

In situ gap analysis includes the following five main steps (Flowchart 7):

1. Select the occurrence data to be used in the analysis.
2. Identify the CWR that do not occur within the existing network of protected areas (individual CWR taxon level).
3. Identify the CWR that do occur within existing protected areas but are not actively managed and conserved (individual CWR taxon level).
4. CWR distribution modelling and field confirmation.
5. Identify gaps at infra-species level, i.e. ecogeographic diversity, genetic and trait levels.

1. Select the occurrence data to use in the analysis. If different levels of geographic precision have been ascribed to each species' occurrences, only the most accurate should be used (e.g use levels 1 to 3 from Table 3).
2. Identify the CWR that do not occur within the existing network of protected areas (individual CWR taxon level). This task involves:
   (i) Surveying the environment and agriculture communities in order to find out whether the target CWR are known to occur within any existing PAs, as this information might not have been picked out during the collation of occurrence data.
   (ii) Overlaying the CWR taxa distribution with the network of protected areas in a GIS (e.g. DIVA-GIS, ArcGIS etc.).

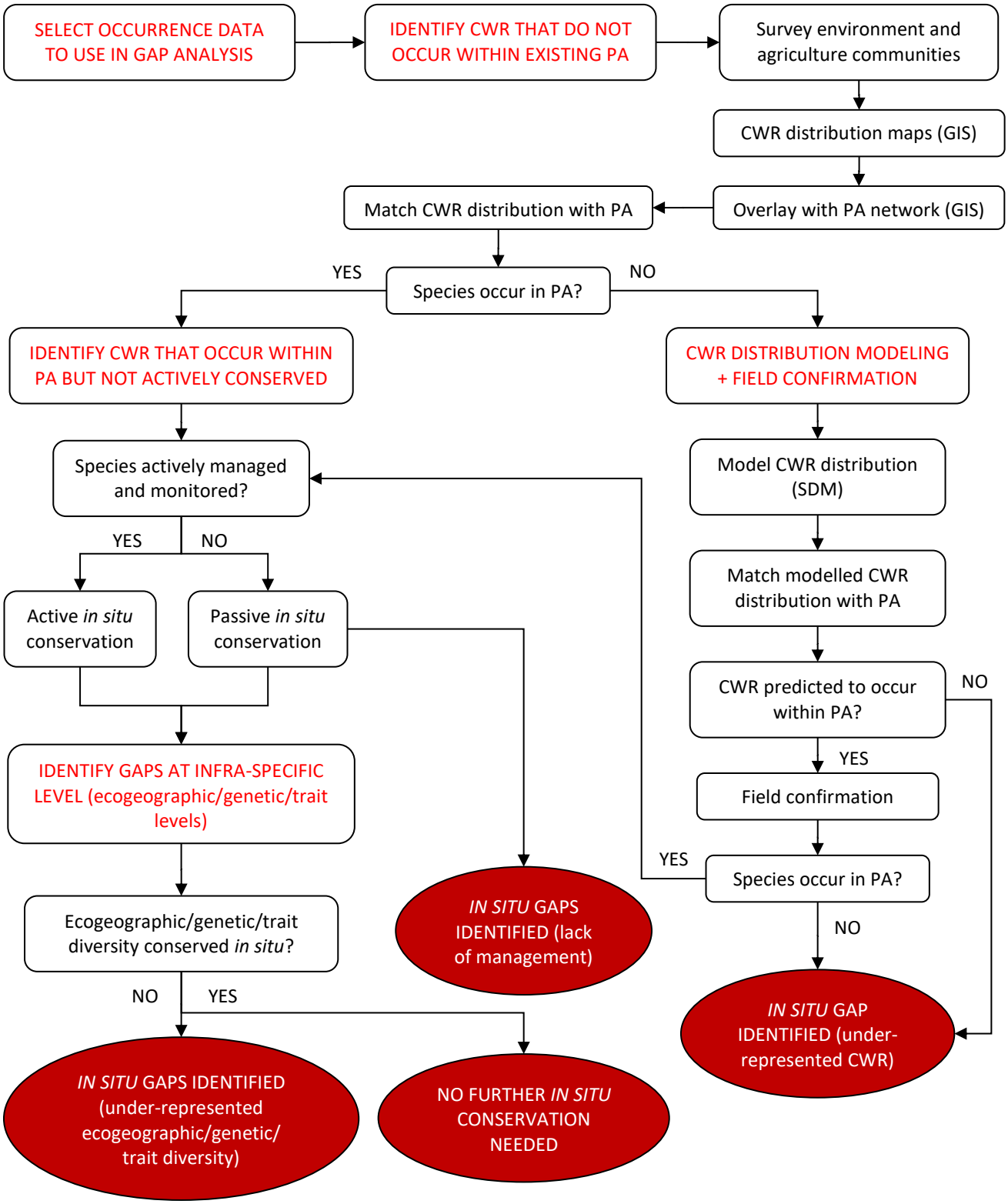
   Further analysis is required for any CWR found only to occur outside protected areas, to confirm their absence (see point 4 below).
3. Identify the CWR that do occur within existing protected areas but are not actively managed and conserved (individual CWR taxon level). In these cases, CWR are only passively conserved. **GAPS = CWR taxa within protected areas but lacking management.**
4. CWR distribution modelling and field confirmation. If target CWR do not occur within any existing PA, their distribution can be predicted using species distribution modelling techniques (see BOX 29). Modelled distributions of CWR can then be matched with the existing network of PA. If the species is then predicted to occur within an existing PA, field work should be undertaken to confirm this. If confirmed, it should then be evaluated to determine if it is actively managed and conserved (though this is very unlikely, as the previous analysis will have shown that there were no records of the species in the PA). If the species is not managed and actively conserved, then this is a gap in its conservation (**GAPS = CWR taxa within protected areas but lacking management**). If the species is not predicted to occur within a PA, then this is also a gap (**GAPS = CWR taxa not actively conserved *in situ***).
5. Identify gaps at infra-species level, i.e. ecogeographic diversity, genetic and trait levels.

At ecogeographic diversity level: determine the range of ecogeographic CWR diversity and identify where it is conserved *in situ*. **GAPS = CWR ecogeographic areas not already conserved *in situ***. This can be achieved using ecogeographic land characterization maps (ELC maps) and the ecogeographic diversity analysis already outlined here. This method identifies known populations of the target CWR that are within ecogeographic gaps (ecogeographic area not adequately conserved) and also helps to determine appropriate areas for *in situ* conservation activities.

- After creating an ELC map (either species-specific or generalist) (to know more about these two different types of ELC map, click here), the Representa tool from the CAPFITOGEN tool set (Parra-Quijano *et al.* 2016) can be used to compare the ELC categories in which the species occurs with the ELC categories containing populations of the species that are already actively conserved *in situ*.
- Gaps in *in situ* conservation can then be identified for each target taxon.
- Priority areas in need of *in situ* conservation can then be identified by producing richness maps of *in situ* ecogeographic gaps (DIVA-GIS can be used to produce such maps) or by complementarity analysis using the Complementa tool from the CAPFITOGEN tool set (Parra-Quijano *et al.* 2016). Both methods use the occurrence points of each priority CWR that are located in the identified ecogeographic gaps, and the richest or most complementary areas for each under-conserved ELC category etc. are determined. How the ecogeographic diversity gaps are incorporated into *in situ* conservation is the responsibility of the researcher.

At genetic/trait level: compare CWR distribution with genetic/trait diversity data and determine which populations are actively conserved. **GAPS = specific CWR populations with genetic diversity/traits of interest not conserved *in situ*.** For more information on genetic diversity analysis of priority CWR, click here.

Regarding the trait level analysis, predictive characterization is a technique that enables the identification of CWR populations (*in situ* or from *ex situ* collections) that potentially harbour traits of interest (e.g. drought tolerance, insect pest resistance) (Thormann *et al.* 2014). It uses ecogeographical and climatic data derived from the specific location of a collecting or observation site to predict traits of interest in order to inform conservation and use options (Thormann *et al.* 2014). Once these traits have been identified, it is possible to assess whether the populations in which they are thought to occur are actually conserved adequately *in situ*. For further information, see this document that has been produced in the context of the SADC Crop Wild Relative project with some guidelines on how to undertake a predictive characterization study.



Flowchart 7 *In situ* gap analysis of CWR diversity.

4.8.1.2 Ex situ gap analysis

Ex situ gap analysis can be carried out at different levels:

(i) *Individual CWR level*: whether the target CWR taxa are adequately represented by existing *ex situ* accessions.

(ii) *Ecogeographic level*: whether the whole ecogeographic range of the CWR is represented *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.

(iii) *Genetic level*: whether specific CWR populations that contain genetic diversity of interest (e.g. high genetic diversity) are conserved *ex situ*.

(iv) *Trait level*: whether specific CWR populations that contain a particular trait of interest (e.g. resistance to drought etc.) are adequately conserved *ex situ*.

Ex situ gap analysis includes the following three main steps, which are very similar to those carried out in an *in situ* gap analysis (Flowchart 8):

1. Select the occurrence data to be used in the analysis.
2. Identify the CWR that are not conserved *ex situ* (individual CWR taxon level).
3. Identify gaps at infra-species level, i.e. ecogeographic diversity, genetic and trait levels.

1. Select the occurrence data to use in the analysis. If different levels of geographic precision have been ascribed to each species' occurrences, only the most accurate should be used (e.g use levels 1 to 3 from Table 3).
2. Identify the CWR that are not conserved *ex situ* (individual CWR taxon level). This task involves comparing priority CWR taxa with *ex situ* accessions of those taxa that are adequately conserved in genebanks and field genebanks (this information should already have been collated prior to this step). This enables detection of CWR not adequately conserved *ex situ*. Note that only *ex situ* accessions conserved under suitable genebank conditions, with enough seed, and that are adequately labelled with good quality passport information (where it is possible to track its original collection site) should be considered, as these are the only accessions that can be utilized. **GAPS = CWR taxa not adequately conserved *ex situ***.
3. Identify gaps at infra-species level, i.e. ecogeographic diversity, genetic and trait levels.

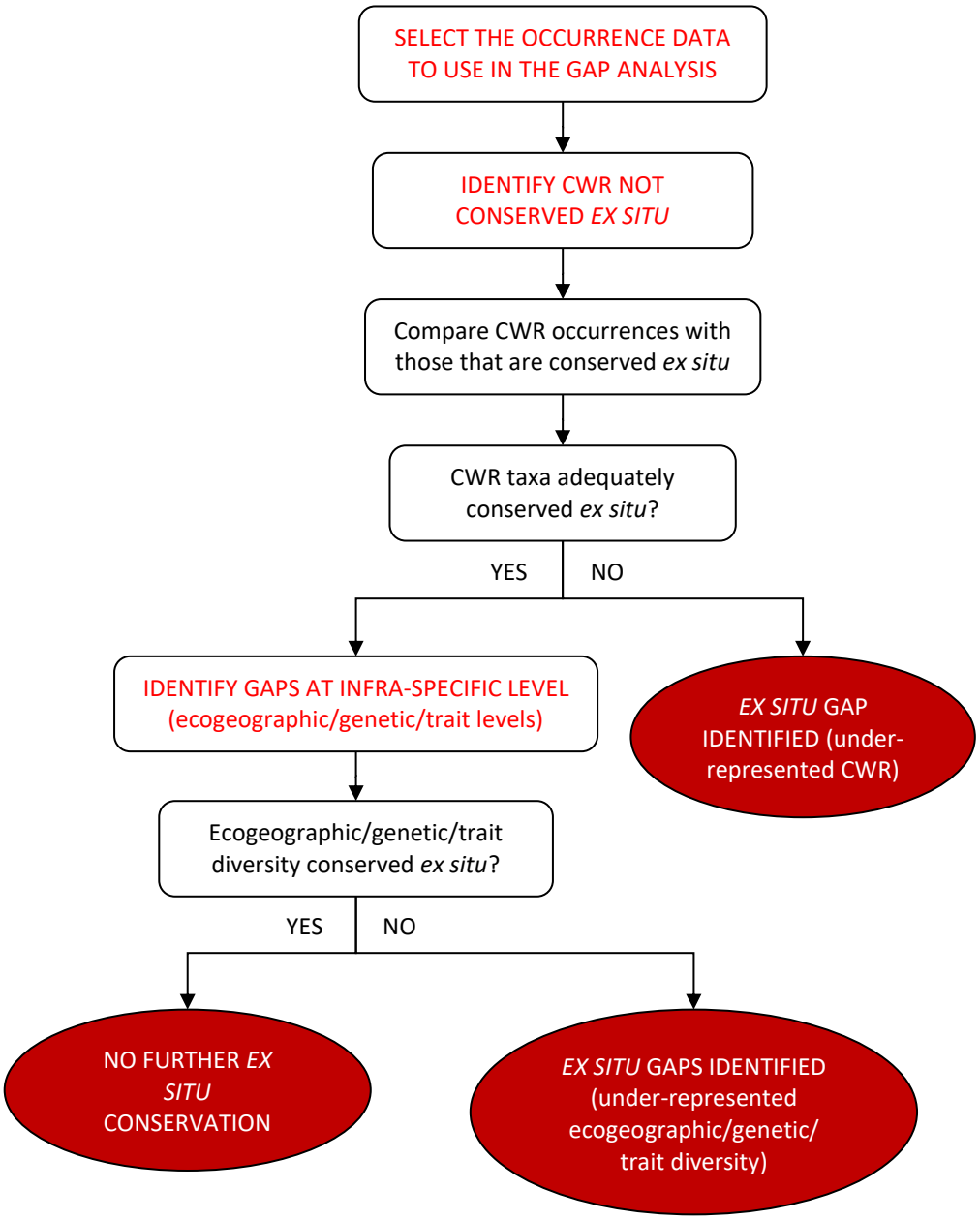
   At ecogeographic diversity level: compare the ecogeographic diversity of priority CWR and the ecogeographic diversity that has already been collected and conserved *ex situ* for those CWR. **GAPS = CWR ecogeographic areas not yet conserved *ex situ***. There are a few alternative methodologies that can be used to carry out an ecogeographic diversity gap analysis:

   - Ecogeographic land characterization maps (ELC maps) and the ecogeographic diversity analysis already outlined here can be used as the basis for a gap analysis. This method identifies known populations of the target CWR that are within ecogeographic gaps (ecogeographic area not adequately conserved) and also helps to determine appropriate areas for *ex situ* conservation activities.
     1. After creating an ELC map (either species-specific or generalist) (to know more about these two different types of ELC map, click here, the Representa tool from the CAPFITOGEN tool set (Parra-Quijano *et al.* 2016) can be used to compare the ELC categories in which the species occurs with the ELC categories containing accessions of the species that are already actively conserved *ex situ*.
     2. Gaps in *ex situ* conservation can then be identified for each target taxon.
     3. Priority areas for *ex situ* collection can then be identified by producing richness maps of *ex situ* ecogeographic gaps (DIVA-GIS can be used to produce such maps) or by complementarity analysis using the Complementa tool from the CAPFITOGEN tool set (Parra-Quijano *et al.* 2016). Both methods use the occurrence points of each priority CWR that were collected from the identified ecogeographic gaps.
   - The Ramírez-Villegas *et al.* (2010) methodology, which consists of identifying gaps in *ex situ* collections based on a combination of sampling, geographic and environmental gaps, can also be used. This method involves the creation of potential distribution models for each target taxon and results in the identification of species of high, medium and low priority for collecting as well as identifying potential

collecting areas for priority species (this is in contrast to the previous method, which only considered known occurrences).

