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## COMMISSION ON GENETIC RESOURCES FOR FOOD AND AGRICULTURE

### ESTABLISHMENT OF A GLOBAL NETWORK FOR THE *IN SITU* CONSERVATION OF CROP WILD RELATIVES: STATUS AND NEEDS

by

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The content of this document is entirely the responsibility of the authors, and does not necessarily represent the views of the FAO, or its Members.

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## SUMMARY

Crop wild relatives (CWR) are species closely related to crops (including crop progenitors). They are potential sources of traits beneficial to crops, such as pest or disease resistance, yield improvement or stability. CWR are a critical component of plant genetic resources for food and agriculture (PGRFA) yet have received relatively little systematic conservation attention.

Many CWR species—and the breadth of genetic diversity they contain—are under increasing threat from anthropogenic factors such as urbanization, habitat fragmentation and intensification of farming practices, but perhaps most importantly, climate change. In order to secure this vital resource for future crop improvement, there is now a need for step change in the *in situ* conservation of CWR, nationally, regionally and globally, as well as ensuring there is adequate *ex situ* backup of key population samples.

In 1989, the Commission on Genetic Resources for Food and Agriculture (CGRFA) called for the establishment of networks of *in situ* conservation areas for PGRFA, for both crops and CWR<sup>2</sup>. The rolling *Global Plan of Action for the Conservation and Sustainable Utilization of Plant Genetic Resources for Food and Agriculture* (GPA) includes conservation of CWR as a priority area, and Article 5 of the International Treaty on Plant Genetic Resources for Food and Agriculture (ITPGRFA) promotes the *in situ* conservation of CWR.

There have been some attempts by individual countries to set up *in situ* conservation areas for CWR, but no systematic effort to create national, regional or global networks of these areas. The objective of this study is to provide sufficient baseline information to allow decision-makers to strengthen efforts for the *in situ* conservation of CWR, including at national level; in particular, by providing the scientific basis for selecting a number of important areas which would be relevant at the global level. Specifically, the study aims to:

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

This background study addresses these issues in four parts. Part 1 is an introduction to CWR: how they are defined, global numbers of CWR, their importance to humankind as gene donors for crop improvement, threats to natural populations, how complementary conservation can be achieved and how CWR might be conserved *in situ* outside of conventional protected areas. Part 2 reviews the elements of a long-term and cost-effective national strategy for the *in situ* conservation of CWR, including presentation of a methodology for the planning and implementation of a national CWR complementary conservation strategy. Part 3 takes a global approach by a) identifying important geographical areas for the *in situ* conservation of a selection of 14 critical crop gene pools, b) pinpointing conservation gaps and c) making recommendations for the steps needed towards establishing an effective complementary conservation strategy for priority species. Part 4 summarises future needs for CWR conservation, stressing the need for a coordinated and collaborative approach, and concludes with a series of recommendations for how to improve the conservation and use of CWR diversity. Recommendations include: establishing national CWR conservation strategies; effecting back-up duplication of CWR diversity *ex situ*; improving consensus-building between biodiversity and agrobiodiversity communities; enhancing availability of CWR for breeders' use; addressing the sustainability of CWR conservation; improving information dissemination; and conducting priority CWR research activities.

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<sup>2</sup> CPGR/89/REP, paragraphs 32-37.

This is the summary version of the background study paper. A full version of the study which includes a number of annexes with more background information on the subject matter will soon be available at [http://www.fao.org/nr/cgrfa/cgrfa-back/en/?no\\_cache=1](http://www.fao.org/nr/cgrfa/cgrfa-back/en/?no_cache=1).

## PART I: INTRODUCTION

### 1.1 Background

CWR are wild species that are found in natural and semi-natural ecosystems. They tend to contain greater genetic variation than crops because they have not passed through the genetic bottleneck of domestication; therefore, they provide a reservoir of genetic variation for improving crops (Vollbrecht and Sigmon, 2005) and are the obvious choice for meeting contemporary food security demands (Feuillet *et al.*, 2008).

The genetic diversity inherent in and between wild CWR populations is constantly changing in response to their environment; therefore, CWR populations are a component of natural ecosystems that cannot effectively just be maintained *ex situ*. Unique and particularly diverse populations of these genetic resources require effective *in situ* maintenance if they are to continue to meet exploitation needs of current and future stakeholders, and via them, global goods. However, the ecosystems in which CWR are found are becoming increasingly unstable due to unsustainable management practices and climate change, putting CWR populations under threat.

There have been few studies of the likely impact of climate change on CWR diversity; however, Jarvis *et al.* (2008) undertook a comparative study of three crop gene pools. They generated climatic envelopes for *Arachis*, *Solanum* and *Vigna* and compared current distribution with the predicted range in 2055. Their results indicated that for the three genera, 16–22% of species would go extinct. The majority of species showed greater than 50% loss of distributional range and the range that remained was highly fragmented, placing the extant species under greater threat of genetic erosion or extinction.

It is likely that many current crop varieties will need replacement to enable them to better suit the new and changing environments under which they will be forced to grow. CWR are likely to contain the breadth of genetic diversity necessary to combat climate change because of the diversity of habitats in which they grow and wide range of conditions they are adapted to (FAO, 2008a). It is therefore of grave concern that the study and conservation of CWR diversity has yet to be systematically addressed. Failure to act now could have a devastating impact on the global economy and social well-being.

It is estimated that between 2% and 6% of global gene bank *ex situ* collections are CWR and of the total number of CWR species, only about 6% have any accessions conserved *ex situ* (see Section 4.3). Apart from a few notable exceptions, such as the Millennium Seed Bank, Kew and the Chinese Germplasm Bank of Wild Species, Kunming, CWR diversity has not been a priority for germplasm collection.

A similar assessment applies to *in situ* CWR conservation. CWR populations have rarely received specific attention in protected area management plans unless their conservation is coincident with other protected area priorities. Further, in many countries, the conservation of CWR has fallen between two conservation sectors; ecological conservation efforts focus on habitats or on charismatic, rare or threatened wild species, while agricultural conservationists focus on crops. As a result their conservation has been neglected (Maxted, 2003).