At genetic/trait level: compare CWR distribution with genetic/trait diversity data and determine which populations have been previously collected and conserved *ex situ*. **GAPS = specific CWR populations with genetic diversity/the traits of interest not conserved *ex situ*.** See here for more on genetic diversity analysis of priority CWR.

Regarding the trait level analysis, predictive characterization is a technique that enables the identification of CWR populations (*in situ* or from *ex situ* collections) that potentially harbour traits of interest (e.g. drought tolerance, insect pest resistance) (Thormann *et al.* 2014). It uses ecogeographical and climatic data derived from the specific location of a collecting or observation site to predict traits of interest in order to inform conservation and use options (Thormann *et al.* 2014). Once these traits have been identified, it is possible to assess whether the populations in which they are thought to occur are actually conserved adequately *ex situ*. For further information, see this document that has been produced in the context of the SADC Crop Wild Relatives project with some guidelines on how to undertake a predictive characterization study.



Flowchart 8 *Ex situ* gap analysis of CWR diversity following a method based on Ecogeographic Land Characterization maps (ELC maps).

BOX 29 SPECIES DISTRIBUTION MODELS

Species distribution models (SDM) are a useful tool to predict potential areas of distribution of priority CWR. They have been commonly used to answer questions related to ecology, evolution and conservation (Elith *et al.* 2006). 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) and to identify high-priority sites for *ex situ* and *in situ* conservation (e.g. Araújo and Williams 2000, Loiselle *et al.* 2003, Castañeda-Álvarez *et al.* 2016).

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. Mastrorillo *et al.* 1997), ecological niche factor analysis (ENFA) (e.g. Hirzel *et al.* 2001, freely available from here), generalized dissimilarity models (GDM) (e.g. Ferrier 2002) and maximum entropy models (e.g. MaxEnt by Phillips *et al.* 2006, freely available from here). 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.

4.8.2 Examples and applied use

Gap analyses for Norwegian priority CWR

Gap analyses were carried out to contribute towards recommendations for the *in situ* and *ex situ* conservation of priority CWR in Norway.

Methods

- CWR checklist: created from the *Crop Wild Relative Catalogue for Europe and the Mediterranean* (Kell *et al.* 2005, 2008) and updated and harmonized with the Flora of Norway (Lid and Lid 2005).
- CWR priority list: obtained by applying the following criteria to the CWR checklist: CWR within the same genera as crops of high economic value as given by gross production value (current million US$) for global production value (2013), within Europe (2013) and within Norway (2013) (from FAOSTAT); CWR present in Annex 1 of the ITPGRFA; CWR highlighted as being of specific importance to Norwegian research, culture and environment; taxa within the Harlan and de Wet inventory (Vincent *et al.* 2013); native taxa only, according to the flora of Norway (Lid and Lid 2005).
- Distribution data were gathered from GBIF for the priority taxa and the following analyses were undertaken:
    - *In situ* analysis: taxon richness and sampling bias maps were created; the Complementa tool from the CAPFITOGEN tool set (Parra-Quijano *et al.* 2016) was used to perform a grid cell and a protected area (PA) complementarity analysis to identify potential PAs for *in situ* conservation; the number of populations conserved within the complementary networks was identified; predicted distribution maps were created for each priority CWR using the MaxEnt algorithm; the predicted distribution maps were then compared to the observed distribution to determine how many taxa were predicted to be conserved within the PA network; an ELC map was created and zones in complementary networks were identified to determine the level of ecogeographic diversity conserved.
    - *Ex situ* analysis: the CAPFITOGEN tool Representa was used to identify gaps in the collection of priority CWR taxa; ELC zones were identified which were under-represented in the *ex situ* collections of taxa.

Main results

- Checklist: 2538 CWR.
- Priority list: 204 CWR.
- *In situ* analysis: the most taxa rich areas are in the south-east of Norway with the north containing the lowest taxa richness. Ten percent of taxa are not found within a PA; the complementarity analysis produced a network of 19 grid cells (10 km^2) that contain all 201 priority taxa; the PA complementarity analysis identified 23 existing PAs that contain 181 taxa (the remaining 20 taxa are not found within a PA); the PA complementarity network covers 17 of the 27 ELC zones and contains an average of 23% of ecogeographic diversity per taxon.
- *Ex situ* analysis: 177 priority CWR are not conserved *ex situ* and these should be targeted for *ex situ* collection; ELC zones 3 and 17 are the highest priority to target for collection of taxa.

Source: Phillips *et al.* (2016)

Ex situ gap analysis for wild relatives of potatoes

An *ex situ* gap analysis was carried out for 73 of the closest wild relatives of potato (*Solanum* section *Petota*), including wild potatoes in the primary and secondary gene pools as well as any distant relatives in the tertiary gene pool that have confimed or potential uses in crop breeding. The aim of this analysis was to establish priorities for further collecting to fill important gaps in germplasm collections.

Germplasm data were obtained from repositories easy to access, namely: EURISCO, GRIN and CIP's biomart portal. Other species occurrence data and additional germplasm accessions passport data were gathered from various online databases and via communications with data managers, including GBIF, CRIA, SINGER, CPNWH, the Atlas of Guatemalan Crop Wild Relatives (Azurdia *et al.* 2011), the PBI Solanum—a worldwide treatment, LAC biosafety, as well as from literature (e.g. Spooner *et al.* 2014), and herbaria (i.e. E, K, L, NY, MA, PH, RB and US). The occurrence data collated and used in this analysis are available here. Potential distribution models were obtained for each species using MaxEnt (Phillips *et al.* 2006) based on a set of 19 bioclimatic variables derived from the WorldClim database (Hijmans *et al.* 2005) at a resolution of 2.5 arc-minutes (approx. 5 km at the equator). Performance of models was assessed based on three criteria: (i) the 5-fold average Area Under the Test ROC Curve (ATAUC), (ii) the standard deviation of the ATAUC for the 5 different folds, and (iii) the proportion of potential distribution where the standard deviation is greater than 0.15 (ASD15). A suitable model had to meet the following conditions: ATAUC >0.7, STAUC <0.15 and ASD15 <10% (Ramírez-Villegas *et al.* 2010). For those species where a suitable model was not obtained (either due to lack of data or low performance of the ensemble model), a convex hull (polygon surrounding the outermost georeferenced points) was prepared.

The gap analysis methodology used was that of Maxted *et al.* (2008a) and of Ramírez-Villegas *et al.* (2010). Three metrics were used to prioritize CWR for collecting: a Sampling Representativeness Score (SRS) (compared the number of germplasm accessions to the total number of samples and provided an overview of the sufficiency of accessions per species), a Geographic Representativeness Score (GRS) [compared the distribution models with the geographic distribution of existing germplasm accession collecting sites, which was estimated by creating circular buffers of 50 km (CA50) around each site where the accession was collected (Hijmans *et al.* 2001), and which assessed the geographic coverage of germplasm collections], an Ecosystem Representativeness Score (ERS) [compared the number of ecosystems currently represented in *ex situ* collections with the total number of ecosystems distributed within the distribution models of each taxon, using a world terrestrial ecoregions map (Olson *et al.* 2001)]. Equal weight was given to these three metrics and an average was calculated to obtain a Final Priority Score (FPS). Collecting priorities were then categorized as follows: high priority species (HPS) when FPS ≤3, or when ten or less accessions were recorded in germplasm collections; medium-priority species (MPS) when 3< FPS ≥5; low priority species (LPS) when 5< FPS ≥7.5; and 'no further collecting of germplasm required' (NFCR) when 7.5< FPS ≥10. The gap analysis was performed using R v2.15.1 (R Core Team 2014) and various packages (see the paper for more details).

Priority areas for collecting *ex situ* gaps identified above were prepared for each species by subtracting the existing germplasm CA50 buffers from the potential distribution models. For those species where a niche

model was not produced, CA50 buffers were prepared around all presence records and germplasm CA50 buffers were subtracted from the CA50 buffers of all presence records. Collecting gap maps for all high priority species were then obtained using the 'Zonal Statistics' tool in ArcMap 10.1 which produced a species richness map of further collecting per country of occurrence.

A total of 32 species (43.8%) were assigned high priority for further collecting, most of them located in Peru, the geographic centre of diversity of potato wild relatives. A total of 20 and 18 species were assessed as medium and low priority for further collecting, respectively, and only three species were considered to be sufficiently represented.

Source: Castañeda-Álvarez *et al.* (2015)

Figure 42 Wild relative of potatoes here pictured in Peru. (Photo: Eve Allen)

Individual CWR taxon 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 occurrence database contained 9,866 unique geo-referenced observations collected between 1932 and 2004. Distribution maps and predicted distribution maps, using climatic models, were obtained and compared using ArcGIS and DIVA-GIS to carry out individual taxon conservation gap analyses. Species priorities were assigned based on *ex situ* conservation status, with 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 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, northwest 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 would need to be established.

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

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Crop Trust (gap analysis video)

4.9 CLIMATE CHANGE ANALYSIS OF PRIORITY CWR

4.10 ESTABLISHMENT AND IMPLEMENTATION OF *IN SITU* CONSERVATION PRIORITIES

What are the* in situ *conservation goals in CWR conservation planning?

The goal of *in situ* CWR conservation planning is 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 should be backed-up with the periodic resampling of CWR populations for *ex situ* collections, which also helps promote sustainable exploitation.

What do we mean by establishment and implementation of *in situ* conservation goals?

Establishment means setting up the foundations of the National CWR *In Situ* Conservation Network for the long-term conservation of CWR, i.e. selecting provisional sites for active conservation based on CWR diversity and gap analyses. Implementation means the execution of this in the field by evaluating the adequacy of each individual site, designating the sites as CWR genetic reserves, developing site and species management plans and involving local communities to ensure CWR conservation is effective.

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

It is possible that CWR populations conserved *in situ*, may not 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. It may also be that the current management practice at the site is 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, in practical terms, *in situ* CWR populations often require active management.

A National CWR *In Situ* Conservation Network may include various types of conservation sites, from single CWR taxon reserves to multiple taxa reserves, within the existing network of protected areas or outside protected areas in more informal management sites or even requiring the extension of the boundaries of existing protected areas so as to include important CWR taxa and populations—appropriate sites may be determined by CWR taxa diversity and/or by infra-specific diversity such as ecogeographic, genetic or trait diversity. To determine the actual number and mix of these different types of CWR genetic reserves that should be established and implemented, it is important to take a pragmatic and scientific approach. Ultimately, however, this is dictated by the resources available for *in situ* conservation, the governmental policy context at both the national and local levels and by NGO and local community involvement. It should be stressed that the practical implementation of the National CWR *In Situ* Conservation Network should have a policy context. Furthermore, national and local commitment is required to ensure the network's long-term survival and to ensure set-up expenditure is not wasted—*in situ* conservation is a long-term and expensive commitment.

BOX 30 SINGLE CWR TAXON GENETIC RESERVES *VERSUS* MULTIPLE CWR TAXA GENETIC RESERVES

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 have the obvious advantage of making the best use of limited conservation resources. However, it will not always be possible to establish multiple CWR sites, because some priority taxa may only occur in sites where no other priority CWR are found. The balance between whether to establish single or multiple CWR *in situ* conservation sites will ultimately depend on the financial and human resources available for, and allocated to, CWR conservation.