In response to these issues, the CGRFA called in the past for the development of a network of *in situ* conservation areas for CWR. The GPA includes conservation of CWR as a priority area, and Article 5 of the ITPGRFA also promotes *in situ* conservation of CWR, including in protected areas.

The objective of this study is to provide sufficient scientific baseline information to allow decision-makers to establish or strengthen *in situ* conservation networks for CWR and other measures to guarantee their conservation and sustainable use, and in particular to:

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

It is important to stress that this report is based on scientific research only (i.e., it does not take account of socio-political factors) and has been possible due to recent advances in access to electronic data sets (e.g., *ex situ* collections and protected area data) and the application of novel methodological approaches to PGRFA conservation. The study aims to provide rigorous and balanced scientific information to decision-makers, which is meant to be policy-relevant but also policy-neutral. It analyses the need for increasing efforts and cooperation at national, regional and global levels, but also for further research where needed. In Part 3 of this report, which addresses global CWR conservation needs on the basis of a selection of priority crop complexes, we have not taken into account political boundaries in the recommendations given. Further, individual nations have not been taken into account in this study; therefore, not all countries are highlighted. However, future research into other globally and/or regionally important crop complexes will broaden the CWR *in situ* conservation network to include more countries and there is a need for all countries, whether they feature in this report or not, to develop national CWR strategies (see Part 2).

We should also stress that this report does not cover all globally and locally important major and minor crop complexes. The groups selected are a sample of crops of global importance for food security and should be viewed as a preliminary selection of crop groups only. Our recommendations for conservation of the wild relatives of these crops can be taken as a first analysis towards establishing a global network for the *in situ* CWR conservation, although further research and intergovernmental discussion is required to ensure their systematic conservation. Further, while we have addressed the national and global approach to CWR conservation in two separate parts of this report, an integrated national, regional and global approach is needed to ensure these species are adequately conserved throughout their range. In particular, regional cooperation will be important for the success of CWR conservation initiatives.

## 1.2. The global and local importance of crop wild relatives

CWR were first routinely used by agricultural scientists to improve major crops in the 1940s and 1950s, and by the 1960s and 1970s this practice was leading to some major breeding improvements (Meilleur and Hodgkin, 2004). Almost all modern varieties of crops contain some genes derived from a CWR and they are now recognized as a critical resource with a vital role in food security and economic stability for the 21st century, as well as contributing to environmental sustainability (Prescott-Allen and Prescott-Allen, 1983; Hoyt, 1988; Maxted *et al.*, 1997a; Meilleur and Hodgkin, 2004; Stolten *et al.*, 2006).

Development in the biotechnology industries has also allowed the transfer of genes from more distantly related species, further enhancing the value of CWR (see Hajjar and Hodgkin, 2007; Hodgkin and Hajjar, 2008). CWR have contributed significantly to improving food production and their value in increasing crop yields worldwide has been estimated at as much as US\$ 115 billion per year (Pimentel *et al.*, 1997). Genes from CWR have also been used to salvage crops in major crisis situations; for example, in the 1970s the US maize crop was severely threatened by corn blight which destroyed almost US\$1000 million worth of maize and reduced yields by as much as 50% in 1978 (FAO, 2005). The problem was quickly resolved through the use of blight resistant genes from Mexican maize CWR (Prance, 1997).

The contribution of CWR is growing and has largely been through the donation of useful genes coding for pest and disease resistance, abiotic stress tolerance and higher nutritional value (Hajjar and Hodgkin, 2008). For example, single gene-controlled traits have been introduced from CWR into



crops to provide 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.). Increased nutritional value of crops has been fulfilled through the introduction of genes for higher protein content in wheat and vitamin C content in tomato. Genes from wild *Brassica oleracea* L. plants have created domestic broccoli with high levels of anti-cancer compounds (Hodgkin and Hajjar, 2008).

Annexe 1 of the full version provides further examples of the use of CWR in crop improvement programmes for 29 major crops.

### 1.3. Definition of a crop wild relative

CWR are commonly defined in terms of wild species that are relatively closely related to agricultural and horticultural crops; therefore, a broad definition of a CWR would be any taxon belonging to the same genus as a crop. This definition is intuitively accurate and can be simply applied. However, application of this broad definition results in the inclusion of a very large number of species that may be either closely or more remotely related to the crop itself. For example, analysis of the European and Mediterranean flora revealed that approximately 80% of species in the region are CWR and other species of socio-economic importance (Kell *et al.*, 2008a). Therefore, there is a need to narrow the definition of CWR so that limited conservation resources can be focused on priority species, either those most closely related to the crop or those that are known to have traits required by breeders.

In the light of contemporary biotechnological advances, most, if not all, species are potential gene donors to a crop. However, while these techniques are rapidly evolving, their cost means that they are likely (at least in the near future) to remain restricted to major crops and advanced breeding companies or institutes, while in the majority of national breeding programmes, exploitation using conventional techniques to cross crops with their close wild relatives will remain the norm. It is therefore important that we apply an accurate definition of the relationship between a crop and its wild relatives, so that conservationists competing for limited resources may objectively prioritize taxa for study (Kell and Maxted, 2003; Meilleur and Hodgkin, 2004; Maxted *et al.*, 2006).

To establish the degree of crop relatedness, one method which could be applied is the Harlan and de Wet (1971) Gene Pool concept—close relatives being found in the primary gene pool (GP1), more remote ones in the secondary gene pool (GP2), and very remote ones in the tertiary gene pool (GP3). However, for the majority of crop complexes, particularly those in the tropics, too little information is available to use this concept. Maxted *et al.* (2006) therefore proposed an alternative solution using the existing taxonomic hierarchy. It can be applied to define a crop wild relative's rank as follows: Taxon Group 1a – crop, Taxon Group 1b – same species as crop, Taxon Group 2 – same series or section as the crop, Taxon Group 3 – same subgenus as the crop, Taxon Group 4 – same genus as the crop, and Taxon Group 5 – same tribe but different genus to the crop. Therefore, for CWR taxa where we have little or no information about reproductive isolation or compatibility, the Taxon Group concept can be used to establish the degree of relationship between a CWR and a crop. The Taxon Group concept can be applied to all crop and CWR taxa and can be used to define relative CWR relatedness, as long as the existing classification of the genus contains an infra-generic structure.

Based on the above arguments, a working definition of a crop wild relative has been proposed by Maxted *et al.* (2006):

“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.”

#### 1.4. Global numbers of crop wild relatives

Recent studies have found that the actual number of CWR species of interest to the food and agriculture community may be much larger than previously recognized. For example, Kell *et al.* (2005) produced the first comprehensive European and Mediterranean CWR Catalogue and, using the broad definition of a CWR (any taxon belonging to the same genus as a crop), listed in excess of 25 000 crop and CWR species that occur in the Euro-Mediterranean region (Kell *et al.*, 2008a). This means that around 80% of the Euro-Mediterranean flora consists of crops and their wild relatives. More than 14 000 of these species are endemic to Europe alone.

Globally, we estimate that there are approximately 50 000–60 000 crop and CWR species (see Annexe 1 of the full version of the study). However, focusing only on those genera that contain the major and minor food crops, analysis of data extracted from Groombridge and Jenkins (2002) and Mabberley (1997) gives a global estimate of 10 739 crop and CWR species that are of direct value for food security. Based on the average percentages of primary and secondary CWR species in the sample of 14 food crop groups included in this study (Table 1), and extrapolating to the 77, we may need to conserve globally around 700 close CWR species worldwide in order to ensure that the highest priority genetic diversity is conserved and made available for use in crop improvement programmes.

**Table 1. Numbers of primary and secondary CWR species**

Crop	Crop taxon	Species genus	in Primary species	CWR	Secondary CWR species	% Priority in genus <sup>1</sup>
Finger millet	<i>Eleusine coracana</i>	9		3	3	66.67
Barley	<i>Hordeum vulgare</i>	16		1	1	12.50
Sweet potato	<i>Ipomoea batatas</i>	600–700		3	11	2.00
Cassava	<i>Manihot esculenta</i>	98		3	13	16.33
Banana/plantain	<i>Musa acuminata</i>	30		10	15	83.33
Rice	<i>Oryza sativa</i>	23		8	9	73.91
Pearl millet	<i>Pennisetum glaucum</i>	80–140		1	2	2.14
Garden pea	<i>Pisum sativum</i>	3		1	2	100.00
Potato	<i>Solanum tuberosum</i>	1000		6	24	3.00
Sorghum	<i>Sorghum bicolor</i>	25		2	2	16.00
Wheat	<i>Triticum aestivum</i>	6+22		6	12	64.29
Faba bean	<i>Vicia faba</i>	140		1	0	0.71
Cowpea	<i>Vigna unguiculata</i>	61		1	3	6.56
Maize	<i>Zea mays</i>	4		1	3	100.00
<b>Totals</b>		<b>2117–2277</b>		<b>47</b>	<b>100</b>	
<b>%</b>		<b>100</b>		<b>2.06</b>	<b>4.39</b>	<b>6.45</b>

1. Percentages based only on the degree of relationship of the species to the crop taxon. In this study, a refinement of this level of prioritization was undertaken based on the degree of threat of these species and to include cases where tertiary wild relatives are also known to be important for crop improvement

Naturally, some countries harbour greater numbers of CWR than others. In general, the greater the number of species in the country's flora, the greater the number of CWR there will be. In those countries with higher numbers of CWR, a greater injection of resources will be needed in order to secure populations *in situ* (as well as in back-up *ex situ* collections). It is not within the scope of this report to address this issue, but it is an issue that, at a global level, will have to be addressed to ensure that these vital resources are adequately conserved within their natural ranges.

### 1.5. Threats to crop wild relative species and genetic diversity

Frankel (1970) and Jain (1975) were among the first to draw attention to the need for *in situ* conservation of CWR (Stolten *et al.*, 2006), realizing that the increasing threat to CWR species and the genetic diversity within them was an escalating problem. It is likely that virtually all CWR species are currently suffering loss of genetic diversity to varying degrees. IUCN's 1997 Red List assessment of plants concluded that 33 798 plant species were threatened or extinct (Walters and Gillett, 1998) (but this was undoubtedly an underestimate as not all plant species were evaluated), while Maxted *et al.* (1997c) estimated that 25–35% of plant genetic diversity would be lost between the ratification of the CBD in 1993 and the 2010 Biodiversity Target date.

The main factors causing loss of biodiversity are associated with anthropogenic influences, including deforestation, logging, plantation agriculture and forestry, industrialized agriculture, dryland destruction and desertification, fire, urbanization, mining and quarrying, invasive species, and climate change. There are also more nebulous but equally detrimental threats to plant diversity, such as the loss of traditional values or indigenous knowledge leading to lower valuation of diversity and resultant careless destruction. Each of these threats is likely to have a significant impact on CWR diversity. However, it is worth bearing in mind that, as pointed out by Jain (1975), most CWR of the major crops are found in disturbed, pre-climax communities, which are the same habitats most subject to increasing levels of anthropogenic change and destruction beyond what has previously been known. Thus, CWR are likely to be disproportionately and adversely impacted by current ecosystem instability and changes to anthropogenic environments, at least compared with non-CWR wild species found in more stable climax communities.

A further threat, unique to CWR is that they are often overlooked as an element of biodiversity. Conservation priorities at international, regional and national levels are primarily established by agencies with a focus on rare and threatened species—the fact that certain species have greater actual or potential economic value is often seen as irrelevant. For example, in Europe, very few CWR species are protected by the EU Habitats Directive. Notably, only four species included in the Habitats Directive Annexes II, IV and V are wild relatives of major food crops out of a total of 153 wild relative species of major food crops that occur in the EU territories, and a further 13 species are included in the minor food crop group, out of a total of 542 (Kell *et al.*, 2008a). The same authors found that only 5% of the CWR species of Europe are found within Important Plant Areas.