BOX 31 CWR GENETIC RESERVES WITHIN AND OUTSIDE PROTECTED AREAS

CWR genetic reserves may be implemented within existing PAs or outside such a formal network. Firstly, it is important to note that the vast majority of PAs in any country are likely to contain CWR populations. However, these PAs have most probably been established to target specific landscapes, habitats or fauna, and not CWR diversity itself. Therefore, in most cases the conservation of CWR within existing PAs is passive (i.e. without any formal management or monitoring plan[*]). Moreover, if individual CWR populations decline or disappear entirely, it might pass unnoticed by the PA manager. On the other hand, if an existing PA is designated as a 'national CWR genetic reserve', the management plan should be amended in order to integrate the genetic conservation of CWR populations occurring within the protected area boundaries. This should result in the implementation of positive management action before any deleterious factor can impact on the CWR populations. So why is it that implementing genetic reserves within existing PA is the most practical option in economic and political terms?

(i) These sites already have an associated long-term conservation ethos and are less prone to hasty management changes associated with private land or roadsides (where conservation value and sustainability is rarely a consideration).
(ii) It is relatively easy to amend the existing site management to facilitate genetic conservation of CWR species.
(iii) It means creating novel conservation sites can be avoided, so the likely prohibitive cost of acquiring previously non-conservation managed land is not necessary (Maxted *et al.* 2008a).

However, the practice of locating genetic reserves within existing PA may be questioned because:

- 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.
- CWR are often found in disturbed, pre-climax plant communities and anthropogenic environments (see Jarvis *et al.* 2015) and these are rarely designated as PA (PA more commonly being established to conserve pristine habitats or ecosystems, or rare or threatened taxa).
- 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.
- 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 and implementation.

In situ conservation of CWR 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 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—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: widening of roads, removal of hedgerows or orchards, cutting of roadside verges at the wrong time of year, use of herbicides rather than physical weed control. To ensure the long-term survival of a 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 is not negatively impacted. By definition, sites outside PAs are primarily managed for reasons other than conservation, so 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. However, the conservation agency will need to monitor the site routinely to ensure efficient management of the target CWR populations. Therefore, informal *in situ* conservation offers an opportunity to conserve populations that may otherwise not be conserved. It 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.

In conclusion, *in situ* conservation of CWR should be planned both within 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 organized in an *in situ* CWR network. National networks could themselves contribute to regional and global CWR networks that together maximize 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.

BOX 31 CWR GENETIC RESERVES WITHIN AND OUTSIDE PROTECTED AREAS (cont.)

*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.

4.10.1 Methodology

The establishment and implementation of *in situ* conservation goals for national CWR diversity involves 12 steps: (i) review *in situ* conservation gaps, (ii) combine *in situ* conservation gaps with the results of the diversity analyses, (iii) incorporate climate change analyses into site selection, (iv) select preliminary *in situ* CWR conservation sites for target CWR, (v) integrate *in situ* conservation priorities with national/international agri-environmental schemes, (vi) ground truth preliminary sites to determine whether sites are suitable for *in situ* conservation of target CWR, (vii) reformulate *in situ* conservation priorities (if necessary), (viii) select final CWR *in situ* conservation sites and actions, (ix) ensure the sites (genetic reserves) comply at least with the minimum quality standards, (x) ensure communities are involved in local CWR diversity conservation and management, (xi) produce *in situ* site and CWR taxa conservation action/management plans and (xii) establish routine collection of CWR diversity for *ex situ* conservation back-up (Flowchart 9).

(i) Review *in situ* conservation gaps. *In situ* conservation gaps at individual taxon, ecogeographic, genetic and trait levels should be reviewed in order to establish priorities for *in situ* conservation.

(ii) Combine *in situ* conservation gaps with the results of the diversity analyses. Diversity analyses include hotspot and complementarity analyses at individual taxon, ecogeographic and genetic diversity levels (see here for information on individual taxon and ecogeographic diversity analyses and here for genetic diversity analyses). *In situ* conservation gaps and the results obtained in the diversity analyses should be integrated into the national *in situ* CWR network of genetic reserves and informal CWR management sites to conserve priority CWR diversity.

(iii) Incorporate climate change analyses into site selection. If you have undertaken a study on how climate change may impact the distribution of priority CWR, then you should take that into account when selecting sites for active *in situ* conservation. The rationale lies in the fact that *in situ* conservation sites should be established and implemented in areas where CWR populations will not be affected negatively by climate change (or the negative impact is minimal) so as to ensure their persistence in the wild and within the genetic reserves (Magos Brehm *et al.* 2016).

(iv) Select preliminary *in situ* CWR conservation sites for target CWR. The *in situ* conservation network is likely to result from the combination of *in situ* conservation gaps, diversity analyses (hotspot, complementarity etc.) and climate change analysis.

- Within or outside protected areas (PA)? If the sites overlap with existing PA, then their implementation is facilitated. Where sites do not overlap with existing PA then informal CWR management sites could be established, the boundaries of existing PA may be extended or novel PA established. See BOX 31 for more information.
- Single or multiple CWR? A selected site may cover a single CWR taxon or may cover multiple CWR taxa. Equally, in a network of sites, some sites may cover only one taxon but others may contain many. If we look at particular ecogeographic/genetic/trait diversity, then a site covering multiple CWR is unlikely to represent the full range of diversity for every CWR, meaning that we would need to look at either sites for a single CWR, choosing the sites that are most diverse, or use a combination of the single and multiple 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 (Dulloo *et al.* 2008). Therefore, if financial and human resources are available, single CWR sites for

exceptionally important CWR populations should be established based on important ecogeographic/genetic/trait diversity.

- How many *in situ* conservation sites? The number of sites depends on how CWR diversity (i.e. ecogeographic/genetic/trait) is distributed within and among populations throughout the target territory. For each CWR, if no studies on ecogeographic/genetic/trait diversity have been carried out, Lawrence and Marshall (1997) have recommended the conservation of five populations from the most ecogeographically diverse sites in order to maximize genetic diversity conservation. The determination of the actual number of sites is, nevertheless, likely to be dictated by the financial and human resources available for implementation. This preliminary site selection should result in an ordered list of potential sites and appropriate conservation actions (i.e. implementing a genetic reserve within an existing PA, extending the borders of an existing PA to include priority populations of target CWR, implementing informal CWR management sites). If more resources are then made available, this list can help guide decisions on where further *in situ* CWR conservation could be implemented.

(v) Integrate *in situ* conservation priorities with national/international agri-environmental schemes. The selected preliminary sites that constitute a national network of genetic reserves and informal CWR management sites should be integrated with agro-environmental schemes (e.g. those funded by the European Commission or other regional agencies) so that their management is nationally coordinated and regionally integrated. Encouragingly, there is a growing effort to strengthen the relationship between agriculture and the provision of ecosystem services (FAO 2010). Activities that promote the *in situ* conservation of PGRFA 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. National Strategic Action Plans (NSAP) for the conservation and sustainable utilization of CWR should also be integrated into national programmes, through the appropriate national focal point(s), for the implementation of the CBD, National Biodiversity Strategies and Action Plans (NBSAPs), the ITPGRFA (ITPGRFA 2001) and the Global Strategy for Plant Conservation (GSPC). 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) Ground truth preliminary sites to determine whether sites are suitable for *in situ* conservation of target CWR. The sites must be 'ground truthed' in order to check whether they are suitable for long-term conservation of the target CWR. Various reasons may exist why even the highest priority potential sites may be unsuitable in practice:

- CWR populations may be absent or below the minimum viable population size.
- Land ownership: understanding whether the site is publically or privately owned is likely to be an important consideration. If the site is publically owned it is more likely that the site's future management can be amended to favour the target CWR population/s, particularly if the implementation of the *in situ* conservation site fulfils government policy objectives. On the other hand, if the site is privately owned the owner may be less amenable to making potential management changes to the site.
- Current land use: if the site is already under conservation management it would be easier to amend the site management for genetic CWR conservation than if it is managed for commercial purposes.
- Whether a site occurs inside or outside an existing PA, and PA status: if the site occurs within an existing PA it is probably easier to adjust the site management to incorporate CWR conservation. Yet, as the existing PA would not have been established for CWR conservation, the objectives of the PA management may not be amenable to adaptation to include CWR conservation (e.g. the management of large herbivores or coniferous trees is likely to conflict with herb CWR management).
- Current and potential threats to the long-term sustainability of CWR populations, their habitats and the sites: threats may be wide-ranging and include those that are the direct result of human actions (e.g. changes in land use or site management, plans to develop the area and urbanize a potential PA site), and those that are the indirect result of human actions that 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). Surveys should be carried out to detect the former, and to estimate the potential impacts. This information can then be considered when making the decision whether to proceed with the protection of the site. In contrast, the latter is likely to require the use of species distribution modelling, which may already have been incorporated earlier in this process to select areas that are the least affected, hence ensuring the long-term preservation of CWR (see step (iii) and here for more details on climate change analysis).

- Local community acceptance/involvement (see step x for more information).

(vii) Reformulate *in situ* conservation priorities (if necessary). The ordered list of potential *in situ* conservation sites produced as part of the preliminary selection is the initial step towards the final list of sites. If the highest priority potential sites are unsuitable, sites further down the ordered list would need to be considered. The process of selecting *in situ* sites is pragmatic and iterative. It continues until a list of suitable sites can be agreed for implemention of conservation action, either in a genetic reserve or informal CWR management site. It should, however, be highlighted that if for some reason there are no suitable sites for the *in situ* conservation of priority CWR taxa or a population of particular interest, then the *ex situ* conservation of those taxa/populations must be carried out.

(viii) Select final *in situ* CWR conservation sites for target CWR. The final selection of *in situ* conservation sites results from screening the preliminary selection using information gathered during the site visit. Pragmatically, priority should be assigned to the sites containing suitable habitats that are not predicted to be altered significantly in the medium to long term. A well balanced set of *in situ* conservation sites may contain a mix of: (i) genetic reserves established in existing PA, (ii) informal CWR management sites, (iii) sites in areas where PA boundaries have been extended, and (iv) sites established as novel PA. Together, each of these will form the National *In Situ* CWR Conservation Network that should be managed as a coherent whole. It should be emphasized that ultimately, the final selection of sites—although a pragmatic decision directed by science—is dictated by the resources available for *in situ* conservation and the governmental policy context at both the national and local levels.

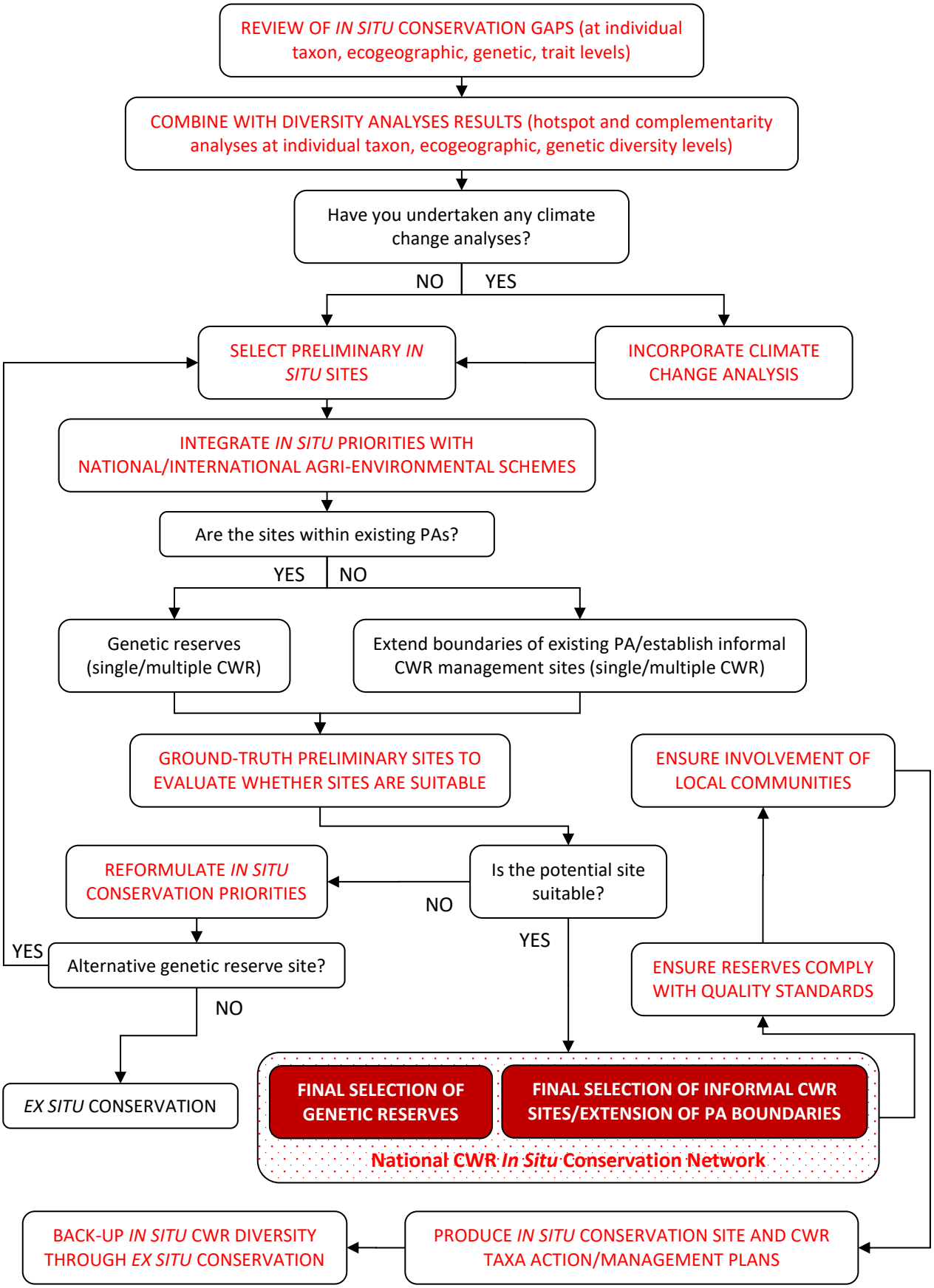
(ix) Ensure the sites (genetic reserves) comply at least with the minimum quality standards. The quality standards for *in situ* CWR conservation sites (Iriondo *et al.* 2012) provide useful guidance for both the practitioners involved in the design of *in situ* conservation strategies for CWR and the PA managers interested in their conservation. The standards have two levels: 'minimum' and 'optimal' quality standards. The minimum quality standards are baseline requirements necessary for any genetic reserve to function and fulfil its conservation objectives, whereas optimal quality standards include a more rigorous set of requirements. Quality standards can be applied to: (a) the genetic reserves themselves, and include traits such as location, spatial structure, target taxa, populations and management, (b) the PAs selected for the establishment of genetic reserves and (c) informal *in situ* conservation areas outside of formal PAs.

(x) Ensure communities are involved in local CWR diversity conservation and management. 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 on private land. Local community training workshops can be carried out and agreements with private owners (e.g. tax incentives) can be made. However, agreements must be linked to some form of guarantee from the land owner to ensure CWR diversity thrives. For example, establishment of a management agreement including a conservation prescription in order to ensure CWR are properly managed, but also to recognize the local communities' role in conserving such a valuable resource. For examples on the integration of conservation into local communities and industry, click here.

(xi) Produce *in situ* site and CWR taxa conservation action/management plans. The first step in formulating a CWR management plan, or amending an existing management plan to include CWR, is to observe the biotic and abiotic dynamics of the site considering both CWR and non-CWR species. A survey of the species present in the site should be carried out to help understand the ecological interactions within the reserve. A clear conservation goal should be decided and a means of implementation agreed. This process 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 actions, threat assessment, uses, additional conservation actions required, research and monitoring requirements, incorporation into existing national or local conservation initiatives and, perhaps most importantly, it summarizes the management interventions recommended for the site and how the CWR are to be monitored to ensure the management is promoting CWR population health (Maxted *et al.* 2008b). As part of the routine site management, a monitoring regime that results in collection time series data of target CWR' populations should be implemented with the aim of facilitating future reviews of project interventions (for more information, click here).

(xii) Establish routine collection of CWR diversity for *ex situ* conservation back-up. CWR diversity within the National *In Situ* CWR Conservation Network should be backed up *ex situ* as an insurance in case there is a reduction of genetic diversity in CWR populations or in case they go extinct (Maxted *et al.* 2008b).



Flowchart 9 Establishment and implementation of *in situ* conservation goals.

4.10.2 Examples and applied use

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 southern Norway, but one rare, annual species of *Beta 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. It was found 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 a field survey, it was found that species population sizes on the two Desertas Islands range between 2,730 and 4,620 individuals. Protection measures undertaken by the Natural Park of Madeira have increased population sizes by 10.8 times, but populations 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.

Figure 44 *Beta patula* Aiton, a primary wild relative of cultivated beets, *B. vulgaris* subsp. *vulgaris*, endemic to two islets in the Madeira archipelago, Portugal, here pictured at the Ilhéu do Desembarcadouro. (Photo: Énio Freitas/BG ISOPlexis)

Figure 43 Habitat of *B. patula* at the Ilhéu do Desembarcadouro, Madeira archipelago, Portugal. (Photo: Énio Freitas/BG ISOPlexis)

Source: Pinheiro de Carvalho *et al*. (2012)

Site selection for the conservation of CWR and landraces in Vietnam

The 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 landraces (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. The project provided technical support to farmers, encouraging effective conservation, development, sustainable management and use of their native landraces and CWR. Identification of sites for the conservation of landraces and CWR were one of the outputs of this project. The selection of these was carried out in two stages:

1. Identification of genetically important areas based on:
    - Presence of target species and their genetic diversity.
    - 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 agrobiodiversity conservation activities. Workshops, stakeholder consultations and meetings between NGOs, local institutes and farmer groups aided this process. Finally, the receptivity of the community to sharing traditional knowledge and practices that promote *in situ* conservation was assessed at each site.

The selected sites encompassed CWR, other species and landraces as well as a range of topographic, climatic and socio-economic conditions (e.g. proximity to markets and community-level associations). Eight genetic reserves were selected; two of them included more than one conservation site (one in a cultivated ecosystem and one in an associated site in an adjoining protected area), and the six remaining reserves consist only of cultivated ecosystems. Most of the targeted sites were diverse in terms of CWR and landraces of each crop and the sites also maintained more than one crop.

Source: Hue and Trinh (2007)

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 to promote community-based *in situ* conservation and sustainable use of both landraces 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 surveys 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 the species to monitor for conservation. The collated species data were then entered in a database and time-series data were analyzed 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 it with new data sent by national survey teams.

The main results of the CWR surveys showed that there is still a wealth of cereals, food and feed legumes, *Allium* and fruit tree CWR species in the region, but that this wealth is 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 of the broader value of CWR species among communities. However, where there is no economic return for farmers and herders changing their practices, national governments need to take the lead in CWR conservation. Further research is required to demonstrate how land management that favours CWR can lead to increased income for farmers and to the effective conservation of target CWR.

Figure 45 Genetic reserve, Al-Haffe, Syria. (Photo: Nigel Maxted)

Figure 46 Informal *in situ* conservation site, Bekaa Valley, Lebanon. (Photo: Nigel Maxted)

Source: Freeman *et al*. (2005)

***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 established by the indigenous Quechua people working in collaboration with CIP (International Potato Center) scientists—has focused attention on the *in situ* protection of potato CWR and landrace diversity. Although, 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 *Solanum tuberosum* subsp. *andigena* and related cultivated species are found in the Tiahuanaco region of southern Peru and northern Bolivia and this region may be suitable for establishment of a further potato park.

Figure 47 *Solanum bukasovii* Juz. ex Rybin (=*S. candolleanum* P.Berthault), a gene pool primary wild relative of cultivated potatoes, pictured here in the *Parque de la Papa*, Peru. (Photo: Eve B. Allen)

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4.11 ESTABLISHMENT AND IMPLEMENTATION OF *EX SITU* CONSERVATION PRIORITIES

What are the* ex situ *conservation goals in CWR conservation planning?

The goal of CWR conservation planning is to develop and implement 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. It is the *ex situ* collections that primarily facilitate access to these resources for crop improvement and research.

Ex situ conservation is the conservation of biological diversity outside its natural habitat. It involves locating, sampling, transferring and storing samples of the target taxa for conservation away from their native habitat (Maxted *et al.* 1997). Since the Convention on Biological Diversity (CBD) (CBD 1992), *ex situ* conservation as been seen—at least for the broader biodiversity conservation community—as a safety back-up strategy to provide security for the favoured *in situ* approach. While recognizing that it would be foolish to implement a National Strategic Action Plan (NSAP) for the conservation and sustainable use of CWR and to establish key national conservation areas without a safety back-up to help guarantee long-term conservation of the populations, it is recognized that CWR diversity has historically been almost exclusively conserved *ex situ*. It can be argued that *ex situ* collections provide the most practical means of access to germplasm by the 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 duplicate diversity *ex situ* for the benefit of the user community. Conversely, *in situ* conservation has a unique role in maintaining the process of adaptation to changing environments, which is not possible with *ex situ* conservation; each *ex situ* accession is a snapshot of that population's diversity at the time of sampling. Both *ex situ* and *in situ* techniques have their advantages and disadvantages and should not be seen as alternatives to one another, but as complementary strategies.

There are a range of *ex situ* conservation techniques available (see BOX 32), but, for CWR, seed storage in genebanks predominates as it is usually the most practical *ex situ* conservation technique. This is because the vast majority of CWR have orthodox seeds, which means they can be dried and stored at -18^{o}C without loss of viability.

BOX 32 *EX SITU* CONSERVATION TECHNIQUES

Like any other plant species, CWR 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 genebank for storage. The samples are usually dried to suitably low moisture content and then kept at sub-zero temperatures (normally at -18^{o}C).
- *In vitro* storage – the collection and maintenance of explants (tissue samples) in a sterile, pathogen-free environment.
- Field genebank – the collection 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 collection 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 collection of DNA or pollen and its storage in appropriate, usually refrigerated, conditions.

Figure 48 Seed collecting. (Photo: Adelaide Clemente)

Figure 49 *Ex situ* seed conservation. (Photo: Adelaide Clemente)

Source: Hawkes *et al.* (2000)

BOX 33 EXAMPLES OF MAJOR *EX SITU* SEED COLLECTIONS

Important national/regional collections include:

- Coffee in Cameroon, Côte d'Ivoire, Ethiopia, Kenya, Madagascar and Tanzania.
- Sesame in Kenya.
- Cassava in Malawi, Tanzania and Zambia.
- Sweet potato in Mauritius, Swaziland, Tanzania and Zambia.

International Maize and Wheat Improvement Centre (CIMMYT) genebank: more than 140,000 accessions (i.e. samples collected at a specific location and time) from more than 100 countries. The maize collection contains around 28,000 seed accessions and includes the world's largest collection of improved maize varieties, maize landraces and maize wild relatives, teosinte and tripsacum.

International Rice Research Institute (IRRI): more than 127,000 rice accessions and wild relatives, the world's largest collection of rice genetic resources.

Millennium Seed Bank at the Royal Botanic Gardens, Kew (MSB): the largest seed collection of 24,000 wild species.

Svalbard Seed Vault: 851,594 accessions from 233 countries of origin, provided by 68 depositor institutions (genebanks, institutes and NGOs) (Asdal pers. comm. 2016).

4.11.1 Methodology

The establishment and implementation of *ex situ* conservation priorities include five steps: (i) review *ex situ* conservation gaps, (ii) formulation of the *ex situ* collecting programme, (iii) germplasm field collection, (iv) genebank seed processing, and (v) post-storage seed care and monitoring (Flowchart 10).

(i) Review of *ex situ* conservation gaps. *Ex situ* conservation gaps at individual CWR taxon as well as at ecogeographic, genetic and trait levels should be reviewed in order to establish priorities for the *ex situ* collection programme.

(ii) Formulation of the *ex situ* collecting programme. The formulation of an *ex situ* collecting programme involves selecting target CWR populations and collecting sites, and planning when and how the collection will be undertaken. The selection of target CWR populations and sites is likely to result from the combination of *ex situ* conservation gap analyses (at individual CWR taxon, ecogeographic, genetic and/or trait diversity levels and, for instance, using a 'hotspot' or a complementarity approach, see here) and climate change analysis. Priority is likely to be assigned to:

- Individual CWR that are not conserved *ex situ* or *in situ*.
- CWR populations (within a single taxon) that are under-represented at ecogeographic, genetic or trait diversity levels as identified by the *ex situ* analysis.
- CWR taxa and populations most likely to be negatively affected by climate change (Magos Brehm *et al.* 2016).

The *ex situ* collecting programme should also include information about the number of sites sampled. Generally, collectors should aim to sample the maximum number of sites possible with the resources available. However, the species' breeding system, seed dispersal mechanism, the ecogeographic characterization of the species and the predicted impact of climate change on its distribution may also be used to determine the number of sites to be sampled.

(iii) Germplasm field collection. CWR should be collected from natural or semi-natural habitats, and the following five factors should be considered when sampling from the field:

- Distribution of sites within the target area: using either the cluster approach where selected sites are close together to pick up micro-habitat associated genetic diversity, or the transect approach where selected sites are along a line to pick up diverse ecosystem associated genetic diversity.
- Delineation of a site: site boundaries should be related to the size of the interbreeding unit. a site may also be delineated by changes in dominant habitat.
- Distribution of the plants sampled at a site: sampling could be carried out randomly throughout the site or, if there are distinct habitats, using a stratified random sampling method that encourages sampling from each habitat type. Collection of off-types or interesting material should be carried out selectively.
- Number of plants sampled per site: Recommendations suggest the collection of at least 2,500 seeds sampled from 40–50 plants, but ideally 5,000 seeds from 100 individuals. These numbers also depend on the species' breeding system and seed dispersal mechanism.
- Indigenous knowledge held by local communities: field collectors should note any knowledge held by local people on the CWR found in their area, this knowledge 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 that it is possible to apply the ideal sampling strategy. For instance, many CWR are found as individual plants or small clumps of plants, not dense stands. Furthermore, ripening is not uniform so not all of the potential fruit produced by a population will be available during one sampling visit. Another important point to consider is that germplasm is virtually worthless unless it has detailed passport data associated with the collection location. Therefore, these 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' taxonomic identification can be checked post-collection.