### 1.6. *In situ* and *ex situ* conservation of CWR diversity

There are two primary techniques used for CWR conservation: *in situ* (i.e., in natural habitats managed as genetic reserves<sup>3</sup>) and *ex situ* (primarily as seed in gene banks, but also as explants in tissue culture

<sup>3</sup> Genetic reserve conservation may be defined as “the location, designation, management and monitoring of genetic diversity in natural wild populations within defined areas designated for active, long-term conservation” (Maxted *et al.*, 1997b). Synonymous terms include ‘genetic reserve management units’ (GRMUs), ‘gene management zones’ (GMZs), ‘gene sanctuaries’ or ‘genetic sanctuaries’ and ‘crop reservations’.

or cryopreserved, or as mature individuals in field collections). Genetic reserve conservation action is long-term because significant resources have to be invested to establish the reserve. *Ex situ* seed conservation is suitable for the majority of CWR species, and as management interventions are fairly minimal once seed is in the gene bank, the annual cost of maintenance may be as little as US\$5 per year for a single accession (Smith and Linington, 1997). However, the CBD and ITPGRFA both stress the desirability of *in situ* conservation; primarily due to the overall need to maintain ecosystem health, but also because it has the advantage that it maintains the dynamic evolution of the CWR diversity itself in relation to parallel environmental changes.

It is generally accepted that CWR genetic reserves would normally be established within existing protected areas (Maxted *et al.*, 1997b; Heywood and Dulloo, 2006; Iriondo *et al.*, 2008a). There are three important reasons for locating genetic reserves within existing protected areas: a) 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 are not considerations, b) it is relatively easy to amend the existing site management plan to facilitate genetic conservation of CWR species, and c) it means creating novel conservation sites can be avoided, thus evading the possibly prohibitive cost of acquiring previously non-conservation-managed land (Iriondo *et al.*, 2008a).

The reason why there is a need to establish genetic reserves, even within existing protected areas, is that the majority of protected areas are established to conserve specific habitats or faunal elements and not the genetic diversity of wild plant species. Few are established specifically to conserve flora and very few specifically for CWR conservation. Therefore, CWR taxa are rarely routinely targeted for demographic monitoring, which means that their conservation is regarded as passive. Without monitoring and active management, the genetic diversity within and between individual CWR populations could be eroded and entire populations could even go extinct.

If our goal is to conserve the maximum genetic diversity within CWR taxa, then we need to study and monitor the genetic diversity and natural dynamics of CWR populations; otherwise, our efforts in establishing protected areas for these taxa may be wasted. Therefore, passive conservation of CWR in protected areas is unlikely to prove effective and active demographic and genetic monitoring and management of target CWR populations is required. It should also be noted that the *in situ* management of CWR may differ significantly from that required for more traditional protected areas whose objective is commonly to sustain climax communities. For example, CWR of major crop plants are often located in pre-climax communities (e.g., *Aegilops speltoides*, *Lens orientalis*, *Sorghum bicolor*) (Jain, 1975; Maxted *et al.*, 1997b; Stolton *et al.*, 2006) where the site management is comparatively intense, or the CWR may be closely associated with traditional farming practices, in which case, genetic reserve management would need to be associated with maintenance of the farming system.

IUCN recognizes six categories of protected areas (IUCN, 1995). Stolten *et al.* (2006) conclude that some IUCN protected area management categories will be easier to adapt to active CWR conservation and are compatible with genetic reserve nomination:

- *Category Ia* – Strictly protected reserves (often small) set aside and left untouched to protect particular species under threat.
  - *Category II* – Large ecosystem-scale protected areas maintained to allow CWR to continue to flourish and evolve under natural conditions.
  - *Category IV* – Small reserves managed to maintain particular species; for example, through controlled grazing or cutting to retain important grassland habitat, coppicing to maintain woodland ground flora, or sometimes even intervening to restore habitat of threatened CWR species.
-

Application of genetic reserve conservation in any of the above categories of protected areas would mean CWR taxa would be given priority for active management within the existing management plan for the site.

### 1.7 CWR conservation outside of formal structures

Although there are obvious advantages to focusing *in situ* conservation within existing protected areas, this may not always be possible, either because the existing network of protected areas is insufficiently comprehensive to provide geographic or ecological coverage, or it does not coincide with a target taxon of restricted distribution. Furthermore, as already noted, many CWR are commonly found in disturbed, pre-climax plant communities; therefore, many may be excluded from or marginalized in established protected areas, which more often aim to conserve pristine habitats, ecosystems or landscapes, or animal species that are now restricted to these environments. When designing a national CWR conservation strategy it is therefore necessary for the genetic conservation of CWR outside as well as inside protected areas to be considered. These areas include roadsides, field margins, orchards and even fields managed using traditional agro-silvicultural practices. Such areas often contain large thriving populations of CWR and can act as important corridors for CWR gene flow and dispersal, and as reservoirs to bolster genetic reserve populations.

If such sites are to contribute to sustainable *in situ* conservation there is a need to establish some level of protection and consistency in management. A management agreement must be reached with the site owner and/or manager to ensure that current site management is not changed to the detriment of CWR diversity. Such agreements are now commonplace for rural roadsides in many North American and European countries. A well-documented example of this kind of local management agreement is those used in the establishment of micro-reserves in the Valencia region of Spain (see Laguna, 1999; Serra *et al.*, 2004). However, there are no known agreements yet in place in the centres of CWR diversity where *in situ* conservation is a priority.