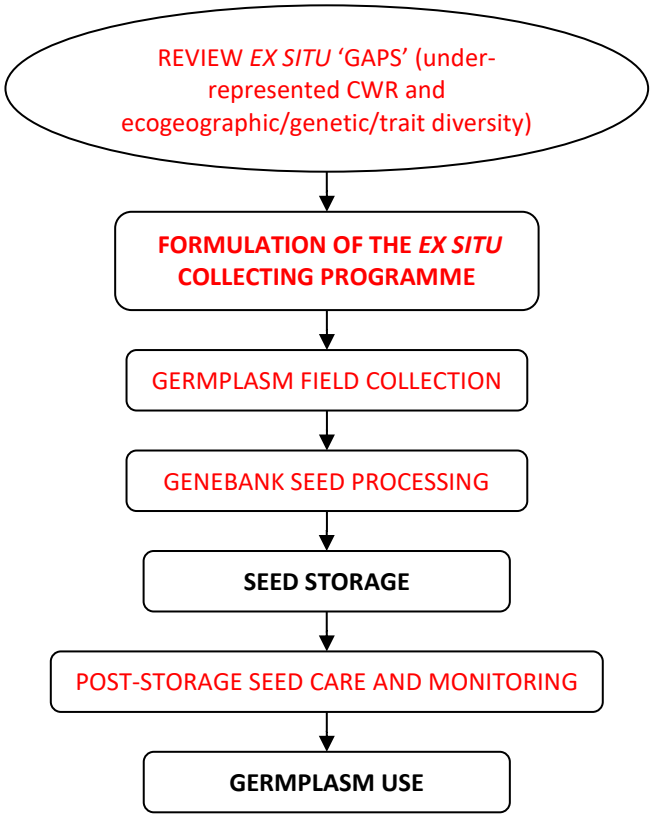
Note that all CWR collections should be undertaken legally with the appropriate national permission and ensuring the collection is not counter to international conventions (e.g. CITES). Collectors are also referred to the FAO International Code of Conduct for Plant Germplasm Collecting and Transfer for further guidance.

(iv) Genebank seed processing. Following collection, the sample arrives at the genebank and is processed according to standard practice. This includes:

- Seed cleaning (to separate chaff and fruit debris from the seed and to ensure the accession is a sample from a single species).
- Seed health evaluation (inspection for seed-borne diseases and pests).
- Dehydration (normally to around 5–6% relative humidity).
- Packaging (usually in glass vials, metal cans or laminated aluminium foil packets).
- Registration (entering an associated record in the genebank management system and making the accession available to users).
- Storage (usually in a -18°C cold room).
- Seed safety duplication.

When a seed sample arrives at the genebank but is not considered large enough to be banked directly (e.g. due to a small *in situ* population size or if the collection was made outside of the peak collecting season for that particular species), there may need to be a seed multiplication cycle before the seed can be processed and incorporated into the genebank or there may need to be further visits to the same population to collect more seed. For detailed genebank methodologies, click here.

(v) Post-storage seed care and monitoring. Once seeds are incorporated into the genebank, their viability will gradually decrease over time. Viability is usually determined via germination tests before the seeds are packed and placed into storage, and subsequently at regular intervals during storage (at approximately 10-year intervals). It is a measure of how many seeds are alive and have the potential to develop into normal plants. Usually expressed as 'percentage germination', a level of viability above 75% is acceptable. When germination falls below 75% the accessions require regeneration. The aim of regeneration is to increase the quantity of seed in an 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 has the potential to compromise the genetic integrity of an accession through: (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) (Sackville-Hamilton and Chorlton 1997). The risks involved with regeneration will vary considerably according to the species. Regardless, it is a costly operation and so the most efficient and cost effective way of maintaining genetic integrity is to keep the frequency of regeneration to an absolute minimum.



Flowchart 10 *Ex situ* conservation of CWR.

4.11.2 Examples and applied use

Ex situ conservation of the world's priority CWR

The project *Adapting agriculture to climate change: collecting, protecting and preparing crop wild relatives* is supported by the Government of Norway and managed by the Global Crop Diversity Trust and the Millennium Seed Bank of the Royal Botanic Gardens, Kew, in partnership with CIAT, the University of Birmingham, national/international genebanks and plant breeding institutes from around the world (Dempewolf *et al.* 2014, also see here). 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 due to:

1. Increasing clarification of the taxonomic and genetic relationships between CWR.
2. Ease of access to large online ecogeographic data resources.
3. Better knowledge and tools for modelling and mapping the distribution of plant species using geographic information systems (GIS).
4. A concerted global desire to implement the International Treaty on Plant Genetic Resources for Food and Agriculture (ITPGRFA 2001).

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 final priority list contains 1,392 CWR species from 193 crop gene pools. It is intended as a tool to help fill the gaps in the collection of CWR diversity for 29 globally important crops and to conserve them *ex situ*, before preparing them for use in plant breeding programmes in order to develop new crop varieties adapted to new climates. So far, the project has resulted in an inventory of CWR, an extensive CWR occurrence dataset of 5.4 million records and a gap analysis to identify the locations of genetic diversity that are not represented, or are under-represented, in *ex situ*

collections; this information can be used to plan germplasm collecting for *ex situ* conservation (see Castañeda-Álvarez *et al.* 2016). The project is currently supporting national partners to collect CWR and duplicate them at the Millennium Seed Bank, Kew for long-term storage and for distribution to pre-breeders. In total, the project will support 20 countries to carry out collecting activities. 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. A spin-off project is also looking at the ideal sites to establish genetic reserves around the globe to conserve these 1,392 priority CWR taxa, to help prioritize global *in situ* conservation actions (Vincent *et al*. in prep).

Source: Khoury *et al.* (2011), Dempewolf *et al.* (2014), Castañeda-Álvarez *et al.* (2016)

***Lathyrus belinensis*: a CWR discovered and almost lost**

In 1987, while collecting legume species near Cavus, Antalya province in Turkey, a new species of the genus *Lathyrus* was discovered and described as *Lathyrus belinensis* Maxted & Goyder. The single population was growing alongside a new road that was 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 hairier vegetative parts. The most striking and economically interesting distinguishing feature of *L. belinensis* is the flower colour, which is yellow with conspicuous red veins. This 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.

Figure 50 *Lathyrus belinensis* Maxted & Goyder, a taxon group 2 wild relative of both sweet pea and chickling vetch.

The type population was found over an area of only 2 km^2 and although the species was published in 1988, no further populations have subsequently been reported. The only known population was threatened by the new road construction and the planting 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 tell if field conservation will save this species in the wild!

Source: Maxted (2012)

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WWW Crop Genebank Knowledge Base

WWW European Native Seed Conservation Network (ENSCONET) (with collecting and curation manuals, database, germination recommendations etc.)

4.12 MONITORING CWR DIVERSITY

What is plant population monitoring and why it is important to monitor CWR populations?

Monitoring of plant populations is the systematic collection of data over time to detect changes, to determine the direction of those changes and to measure their magnitude (Iriondo *et al.* 2008). The monitoring of CWR populations and the habitats in which they occur has specific objectives: (i) to provide data for modelling population trends, (ii) to assess trends in population size and structure and to detect changes that may indicate demographically unstable populations, (iii) to assess trends in population genetic diversity, and (iv) to determine the outcomes of management actions on populations and to guide management decisions (Iriondo *et al.* 2008).

CWR can be monitored at different levels: (a) monitoring of specific target CWR populations conserved *in situ* (either informally or within formal genetic reserves) (addressed in this section), (b) monitoring of *ex situ* conserved accessions (addressed here), and (c) monitoring of higher level indicators of CWR conservation (see BOX 34).

The aim of *in situ* genetic conservation of CWR populations is normally to maintain the original levels of genetic diversity in the target populations and to ensure the viability of the populations from a demographic, genetic and ecological perspective. However, where the original status of a conserved population is not at its optimum, or when the population has experienced a catastrophic event, the objectives may concentrate more on achieving specific targets regarding population size, structure and genetic diversity. Therefore, CWR populations need to be monitored regularly to assess any short-term and longer-term changes that could potentially lead to genetic erosion, or even species extinction (see Figure on the right). This information can then be used to help evaluate the effectiveness of management strategies in achieving the initial objectives, and it can also be used to provide supporting evidence to justify maintaining or modifying current management practices (Ringold *et al*. 1996).

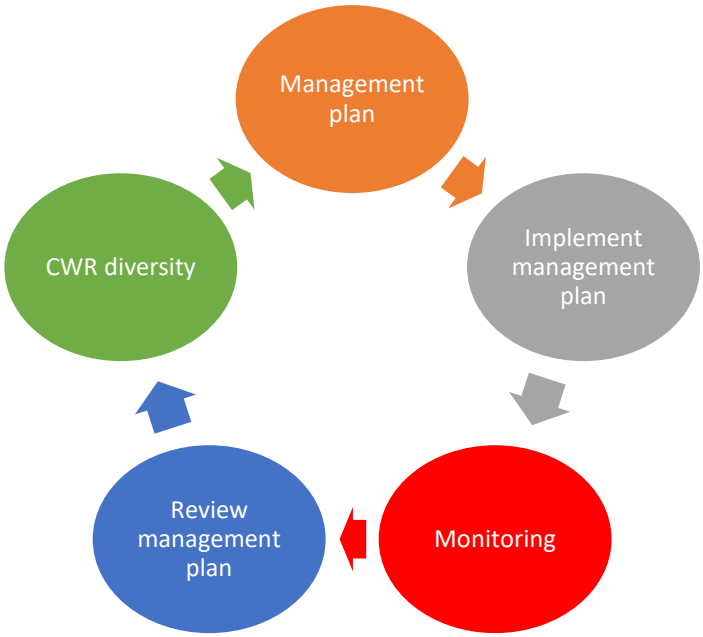

Figure 51 The management and monitoring cycle (Source: Maxted *et al.* 2016).

The objectives of the monitoring to be undertaken, and the questions that need to be answered, will determine the appropriate method to use (i.e. whether demographic, ecological, anthropogenic and/or genetic data should be collected to monitor populations). Collection of demographic data is perhaps the most commonly used method for monitoring plant populations. However, in the absence of this type of data,

ecological data can be collected in its place to infer population trends. Monitoring using ecological data identifies changes in the physical environment that shape the target CWR population and that affect the dynamics and composition of the living communities with which it is associated. Overall, a combined approach, using demographic, ecological and anthropogenic parameters, is desirable. In this way, the target species is monitored directly, but also the biotic and abiotic conditions and the human activities that might contribute to changes in population dynamics are examined and taken into account. Genetic diversity monitoring programmes may also be carried out. However, given that this type of monitoring requires staff with specific skills, specialized equipment and/or higher financial resources, it is recommended that it is only performed if needed, i.e. to answer very specific questions regarding population health and persistence in nature.

Table 5 provides an overview of these monitoring methods. For each method it outlines its main strengths and constraints, the representativeness of the sampling, its replicability and its sustainability in terms of long-term monitoring programmes.

Table 5 Comparison of methods for monitoring CWR populations.

	DEMOGRAPHIC/ECOLOGICAL/ANTHROPOGENIC	**GENETIC**
PRACTICALITY	Very practical: usually requires staff trained in species identification and monitoring methodologies. Field forms and small equipment are usually needed	Not practical: very specific skills are needed for molecular work and/or data analysis, as well as the provision of specialized equipment
TIME-SCALE	Relatively quick to collect and analyze the monitoring data	Time-consuming to perform the molecular work and data analysis
REPRESENTATIVENESS OF SAMPLING	Sampling should be designed to be representative of species diversity in both approaches	
NATURE OF DATA OBTAINED	Robust, qualitative and quantitative	
APPLICABILITY	Applied	Applied, but results may differ depending on the molecular marker used
REPLICABILITY	Replicable, but there is a degree of subjectivity when collecting the monitoring data in the field	Depends on the molecular marker used
CONVENTIONAL vs PARTICIPATORY	Conventional	
COST	Low cost, but monitoring can be quite frequent (depending on life form, expected rate of change, trend of the target species, rarity, degree of threat etc.)	Expensive, but frequent monitoring of population genetics is not necessary
SUSTAINABILITY (stakeholder incentive and involvement)	Sustainable	Not so sustainable as it can be expensive

In all cases, an efficient monitoring method for CWR populations or habitats should be reliable (will not lead to false conclusions), powerful (sensitive enough to detect changes) and robust (measurement techniques provide data that are independent of the technique used) (Brady *et al*. 1993). Finally, a monitoring programme should be able to distinguish between the significant biological changes that negatively impact target population health and normal seasonal variations that need not trigger changes in management.

BOX 34 MONITORING CWR CONSERVATION IMPLEMENTATION

The implementation of CWR conservation actions should be monitored to ensure that CWR diversity is properly conserved and available for utilization.

The CBD Strategic Plan (CBD 2010) developed the concept of SMART (Specific, Measurable, Attainable, Relevant and Timely) objectives. They highlight the need for monitoring outcomes that include time-series data to be analyzed against key performance indicators to evaluate success in achieving a strategic goal. SMART objectives also help towards identifying potential intermediate actions that can be implemented to achieve conservation goals. Additionally, in 2011, the Second Global Plan of Action for the Conservation and Sustainable Utilization of Plant Genetic Resources for Food and Agriculture (FAO 2011) was agreed by the Commission on Genetic Resources for Food and Agriculture at its 13th Regular Session. Its objective is "*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*" (CGRFA-13/11/Report, paragraph 98). In 2012, a technical consultation was held in Madrid, which generated "*revised draft indicators for monitoring the implementation of the Second Global Plan of Action for Plant Genetic Resources for Food and Agriculture*" (FAO 2011).

For CWR, these indicators were focused on *in situ* conservation:

- Number of CWR surveyed/inventoried.
- Number of *in situ* CWR conservation and management actions with government support.
- Number of conservation areas with management plans addressing CWR.
- Number of CWR actively managed *in situ*.

Higher-order indicators, mostly related to *ex situ* conservation, were also identified for CWR as follows:

- Number of threatened crop germplasm accessions.
- Number of CWR surveyed/inventoried.
- Number of accessions resulting from collecting missions in the reporting country.
- Percentage/number of target taxa where a collecting gap exists.
- 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 with safety duplicates.
- Number of accessions in need of regeneration.
- Percentage of accessions in need of regeneration.
- Number of accessions in a collection compared to the number of traits characterized.
- Number of accessions distributed from collections.