Many CWR species are also found growing as weeds in agricultural, horticultural and silvicultural systems. For example, the Dryland Agrobiodiversity Project in West Asia found that many intensively cultivated areas contain significant CWR diversity at their margins in field edges, habitat patches or roadsides (Al-Atawneh *et al.*, 2008). In the base of the Beqaa Valley, Lebanon, which is industrially cultivated, there are globally significant populations of rare CWR found along the roadsides, while in the Hebron area of Palestine and Jabal Al-Druze in Syria, very rare wheat, barley, lentil, pea and bean CWR are common in modern apple orchards.

However, in many areas of the world this group of weedy CWR species is particularly threatened because of the widespread abandonment of these traditional cultivation systems. Several national governments in developed countries are responding by providing incentives or even financial subsidies to maintain these systems (at least partially), to secure continued cultivation and through cultivation to maintain the wild species that thrive in such anthropogenic habitats. Such grants are unlikely to be a practical option in many developing countries, but there is an opportunity for the integration of on-farm landrace conservation with that of CWR diversity in these and other countries.

Conservation of CWR is just as feasible outside of conventional reserves as it is within fully designated genetic reserves. However, there are advantages and disadvantages to this approach. A major advantage of CWR conservation outside protected areas is that the management interventions at the site are likely to be minimal and may simply involve maintaining current regimes, along with an agreement with the site manager not to make management changes without discussion with the overseeing conservation officer. However, as for CWR populations within protected areas, routine monitoring of these sites is necessary to ensure the site management is actually maintaining the target CWR populations. A major disadvantage of CWR conservation outside protected areas is that they are more likely to suffer from changes in land ownership and national or local policy, as compared with formal genetic reserves, which are likely to be more sustainable in the long-term because to abandon them would waste the considerable resources already committed to setting them up. Therefore, special

measures need to be in place to ensure that regular checks are made of unprotected sites supporting populations of CWR (particularly of critical populations) and ideally an early warning system should be put in place to alert authorities of any pending changes in land ownership or management.

### 1.8 Systematic approaches to CWR conservation

There are numerous potential approaches to achieving the systematic conservation of global CWR diversity, but three distinct (though complementary) approaches may be characterized as individual, national and global (Maxted *et al.*, 2007):

- *Individual approach* – The individual approach involves an individual protected area or gene bank manager actively promoting CWR conservation within the protected area or gene bank that they manage. By promoting the presence of the CWR diversity, the manager can add an additional dimension to the public attraction of the reserve, increase its conservation significance, and in times of limiting financial resources for protected area maintenance further underpin the value of the site. The value could be further enhanced by advertising the presence of the CWR diversity to potential user communities (e.g., plant breeders, research institutes, local people), as long as any utilization that ensues does not put the populations at risk of genetic erosion.
- *National approach* – The national approach involves an individual country developing a CWR conservation strategy that results in the systematic representation of the nation's CWR diversity in an *in situ* network of genetic reserves and, as a back-up measure, *ex situ* storage of genetically representative population samples in national gene banks. The objective is to maximize the protection of the nation's CWR diversity and to link the conserved diversity to its actual or potential utilization. The strategy has policy implications for the plant conservation and exploitation agencies that are responsible for its implementation. Critically, as genetic reserves are likely to be established within existing protected areas, national PGRFA and nature conservation communities need to work together to achieve systematic national CWR conservation.
- *Global approach* – The global approach involves a strategy that is independent of national political borders and focuses on worldwide priority crop gene pools. Using this approach, CWR diversity can be conserved systematically via a global network of *in situ* genetic reserves and in back-up *ex situ* collections. The sites selected for inclusion in a global network of *in situ* genetic reserves must initially focus on the crop diversity that is considered to be critical for food security. They are most likely to be associated with the Vavilov 'centres of diversity', rather than spread evenly across the globe.

Each of these three complementary approaches aims to incorporate CWR conservation within existing protected areas and to be truly effective needs to include *ex situ* duplication of the *in situ* conserved diversity. However, the long-term sustainability of both *in situ* and *ex situ* conserved diversity can only really be assured if that diversity is seen to have value; therefore, the use of conserved CWR diversity is an important component of the conservation strategy. Importantly, the individual, national and global approaches outlined above should not be seen as alternative approaches but rather as a holistic matrix needed to conserve overall CWR diversity.

## PART II: NATIONAL CWR CONSERVATION STRATEGIES

There are many potential approaches to systematic CWR conservation. But as every country contains CWR diversity, they are obliged as signatories to the CBD and ITPGRFA, or other policy instruments, to adopt a national approach to systematically conserve this diversity. This section outlines how a national approach to developing a CWR conservation strategy can be implemented, including both complementary *in situ* and *ex situ* measures. For more details of the approach, see Annexe 2 of the full version of the study.

### 2.1 Introduction

The steps involved in developing a national CWR strategy are illustrated in Figure 1. The application of this model is described in Annexe 3 of the full version of this study: Case study: National CWR conservation strategy for the UK, which outlines how the UK National Inventory of CWR was prepared.