These indicators are well defined, easily measurable, the necessary data is readily attainable, the data relates clearly with the goal and they can periodically be assessed to provide a time-series comparison. When implemented by national PGR programmes, countries can check their compliance with international conventions/treaties, assess their conservation efficiency and specifically meet the country's obligation on CWR data reporting to the Second Global Plan of Action for the Conservation and Sustainable Utilization of Plant Genetic Resources for Food and Agriculture (FAO 2011). It should however, be noted that these indicators are relatively new, and tried and tested methodologies are not yet available.

BOX 35 MAJOR ACTORS INVOLVED IN A MONITORING PROGRAMME

In a CWR monitoring programme, different expertise are needed at various stages: (i) conservation managers/scientists are needed to design and implement the monitoring scheme, as well as to perform the analysis of monitoring data and to decide on changes in population management based on the results, (ii) statisticians are needed to help design the monitoring plan, taking into consideration the statistical tests needed in the data analysis, and (iii) staff of conservation areas are needed who are able to identify target species in the field and are trained in the field monitoring methodologies to collect data throughout the monitoring period.

Figure 52 Monitoring CWR populations in the West Bank, Palestinian Territories. (Photo: Nigel Maxted)

Source: Maxted *et al.* (2016)

4.12.1 Methodology

Regardless of where the monitoring of CWR populations takes place (within formally recognized genetic reserves or informal *in situ* conservation areas) the monitoring is likely to be implemented as follows (Figure 53):

(i) Identification of monitoring objectives for target CWR.
(ii) Identification and selection of variables to monitor.
(iii) Design of the sampling strategy.
(iv) Selection of the sampling units.
(v) Positioning of sampling units.
(vi) Determination of the timing of monitoring.
(vii) Determination of frequency of monitoring.
(viii) Implementation of a pilot study.
(ix) Data analysis.
(x) Adjustment of the monitoring plan.

(i) Identification of monitoring objectives for target CWR. The initial step is to define the specific objectives of the monitoring programme, for example whether to assess trends in population size and structure and/or in population genetic diversity. Ideally, genetic diversity monitoring should be carried out but, as it is costly, it should only be used if specific questions need to be answered (see Iriondo *et al.* 2008 for

recommendations on how, when and why to use genetic monitoring). Monitoring of genetic diversity may be needed (i) to recognize situations where an overall reduction of fitness has occurred, (ii) to decide what to do if a conserved population or population being considered for protection has severely declined in population size and (iii) to assess the extent of gene flow among populations that are, or have become, fragmented in a conservation area.

(ii) Identification and selection of variables to monitor. These variables may include demographic, ecological, anthropogenic and/or genetic parameters (see Table 6, Table 7 and Table 8 for a description of these variables). Life form and breeding system of target taxa and the resources available for monitoring should be taken into account.

(iii) Design of the sampling strategy. This involves making decisions on the type, size, number and position of the sampling units and the timing and frequency of sampling (Elzinga *et al.* 2001). It should be based on both a literature review of target taxa or of taxa with similar life forms and biological traits and on consultation with experts.

(iv) Selection of the sampling units. Sampling can be carried out using various methods:

- Plots (or quadrats): diversity is sampled within areas of standard size. The establishment of permanent quadrats is perhaps the most used monitoring method.
- Transects (banded transects or intercept transects): diversity is sampled within a defined distance either side of a central line, often one metre either side, making a two-metre-wide transect. The intercept method samples diversity that actually touches the transect line.
- Monitoring of individual plants (or plant parts) for particular attributes (e.g. plant height, number of seeds per fruit) (Iriondo *et al.* 2008).

(v) Positioning of sampling units. This should be random and ideally distributed throughout the entire distribution of the population. Simple random sampling involves the selection of a combination of sampling units that each have the same probability of being selected. Equally, 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 individuals within the same group share common features, and simple random samples then are taken within each group (Iriondo *et al.* 2008).

(vi) Determination of the timing of monitoring. Populations of CWR should be monitored regularly in order to detect any changes. Monitoring should be scheduled at the same phenological time each year to ensure data are directly comparable between monitoring events. It is often most effective during flowering or fruiting, because taxa can be easily identified. However, it may also be possible when leaves are unusually coloured or about to fall, or when the surrounding vegetation does not obscure the target species or a particular character of the target species.

(vii) Determination of frequency of monitoring. This depends on the life form, the expected rate of change, the rarity and trend of the target species, as well as the resources available for monitoring. It can be as frequent as every month during several growing seasons (e.g. rare or very threatened annuals), or much less frequently (e.g. perennials). In many cases working with both annuals and perennials, monitoring is performed annually.

(viii) Implementation of a pilot study. Once the monitoring scheme has been designed, a pilot study should be carried out before the implementation of a long-term monitoring strategy. This provides an opportunity to assess whether the experimental design and the field techniques are efficient or whether they need some adjustment.

(ix) Data analysis. The results of the pilot study should be analyzed in order to detect possible problems with the monitoring design and field methodologies. Statistical tests that provide meaningful conclusions need to be chosen at this stage.

(x) Adjustment of the monitoring plan. Refinement of the monitoring plan will often be necessary. If variables such as the chosen sample size, or the position of sampling units etc. are found to be inadequate in detecting meaningful changes in the population they will need to be adjusted. Nevertheless, it is

important to note that changes to the monitoring regime may impact data comparison, so any changes need to be considered carefully, possibly with the help of a statistician, before being implemented.

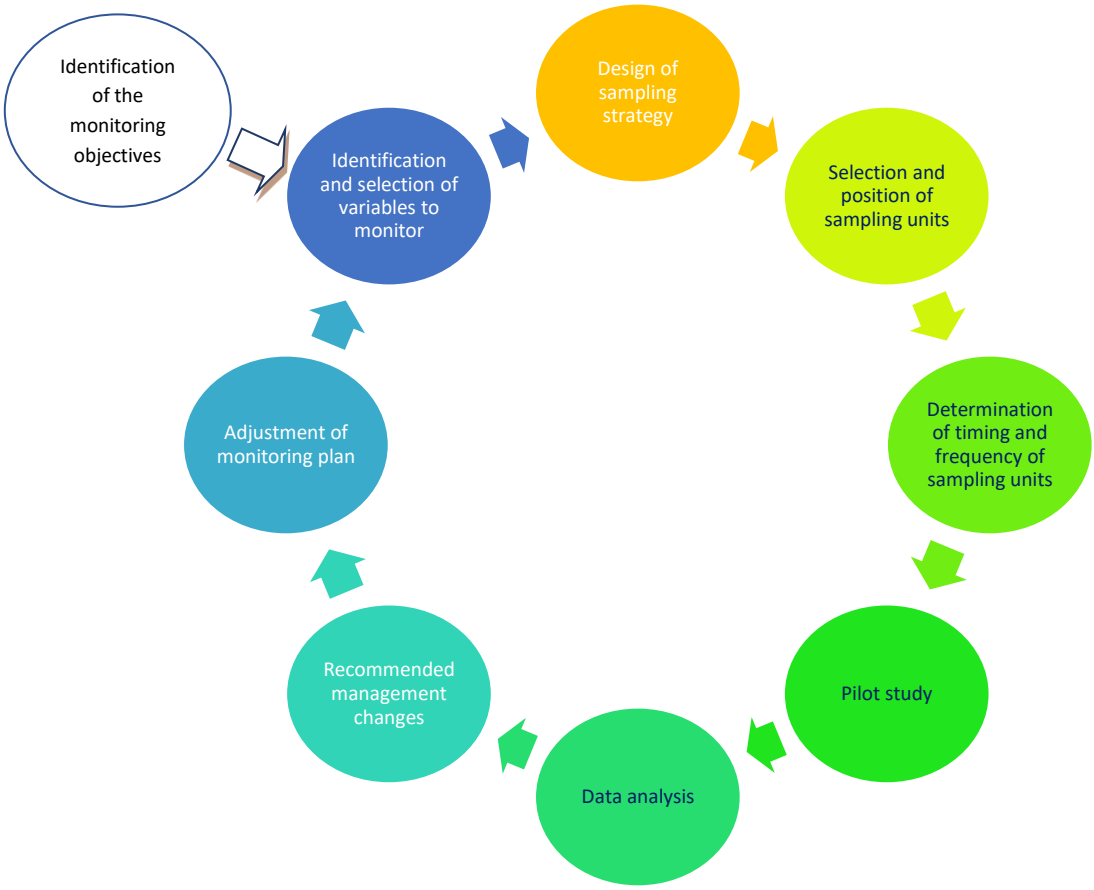

Figure 53 Development of a monitoring plan at the individual CWR level.

Table 6 Monitoring parameters for CWR to detect changes in diversity (see Iriondo *et al.* 2008 for more detail on each parameter).

LEVEL OF MONITORING	PARAMETERS TO MEASURE	EXPLANATION	OBJECTIVES	FURTHER INFORMATION
Demographic: individual CWR	Population size	Total number of individuals in a population	To assess viability of populations using: • Population trends • Extinction risk • Population viability analysis (PVA)[1] To identify demographic factors that are most relevant to population viability	See Table 7 for recommendations on which parameters to use in relation to population size and threat status of the target taxon
	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> • Temperature, precipitation, solar radiation, wind, cloud cover, atmospheric pressure, humidity • Soil moisture, texture, pH, nutrients, salinity, redox potential, cation exchange capacity	Environmental conditions of the habitat where the plant occurs	To identify changes in the physical conditions that characterize CWR and their associated communities; it can be used as a surrogate to infer population trends when demographic data are not available	–
	<u>Biotic components:</u> • Density, dominance, frequency, cover and importance value of all taxa that occur in the community	Description of the living organisms that occur in the habitat of the target taxon		See Table 8 for the equations for each of these parameters

	• Density and frequency of pollinators, seed dispersers, predators and parasites • Identification of pathogens and intensity of pathogen infection			
	<u>Disturbance:</u> • Natural (fire, flooding, slope movement, wind damage, extreme temperatures, trampling, erosion) • Human-induced disturbance (mining, logging, livestock grazing, recreation, road construction or maintenance, weed control)	Threats to the populations of the target species		See the IUCN's Threats Classification Scheme
	<u>Climate change:</u> • Annual recordings of susceptible species and habitats • Phenology • Changes in composition of communities	–		–
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 for the subsequent generation	• To evaluate the genetic diversity within populations • To understand the dynamics of populations • To recognize the reduction of fitness of a population • To determine the level of inbreeding/outbreeding of the target species • To determine which populations should be targeted for protection	–
	Effective population size (*Ne*)	The size of a hypothetical population that would lose genetic diversity at the same rate as the population under study		
	• Genetic diversity • Gene flow and population structure (*F* statistics)	• Both genetic 'richness' (the total number of genotypes or alleles regardless of frequency) and 'evenness' (the frequencies of different alleles or genotypes) can be measures of genetic		

		diversity; Nei's expected heterozygosity is also a measure of genetic diversity • Gene flow among populations, inbreeding within populations and differentiation between populations.	• To determine what to do if a protected population has suffered a severe decline in population size	
	Minimum viable population	The minimum size of a population needed to maintain genetic variation, avoid inbreeding depression and retain evolutionary potential		

[1]Population viability analysis (PVA) uses demographic modelling methods to predict the future status of a population, therefore aiding conservation and management decisions (Iriondo *et al.* 2008).

Table 7 Demographic parameters that should be monitored according to the population size and threat status of the target taxon (Source: Iriondo *et al.* 2008).

POPULATION SIZE	THREAT STATUS	DENSITY, FREQUENCY or COVER	POPULATION STRUCTURE	VITAL RATES THROUGH INDIVIDUAL MONITORING
Large (>5000)	Non-threatened	✓		
Small (<5000)	No evident threats	✓	✓	
Small (<5000)	Threatened	✓	✓	✓

Table 8 Parameters and equations for monitoring plant community structure (Source: Cox 1990).

PARAMETERS	EQUATIONS
Density	Number of individuals/area sampled
Relative density	(Density for a species/total density for all species) × 100
Dominance	Total basal area or aerial coverage values/area sampled
Relative dominance	(Dominance for a species/total dominance for all species) × 100
Frequency	Number of plots in which a species occurs/total number of plots sampled
Relative frequency	(Frequency value for a species/total frequency values for all species) × 100
Importance value	Relative density + relative dominance + relative frequency

BOX 36 ISSUES TO CONSIDER BEFORE DESIGNING A MONITORING PROGRAMME

Before designing a monitoring programme for CWR populations, some basic issues should be considered:

1. Available financial and human resources.
   - A monitoring programme needs to be sustainable both in the short and the long term because it involves the collection of data over a certain period of time.
   - The availability of skilled personnel and/or access to professionals with specialized skills as well as field equipment, should also be taken into consideration.
2. Baseline information regarding the taxon and its site during genetic reserve establishment.
   - Baseline information regarding the target taxon and its site should be collected to be able to compare the results with future monitoring events.
   - The study initially undertaken for genetic reserve establishment may be inadequate to detect future changes, because the necessary type and intensity of monitoring will often remain unknown until a pilot study is completed.
3. Intensity of the monitoring programme. This will mostly be determined by the level of priority given to the target CWR species in the management plan: high-intensity qualitative monitoring is expected for rare or highly threatened CWR or when there is high political sensitivity on potential decisions.
4. Spatial scale. Questions regarding whether the monitoring should target all populations, single populations or parts of single populations need to be addressed as it will influence later decisions and design.
5. Variables. Whether the monitoring will detect a percentage change, an absolute change, a target value or a threshold value should also be determined. Depending on the management objective for the target CWR species, it may be necessary to define a desired increase, a critical decrease or a target population size. In any case, the quantity should be measurable and biologically meaningful (Elzinga *et al*. 1998).

Source: Magos Brehm *et al.* (in press)

BOX 37 MONITORING DATA COLLECTION AND DOCUMENTATION SYSTEMS

Once the monitoring design has been finalized, monitoring data should be collected at the frequency determined in the design stage, and analyzed to detect significant biological changes that may negatively impact target population health. Table 6 shows the parameters and metrics that can be used.

Data collection methods need to be consistent across all target CWR populations and at each monitoring event. If monitoring of different populations of the same species is being carried out, it is extremely important that the same procedures are followed, to allow for reliable comparisons and to ensure that the results obtained reflect the real status of the monitored populations. In addition, monitoring methods must be clearly explained so that measurements in successive monitoring events are taken in exactly the same manner.

A consistent and comprehensive monitoring documentation system that clearly describes the monitoring methodology is of utmost importance. Monitoring data should be clearly recorded using field data forms, portable computers or personal digital assistants (PDAs). Iriondo *et al.* (2008) recommends filling the field forms with as much information as possible before going out into the field and use predefined codes to avoid repetitive writing and to reduce mistakes. Elzinga *et al*. (1998) highly recommended taking detailed information on the data collection methods defined in the monitoring plan. Collected data are then generally transferred to a spreadsheet or statistical software for subsequent data analysis. After each monitoring cycle, the data collected need to be properly analyzed using appropriate statistical tests selected during the monitoring design. In this way, any problems regarding the monitoring design or the health of a species can be identified and addressed in a timely manner.

Source: Maxted *et al.* (2016)

BOX 38 COST OF CWR MONITORING PROGRAMMES

It is not possible to give a precise cost of the application of these monitoring methods because there are numerous variables to consider. In practice, monitoring cost is often a compromise between the objectives initially set, the level of accuracy of the monitoring required and the resources available to the conservation team; the more resources, the more sophisticated the techniques that can be applied and the more accurate the results that can be obtained. The overall costs of monitoring CWR populations include those associated with establishing the monitoring programme, collecting the baseline data and then subsequent routine monitoring. It is likely that routine monitoring will be less costly than the establishment of the programme and the collection of baseline data.

Source: Maxted *et al.* (2016)

4.12.2 Examples and applied use

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 landraces and CWR of wheat, barley, lentil, chickpea, faba bean and several species of forages, range species and dryland fruit trees. Little is known of the status and trends of the diversity of these species according to both the First and Second reports on the State of the World on Plant Genetic Resources produced by FAO (FAO 1998, 2010). ICARDA, together with national research institutes in Jordan, Lebanon, Palestinian Authority and Syria, conducted population surveys across more than 65 monitoring sites between 2000 and 2005 as part of a GEF-supported regional project on promoting *in situ* conservation of dryland agrobiodiversity in the four countries. Further surveys were continued across 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 sites outside of Syria. The sites originally selected for the presence of large, healthy CWR populations—in Aarsal in Lebanon and Hebron in the West Bank—when re-surveyed, were found to be completely 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 a natural reserve in 2008.

Source: Amri A (pers. comm.)

Indirect genetic erosion monitoring of *Vicia* CWR — an example of demographic and anthropogenic monitoring

Between 1986 and 2006, monitoring was carried out to detect changes in genetic diversity of 18 populations of five *Vicia* species (section *Narbonensis*) from two regions in Syria (Kesab, Lattakia province, and Tel Kalakh, Homs province).

A threat assessment to indirectly detect genetic erosion was based on the methodology suggested by Guarino (1995) and modified by de Oliveira and Martins (2002). A quantitative comparison of changes was undertaken using a scoring system of factors related to increased risk of genetic erosion and based on the information obtained from interviews with local farmers, agricultural extension officers and data from initial collections. Each site was scored from 0 to 10 in relation to 18 factors. The overall score, a sum of the scores of all 18 factors, inferred the risk of genetic erosion at each site (rather than for each population).

Population size was classified in both 1986 and 2006 according to the following categories: (i) large (>100 plants), medium (50–100 plants), small (10–50 plants) and very small (<10 plants). An 'extinct' category was used in 2006 given that some populations had become extinct. Population size changes (1986 *vs* 2006) were then grouped using six size classes (Table 9 below). A Spearman's rank correlation was applied to evaluate the relationship between temporal changes in genetic erosion threat and demographic changes.

Table 9 Population size change classes for population characterization

CLASS	CHANGE	EXAMPLE
1	Decrease in 3 or more steps	Large → extinct
2	Decrease in 2 steps	Large → small
3	Decrease in 1 step	Large → medium
4	No change	Small → small
5	Increase in 1 step	Medium → large
6	Increase in 2 steps	Small → large

Source: Keiša *et al.* (2008)

Population dynamics of *Erodium paularense* Fern.Gonz. & Izco — an example of demographic monitoring of a wild relative of an ornamental crop

Figure 54 *Erodium paularense* Fer.Gonz. & Izco, wild relative of an ornamental crop, endemic to central Spain. (Photo: José Maria Iriondo)

A demographic study was carried out on *Erodium paularense* Fern.Gonz. & Izco (Geraniaceae), a woody chamaephyte that is endangered (VV.AA. 2000) and endemic to central Spain. This species is characterized by a narrow distribution, small populations, very low reproductive success (González-Benito *et al*. 1995, Albert *et al*. 2001), seed predation by ants and low seedling recruitment; its populations are also subject to human activity (cattle herbivory, recreational activities and plant collection). A population viability analysis (PVA) was carried out with data from the smallest population (area of occupancy of 443m^2) (Albert *et al.* 2004). Taking into account the plant size and their ability to produce flowers, plants were grouped into four life stages: one vegetative and three reproductive. These stages were obtained using cluster classification of field data: juvenile (<6cm), adult I (6–12cm), adult II (13–21cm), adult III (>21cm).

A metapopulation model was implemented with five subpopulations, four located in a rock microhabitat and one in lithosol. The model was built using spatial and demographic data gathered since 1993. Extinction risk and population decline under present and possible future scenario were estimated and the effectiveness of different conservation actions was evaluated.

Source: Albert *et al.* (2004)

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4.13 PROMOTING THE USE OF CONSERVED CWR DIVERSITY

Why link conservation to use?

Some conservationists argue that conservation is an end in itself, 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 in the case of PGRFA, for the following reasons:

- Cost of conservation — conservation does have a real and often significant cost—according to Hawkes *et al.* 2000, the annual cost of PGRFA *ex situ* conservation was estimated at US$ 30.5 million. These funds might otherwise be used to feed the starving, heal the sick or educate the illiterate. So why should humankind meet this cost and why should politicians and the 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 (according to ten Kate and Laird 1999, annual income from using PGRFA in 1999 was US$ 500–800 billion), so conserving PGRFA is a sound economic investment.
- Conservation sustainability — *in situ* CWR conservation, particularly, requires a relatively high and long-term investment, as wild populations and *ex situ* accessions of CWR need to be managed and monitored over time. On-going use of the conserved diversity hence offers a means of underpinning their value and reinforces conservation sustainability.
- Human altruism — humans are unable to see the world dispassionately and when men, women and children are suffering from malnutrition, there appears to be no practical alternative than to give CWR species, which are of direct use to humankind, the highest conservation priority.

Therefore, conservation of PGRFA and its sustainable utilization is intimately linked. This linkage forms the basis for enduring human food security and well-being, and ultimately the continuing survival of humankind itself.

CWR are defined by their potential for utilization, i.e. the ability of CWR to donate useful traits to crops. The CBD (2010) 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". Maxted and Kell (2009) reviewed the use of CWR in crop improvement for 29 major crops and noted the following points:

- For the 29 major crops studied 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. Use is particularly prominent in barley, cassava, potato, rice, tomato and wheat, but rice and wheat are the 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 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% of all references for the 29 major crops. Pest and disease resistance accounts for 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. Two percent of citations were recorded prior to 1970, 13% in the 1970s, 15% in the 1980s, 32% in the 1990s and 38% after 1999.
- 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 be a close reflection of the actual use of CWR in commercial crop breeding because: (a) the reporting of a useful trait transfer from a CWR to a crop does not mean that it has resulted in a novel

variety and (b) breeders are unlikely to be forthcoming about their use of CWR due commercially sensitive issues. Therefore, the use of CWR in crop improvement is significant but imprecisely defined.

- The use of the potential diversity contained in CWR species remains *ad hoc*, as CWR use by breeders has not been systematic or comprehensive.

The review concludes that there is a wealth of novel traits available for crop improvement in CWR and so far the vast majority of CWR diversity is untapped in terms of its potential utilization value. Also see BOX 39 for more information.

There are numerous ways in which the use of CWR diversity for crop improvement can be promoted, but traditionally this has focused on identifying traits of interest through phenotypic characterization and evaluation. However, in many cases this has proved prohibitively expensive. The First SoW Report (FAO 1998) highlights the fact that two thirds of globally conserved *ex situ* germplasm lacks basic passport data, 80% lacks characterization data and 95% lacks evaluation data, making the use of such germplasm—including CWR germplasm—much more difficult than it need be. The SoWPGR-2 (FAO 2010) 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".

Figure 55 Using wild emmer wheat to increase diversity in cultivated wheat, National Institute of Agricultural Botany field plots. (Photo: Nigel Maxted)

The bottleneck of systematic characterization and evaluation has been acknowledged almost since the late 1960s and early 1970s when the need for their conservation was recognized (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 CWR diversity. However, novel techniques such as 'next generation technologies'—that enable the screening of thousands of samples of germplasm for interesting gene variants that are adaptively important (Nordborg and Weigel 2008)—and 'predictive characterization'—where spatial analysis of germplasm passport data is used to predict which germplasm accessions might have desired traits (see Bhullar *et al.* 2009, Thormann *et al.* 2014)—offer an alternative to conventional characterization and evaluation. Ultimately, the use of conserved CWR (and indeed of all PGRFA) diversity is not likely to improve unless the professionals involved with CWR conservation can ensure that conserved germplasm is more accessible to breeders and other user groups, removing the barrier between conservation and use.

BOX 39 SOME EXAMPLES OF CWR USE IN CROP IMPROVEMENT

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:

(i) Desirable traits from wild sunflowers (*Helianthus* spp.) are worth an estimated US$267 million to US$384 million annually to the sunflower industry in the United States.

(ii) A single wild tomato species (*Lycopersicon peruvianum* (L.) Mill.) has contributed to a 2.4 per cent increase in solids content worth US$250 million.

(iii) Three wild peanuts (*Arachis batizocoi* Krapov. & W.C. Gregory, *A. cardenasii* Krapov & W.C. Gregory and *A. diogoi* Hoehne) have provided resistance to the root knot nematode, which costs peanut growers around the world US$100 million each year.

(iv) In the 1970s the US maize crop was severely attacked by corn blight, reducing yield by 50% and resulting in an economic loss of almost US$1,000 million, but was resolved by blight resistant genes from *Tripsacum dactyloides* L.

(v) Single gene-controlled traits have been transferred from CWR to confer 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.).

(vi) Genes from wild *Brassica oleracea* L. have produced domestic broccoli with high levels of anti-cancer compounds.

(vii) A wild Sicilian relative was crossed with cultivated broccoli to breed a variety that contains 100 times more of the cancer fighting chemical, sulforaphane, an anti-oxidant that destroys compounds that can damage DNA.

(viii) *Triticum turgidum* var. *dicoccoides*, a wild relative of wheat from the eastern Mediterranean, was used to increase the protein content of bread and durum wheat.

(ix) Genes from wild Mexican *Solanum demissum* Lindl. saved the world from potato blight by developing a blight resistant commercial variety.

Source: Mulongoy and Gidda (2008), Maxted and Kell (2009) and Hunter and Heywood (2011)

BOX 40 DO FARMERS BENEFIT DIRECTLY FROM CWR DIVERSITY?

It is interesting to question whether CWR are of any direct value to farmers. There are very few reports in the literature of farmers deliberately growing their crops near CWR to facilitate trait transfer between them. However, Mexican farmers, for example, encourage teosinte (*Zea mexicana* (Schrad.) Kuntze) to grow alongside cultivated maize (*Zea mays* L.) to permit natural crossing between the CWR and the crop. The corn producers mention that in approximately four years they can obtain a new, better adapted maize variety that will out-compete traditional varieties or hybrid maize. This case does seem counter intuitive, and contradicts the experience of many plant breeders. Plant breeders often state that the reason they are reluctant to use CWR in their breeding programmes is because crossing their elite breeding lines with CWR may not only transfer potentially beneficial traits, but there is a very high possibility that deleterious characters will be introduced from the CWR to the crop. It then takes significant resources to select out the unwanted deleterious characters whilst retaining 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 crop, potentially reducing yield and the adaptive characteristics of the crop as well as reducing the farmer's income in the short term. The degree of CWR to crop introgression is also likely to vary from crop to crop and will be very limited for inbreeding crops.

Overall, despite the case mentioned above, it seems likely that 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. Therefore, greater effort needs to be placed on raising public and professional awareness of the value of CWR diversity.