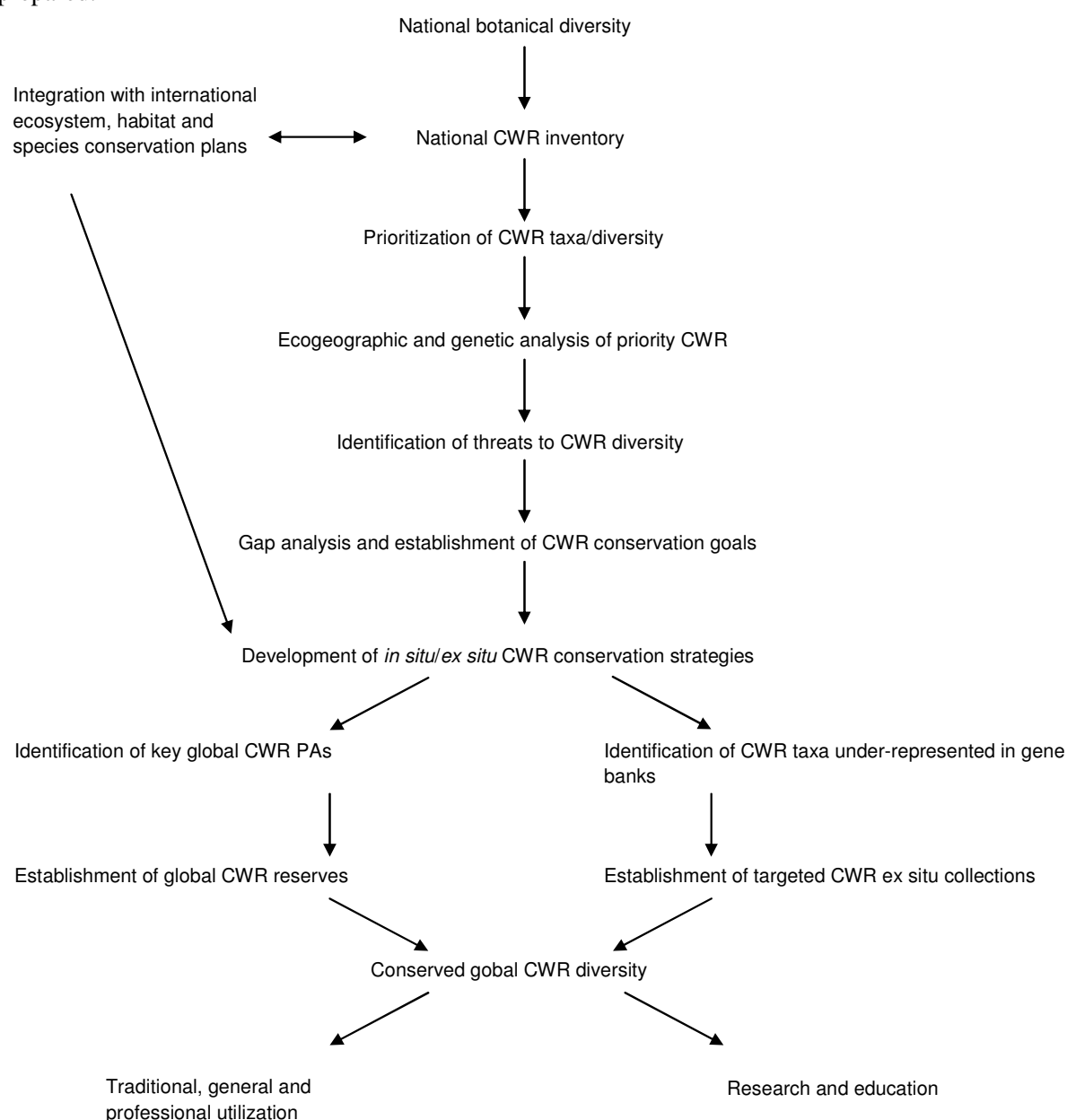


Figure 1. Model for the development of national CWR strategies (Maxted *et al.*, 2007)

The steps shown in the model require input at two organizational levels: the national (conservation or more specifically PGR authority) level for the production of the inventory, establishment of taxon and site priorities and ensuring the conserved diversity is used; and the individual site level (PAs or other sites outside PAs that are rich in CWR diversity, such as agricultural field margins or roadsides).

Although the two levels of responsibility (national and individual) are interconnected, they can also be seen as distinct and with quite separate goals. The national CWR strategy aims to ensure the conservation of the maximum taxonomic and genetic diversity of the country's CWR. It results in the conservation of priority CWR taxa in key protected areas, with back-up in *ex situ* collections. For individual CWR protected area or gene bank managers, the aim is not only to ensure the conservation of the maximum CWR taxonomic and genetic diversity, but also to promote the use of the conserved diversity.

## **2.2 Creating the national CWR inventory**

The starting point for preparing a national CWR conservation strategy is the national CWR inventory, which is likely to be derived from a national botanical checklist. Most countries have some form of floristic checklist, even if it is relatively old and not digitized. For areas where there is no adequate Flora or the Flora is written in an unfamiliar language, it may be possible to make use of the Flora of a neighbouring region. Thus, for example, the Flora of Turkey lists many of the species found in Syria.

Having identified the national botanical checklist, the CWR can be extracted by applying a definition of a CWR to the taxa in the list. Broadly speaking, because the taxa found in the same genus as a crop are by definition in close taxonomic proximity to the crop, they may be regarded as CWR taxa. Using this broad definition, the process of producing a national CWR inventory is one of identifying which genera contain crop taxa and extracting the taxa within those genera from the national botanical checklist.

Having established the national CWR inventory, there are two routes for potential interactions with individual conservationists:

- Sites or taxa of national importance can be identified and appropriate conservation action taken;
- Individual conservationists, whether managing protected areas or collecting accessions for *ex situ* conservation, may consult the national CWR inventory to enact appropriate CWR conservation policies.

## **2.3 Prioritizing CWR taxa/diversity**

A strategy is needed for prioritizing the CWR that require most immediate conservation action. Opinions vary as to how this prioritization should be done. However, there is some consensus for an initial, simple prioritization on the basis of economic value and relative threat alone (Magos Brehm *et al.*, 2007; Barazani *et al.*, 2008; Ford-Lloyd *et al.*, 2008). Some proxy for threat may be necessary if the taxa have not already been assessed using the IUCN Red List criteria (IUCN, 2001). For example, a simple assessment of geographic distribution may be used, with endemic and narrowly distributed taxa being given higher priority than more widely distributed taxa, the assumption being that they are more likely to be threatened. But however prioritization is achieved and whatever criteria are used, the total number of target CWR species must be reduced to a number that can be actively conserved using the available resources.

## **2.4 Ecogeographic and genetic diversity analysis of priority CWR**

Once the priority list of CWR species is identified, there is a need to collate the ecogeographic and genetic diversity information that is available to assist in further formulation of the CWR conservation strategy.