Figure 56 *Zea mexicana* (Schrad.) Kuntze (teosinte), a primary genetic relative of maize. (Photo: César del Ángel Hernández-Galeno)

4.13.1 Methodology

The potential users of CWR diversity and the stakeholders involved in CWR conservation can be categorized into four categories, each of which has different associated challenges:

1. Policy-makers. People who are responsible for, or are involved in, formulating policies related to CWR conservation and use. Ultimately, policy-makers decide the future of CWR conservation by developing and implementing policies that contribute to the long-term conservation of CWR and therefore both food and economic security. Policy-makers can be made aware of CWR value and the need for their conservation through the National Strategic Action Plan (NSAP) for the conservation and use of CWR. For example, they can be involved in all steps of the NSAP, they can be provided with policy-briefs etc.
2. Professional users (researchers, pre-breeders, breeders, farmers).
   Associated with the professional use of CWR diversity is the need to characterize, evaluate and screen the germplasm (either *in situ* or *ex situ*) for novel traits which are then used in crop breeding programmes. Plant breeding capacity ought to be strengthened and greater pre-breeding initiatives that transfer adaptive traits, and avoid linkage drag of deleterious traits, from what many breeders regard as exotic

backgrounds to more acceptable breeding material, should be encouraged. As a result, a close working relationship between the conservation and breeder communities needs to be encouraged to facilitate access to genetic diversity.

Professional users can utilize CWR germplasm conserved in *in situ* conservation sites, but more often they will utilize the samples of these populations stored *ex situ* in genebanks. Nevertheless, managers of genetic reserves, together with the support of relevant conservation authorities, should attempt to work with the professional user community to characterize, evaluate and publicize the germplasm found at *in situ* sites. Farmers have been included in this category as there may be some examples where they are using CWR diversity for crop improvement. However, there are very few known cases where this has been recorded (see BOX 39 to know more).

Useful traits can be identified using various techniques, but predictive characterization is a powerful technique that allows identification of *in situ* populations/*ex situ* accessions that potentially harbour specific traits. This technique is able to reduce the great amount of available diversity to a much smaller sample of diversity from which the pre-breeder can then test for relevant traits. In addition, *in situ* CWR conservation sites can be seen as *in situ* research platforms for field experimentation. Specific research questions that can be addressed include: species dynamics within conservation areas to aid their sustainable management, ecology and genetic diversity of *in situ* conserved CWR etc.

3. General users (the public). Through paying taxes, the general public fund most CWR conservation. Their support is therefore 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 genebanks. Yet how can public awareness of the value of CWR and the need for their conservation be promoted? This could be achieved by (i) promoting visits to CWR genetic reserves through a media campaign, (ii) providing various formal and informal education material as well as nature trails, guided tours, lectures etc. in the genetic reserve, (iii) publishing CWR-based cook books, (iv) encouraging agrobiodiversity ecotourism, (v) facilitating art competitions, (vi) promoting CWR on TV and in newspapers and bulletins etc. and vii) including CWR in school curricula etc.
4. Traditional users (local communities who live in the vicinity of CWR populations). Local communities are likely to have an extensive history of local plant collecting and utilization, and possibly of the CWR themselves. They often possess extensive knowledge of the ethnobotanical value and direct uses of plants, and a high proportion are likely to be CWR as so many plant species are CWR; although their use may be incidental to their value as a wild relative. It is worth noting that whether a genetic reserve is to be implemented, 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 its conservation. As a result, if the support of the local community for CWR conservation is to be obtained, active CWR conservation should not hinder local resource use, except 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 Europe (Kell *et al.* 2012), local communities do not always permit the sustainable management of their resources, even if mismanagement is likely to adversely impact their longer-term interests. For example, if private landowners decide to sell their land for development, there is seldom anything 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 members as it is about practical conservation implementation. A successful resolution will ensure the continued use of PGR resources by the local community while achieving sustainable conservation. It is apparent that there is a

Figure 57 Involving local communities in CWR conservation decision making, Sweida, Syria. (Photo: Nigel Maxted)

key role for the conservationist to play in educating both policy-makers and local people about the importance of these critical genetic resources.

4.13.2 Examples and applied use

Promoting the value and use of CWR in Zambia

In the context of the SADC Crop Wild Relatives project, the Zambia Agriculture Research Institute (ZARI) produced a video to promote the value and use of CWR in the country which was distributed among national stakeholders and broadcasted on TV. Please see the video here.

Raising the profile of CWR using social networks

The Crop Trust has been very active in disseminating the importance of agrobiodiversity including CWR and especially the results of the 10 year project, Adapting Agriculture to Climate Change: Collecting, Protecting, and Preparing Crop Wild Relatives. Facebook (Crop Wild Relatives) and Twitter (@CropWildRelativ) pageshave been the main vehicles of dissemination information regarding CWR and their use in crop improvement. In addition, researchers of the Crop Trust and partners of the project have their personal accounts which are also used for this purpose. The use of social networks has thus been essential and extremely effective in raising the profile of CWR worldwide.

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4.13.4 Additional materials and resources

Linking CWR conservation to use:

For references on genetic studies for breeding, click here.

Den Nijs HCM, Bartsch D and Sweet J (eds) (2004) Introgression From Genetically Modified Plants Into Wild Relatives. CAB International, Wallingford, UK.

Hunter D and Heywood V (eds) (2011) Crop Wild Relatives, A Manual of *In Situ* Conservation. Issues in Agricultural Biodiversity. Earthscan, London. (Available in English and French).

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Maxted N, Ford-Lloyd BV, Kell SP, Iriondo J, Dulloo E and Turok J (eds) (2008) Crop Wild Relative Conservation and Use. CAB International, Wallingford, UK.

Maxted N, Dulloo ME and Ford-Lloyd BV (eds) (2016) Enhancing Crop Genepool Use: Capturing Wild Relative and Landrace Diversity for Crop Improvement. CAB International, Wallingford, UK.

Sousa-Correia CM, Abreu JM, Ferreira Dias S, Rodrigues JC, Alves A, Maxted N and Ford-Lloyd BV (2008) "Linking conservation with sustainable use: *Quercus ilex* subsp. *rotundifolia* (Lam) O. Schwartz in traditional agro-sylvo-pastoral systems in Southern Portugal." In: Maxted N, Ford-Lloyd BV, Kell SP, Iriondo JM, Dulloo E and Turok J (eds) Crop wild relative conservation and use. CAB International, Wallingford, UK, pp. 638–648.

Dempewolf H (2013) Wild relatives in pre-breeding: Fishing the genepool with dynamite. EUCARPIA Genetic Resources section meeting: Pre-breeding – fishing in the gene pool. 10–13 June, Alnarp, Sweden.

Frese L (2016) Linking conservation to use. Nordic/ECPGR Joint Workshop. Plant genetic resources for food and security and ecosystem services. Planning and implementing national and regional conservation strategies – CWR conservation strategies. 19–22 September, Vilnius, Lithuania.

Project Adapting Agriculture to Climate Change: Collecting, Protecting, and Preparing Crop Wild Relatives has a dominant use component.

Project Enhancing the Link Between *In Situ* Conservation and Use of Crop Wild Relatives (CWR) in the SADC Region to Underpin Regional Food Security and Mitigate Predicted Adverse Impact of Climate Change (SADC Crop Wild Relatives) has a pre-breeding component.

Project Novel Characterization of Crop Wild Relative and Landrace Resources as a Basis for Improved Crop Breeding (PGR Secure).

Promoting the use of CWR:

Curtis S (2008) "Use of wild plant species: the market perspective." In: Maxted N, Ford-Lloyd BV, Kell SP, Iriondo JM, Dulloo E and Turok J (eds) Crop Wild Relative Conservation and Use. CAB International, Wallingford, UK, pp. 632–637.

Heywood VH (2008) "The use and economic potential of wild species: an overview." In: Maxted N, Ford-Lloyd BV, Kell SP, Iriondo JM, Dulloo E and Turok J (eds) Crop Wild Relative Conservation and Use. CAB International, Wallingford, UK, pp. 585–604.

Crop Wild Relatives, Public Awareness Program (Sri Lanka).

Karunagoda K (unknown date) Effectiveness of public awareness of CWR.

4.14 A NOTE ON CWR DATA MANAGEMENT IN CONSERVATION PLANNING

CWR conservation planning (along with the development of National Strategic Action Plans (NSAP) for the conservation and utilization of CWR) involves significant data collation, analysis and management (see Figure 58).

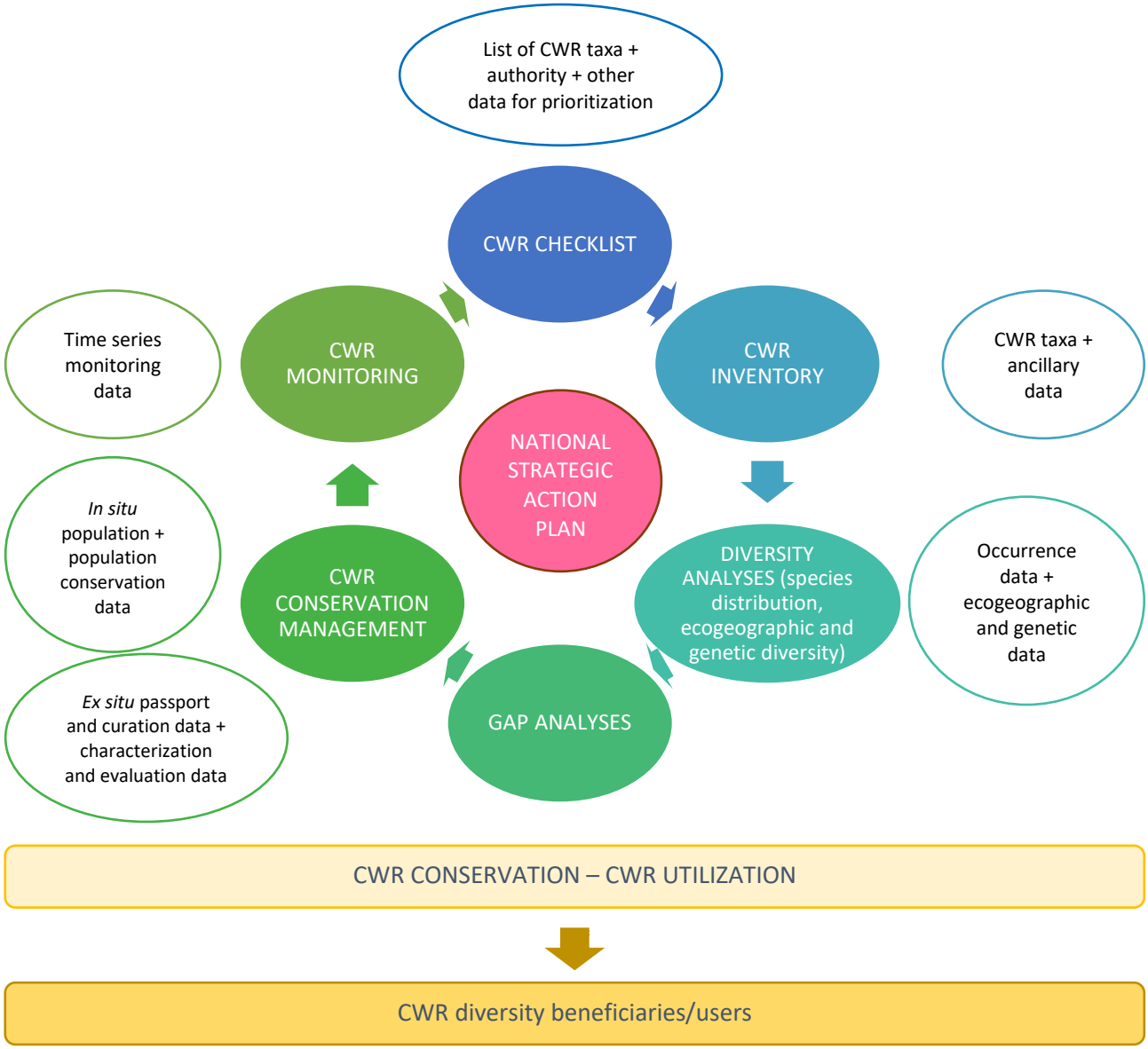

Figure 58 Summary of data flow in CWR conservation planning.

1. *CWR checklist* – normally a simple table of the Latin names of the CWR taxa present in the country. In order to prioritize CWR for active conservation further information for each CWR might be needed (to know more about annotated checklists, see here), in which case the checklist will consist of a list of Latin names of CWR taxa together with relevant data.
   CWR inventory – normally a list of a subset of the taxa in the checklist that have been identified as priority. The inventory will also include the prioritization information from the annotated checklist and further relevant information associated with each priority CWR taxon. A CWR checklist and inventory template is currently being developed which will facilitate the compilation of CWR checklists and inventories.
2. *Diversity and gap analyses* – the CWR checklist and inventory are primarily taxon-based, but diversity analyses of priority CWR are based largely on data associated with individual occurrences and genetic

data that represent those taxa. Normally significant resources are invested in the collation of large occurrence datasets and these can be collated into the Occurrence data collation template.

3. *CWR conservation management and monitoring* – the data associated with management and monitoring varies depending on whether it is associated with *in situ* or *ex situ* conservation. However, in general it falls into three basic categories: *in situ* populations (*in situ* population, conservation status and actions etc.), *ex situ* accessions (passport data, curation data, characterization and evaluation data) and both *in situ* and *ex situ* monitoring.
4. *Promotion of use* – CWR conservation should be directly linked to utilization. Characterization and evaluation data (mentioned in the previous point) are of extreme importance so that potential users have some basis on which to select the accessions they wish to utilize. The data associated with characterization and evaluation is often lacking and is seldom available to the user community. In Europe, the web-enabled European Cooperative Programme for Plant Genetic Resources (ECPGR) Central Crop Databases hold passport data and, to varying degrees, characterization and primary evaluation data of the major crop-related collections in Europe.