In terms of *in situ* conservation, the culmination of the ecogeographic and genetic diversity analysis should be a set of areas with high concentrations of the priority CWR species.

In terms of *ex situ* conservation, the culmination of the ecogeographic and genetic diversity analysis will be populations of CWR taxa containing or thought to contain unique genetic diversity that is not already conserved *ex situ*, and once identified, this material may be collected and conserved in the appropriate gene banks. It is important to note that while accessions of CWR taxa may be held in *ex situ* collections, this does not mean necessarily that they are genetically representative samples—a single accession in a gene bank does not mean the taxon's genetic diversity is effectively conserved *ex situ*.

## **2.5 Identification of threats to priority CWR taxa and important CWR areas**

As well as assessing threat in relation to individual CWR taxa (in order to assist prioritization for conservation), there is also a need to assess threat in relation to conservation planning (i.e. to identify those important CWR areas most likely to be threatened).

Among the region's or country's Important CWR Areas there is a twofold requirement: first, to focus conservation effort in areas least threatened by such factors as changes in cultivation practices, civil strife, habitat fragmentation, over-exploitation, overgrazing, competition from exotic invasive species, increased urbanization and of course climate change, so that the sites selected maximize long-term sustainability; and second, where there is a real prospect of genetic erosion or extinction of CWR taxa, to eliminate or minimize the threats to CWR taxa and ensure the CWR taxonomic and genetic diversity located in the area is adequately represented in *ex situ* collections.

## **2.6 CWR gap analysis**

The assessment of taxonomic and genetic conservation efficiency effectively involves a comparison of natural *in situ* CWR diversity with the diversity that has been sampled and conserved either *in situ* or *ex situ* (Maxted *et al.*, 2008a).

In the absence of 'real' genetic diversity information it is necessary to employ the proxy of ecogeographic diversity. For example, if a priority CWR species is distributed throughout a country, and unless there is evidence to the contrary, it can be assumed that genetic diversity is partitioned in relation to ecogeographic diversity, and sampling from the maximum diversity of locations will result in the most genetically diverse samples. In this case, disparate ecogeographic locations would be identified for the establishment of genetic reserves or the sampling of populations for *ex situ* conservation.

## **2.7 Development of *in situ/ex situ* CWR conservation strategies**

### **2.7.1 *In situ* CWR conservation**

The result of the ecogeographic and gap analysis is a list of Important CWR Areas known to contain prioritized CWR species. The next step is to identify which combination of these sites contains the optimal or 'best' sample of CWR species in the minimum number of protected areas. The first protected area chosen is likely to be the site that contains the highest concentrations of actual and predicted CWR richness. The second site selected is the one with the highest concentrations of actual and predicted species not present in the first site, and so on (Pressey and Nicholls, 1989; Pressey, *et al.*, 1993; Rebelo, 1994). It is also advisable to select protected areas located in diverse locations—for example, in the extreme north and south of the country, or at sea level and on high land, etc.

Determination of the actual number of specific CWR genetic reserves will ultimately be pragmatic—dictated by the resources available for *in situ* CWR conservation as well as the size of the country and richness of its CWR flora. For example, in UK 17 sites in existing protected areas (nine in Special

Areas for Conservation and eight in Sites of Special Scientific Interest) were nominated to ensure 226 or 67% of CWR taxa were conserved *in situ*. As a result two thirds of the priority CWR taxa were located in the network of UK CWR genetic reserves.

As noted previously, existing protected areas are likely to have been established to conserve habitats or mega-fauna rather than CWR species, so the number of CWR species monitored is unlikely to be large. It is therefore important that if an existing protected area is provided with the designation as part of a 'network of national CWR genetic reserves', the management plan is amended to give priority to active CWR conservation.

Establishing key national CWR protected areas provides an opportunity to monitor and assess short and longer term changes in CWR diversity as a contribution towards the CBD's Biodiversity Target of a significant reduction of the current rate of biodiversity loss at global, regional and national levels by 2010 (CBD, 2002).

### **2.7.2. *Ex situ* CWR conservation**

Establishing *ex situ* CWR conservation priorities involves comparing the CWR taxon's actual distribution to the pattern of distribution based on sampled gene bank holdings for the same taxon. Non-congruence between the two distribution patterns will highlight priority areas for future collection and *ex situ* conservation.

## **2.8 CWR utilization**

The establishment and management of the national CWR reserves is not an end in itself—genetic conservation must facilitate utilization, either now or in the future. Such utilization should be 'sustainable' and 'meet the needs and aspirations of present and future generations' (CBD, 1992).

The general users of protected areas are people at large, and whether local, national or international, their support may be essential for its long-term political and financial viability (in fact, in some countries, the general public ultimately finance the establishment and continuation of protected areas through taxation). Design of protected areas should ideally take into account the needs of visitors by including visitor centres, nature trails, lectures, etc.

The long-term sustainability of protected areas can only be ensured through the use of the diversity in the protected area, as used diversity is more likely to attract longer-term funding for its conservation; therefore, interest among stakeholders in the biodiversity located in the protected area needs to be stimulated.

Professional utilization of CWR species conserved in a protected area is similar to professional utilization of *ex situ* conserved germplasm. Protected area managers should attempt to characterize, evaluate and publicize the germplasm that can be found at the site, possibly in collaboration with those likely to use the material. The onus is on protected area managers, just as it is on gene bank managers, to promote utilization of the material in their care.

## **2.9 Research and education**

There is a real need for a better understanding of species dynamics within protected areas to aid the sustainable management of the specific taxa, but also as a more general experimental tool for ecological and genetic studies of *in situ* conserved species. Research activities based on the material conserved should be encouraged as they provide another use for the material conserved and another justification for maintaining the protected area.

Raising public and professional awareness of the need to conserve CWR can only engender sustainability, both for specific protected areas and conservation actions in general.

## **2.10 Linkage to *ex situ* conservation and duplication**

A safety back-up is needed to ensure the conservation of CWRs conserved *in situ*, and population samples should be collected and deposited in appropriate *ex situ* collections. Although both *ex situ* and *in situ* techniques have their advantages and disadvantages, they should not be seen as alternatives or in opposition to one another—rather, the two strategies are complementary. Similarly, taking national and global strategic approaches to CWR conservation should not be seen as alternatives—they, along with the individual approach, should form a holistic matrix to conserve overall CWR diversity. As well as ensuring the conservation of national CWR diversity, the national network of CWR genetic reserves may also contribute to a global network of CWR genetic reserves if they contain CWR of global importance. Thus, some national CWR genetic reserves, particularly those in Vavilov centres of diversity, may also be designated as CWR genetic reserves of international importance and be part of a global network. Conversely, it is logical that each protected area included in a global network is also nominated as part of a country's national CWR genetic reserve network.

### PART 3: IMPORTANT AREAS AND CONSERVATION GAPS FOR CWR

As outlined in Part 1 of this report, there are two primary strategic approaches to systematic CWR conservation—national and global. Having outlined how a national approach might be taken (Part 2), we now turn to the application of the global approach and the establishment of a global network of CWR genetic reserves.

This section explains the justification for selecting priority crop gene pools, how to prioritize taxa within these gene pools and the application of *in situ* gap analysis to identify priority sites. The intention is to provide preliminary recommendations for the *in situ* conservation of a selection of important food crops, while also providing a platform for further research into these and other important crop groups in the future.

For full details of the approach and the outcomes, see Annexe 4 of the full version of the study.

#### 3.1. Methodology

##### 3.1.1. Selection of priority crop gene pools

The crops included in this background study are primarily those that have been identified as being of major importance for food security in one or more subregion of the world (FAO, 1997) and are listed in Annex I of the ITPGRFA (FAO, 2001). These are: finger millet (*Eleusine coracana*), barley (*Hordeum vulgare*), sweet potato (*Ipomoea batatas*), cassava (*Manihot esculenta*), banana/plantain (*Musa acuminata*), rice (*Oryza sativa*), pearl millet (*Pennisetum glaucum*), potato (*Solanum tuberosum*), sorghum (*Sorghum bicolor*), wheat (*Triticum aestivum*) and maize (*Zea mays*). In addition, we have included three further crops that are listed in Annex I of the ITPGRFA, are regionally important, and for which data are readily available—cowpea (*Vigna unguiculata*), faba bean (*Vicia faba*) and garden pea (*Pisum sativum*).

This does not constitute a definitive list of staple or important food crops. However, it includes examples of different crop groups (cereals, food legumes, roots and tubers), species with different breeding systems (cross-pollinating, self-pollinating, clonally propagated) and crops of temperate and tropical origin (FAO, 1997); thus, lessons learned in the *in situ* conservation of these crop gene pools will be useful for other crop groups.

A further consideration in the selection of crop gene pools has been the inclusion of crop groups that occur within each of the eight Vavilov ‘centres of diversity’:

1. Tropical Centre (South China, India and Southeast Asia)
2. East Asiatic Centre (Central and West China, Korea, Japan and Taiwan)
3. Central Asia and Northwest India (Uzbekistan, Kazakhstan, Kirgizstan and India)
4. South West Asiatic Centre (Turkey, Iran and Afghanistan)
5. Mediterranean Centre (countries bordering the Mediterranean sea)
6. Abyssinian Centre (Ethiopia)
7. Central American Centre (South Mexico and Central America)
8. Andean Centre (Peru, Ecuador, Bolivia and Chile).

Therefore, the crop groups selected present a global representation of crop and CWR diversity.

### 3.1.2. Selection of target species

Within each crop gene pool, the wild relatives that are most closely related to the cultivated taxon are generally given priority over the more distantly related species because these are the taxa that can more easily be used in crop improvement using conventional breeding methods. However, we have also reviewed the literature for information on the known uses or potential uses for crop improvement of all species within the same genus as the crop, and in cases where a more distantly related taxon has been highlighted as a gene donor (or potential gene donor) these are also afforded conservation priority. Of these prioritized taxa, those in most urgent need of conservation action are given precedence (i.e., those with a very limited geographic range—often endemic taxa—and/or known to be under threat).

Other distantly related taxa that have not yet been identified as potential gene donors for crop improvement may be important as gene donors in the future, particularly in the light of climate change; therefore, they should not be ignored in conservation planning for crop gene pools in general and in future expansion of the network of CWR genetic reserves. Widespread and common taxa may also be overlooked, based on the assumption that no active conservation is necessary. However, there is a danger that many of these taxa could become more restricted and threatened in the future. Furthermore, individual populations of these taxa may harbour important genes adapted to particular environmental conditions—genes that may confer important traits to improve crops in the future.

Therefore, while this study primarily targets the rare and threatened taxa that are most closely related to the crop species or that have shown promise in crop improvement programs, the *in situ* network of CWR reserves should in the long term be expanded to ensure that all taxa of potential importance for crop improvement (both closely and more distantly related and both rare and widespread) are actively conserved, both *in situ* and *ex situ*.

In this study, where genetic information is available and taxa have been classified using the Gene Pool concept (Harlan and de Wet, 1971), wild relatives in GP1B and GP2 are generally afforded conservation priority, except for some specific cases where taxa in GP3 have shown promise as gene donors and/or are very rare, highly threatened or have restricted distributions. For those crops where this information is not available, we have applied the Taxon Group concept (Maxted *et al.*, 2006), and where applicable afforded priority to those taxa within TG1b and TG2. For crop genera that have not been subclassified into sections or subgenera, the available information on genetic and/or taxonomic distance has been analysed to make reasoned assumptions about the most closely related taxa.

In order that each crop case study in this report is consistent in the data presented, whichever classification of the degree of relatedness of the wild relatives to the crop has been used, we have presented them as being either primary, secondary or tertiary wild relatives, and in each case, the appropriate reference or explanation for the classification is given. In cases where there are many taxa in the tertiary wild relative group, we have not listed individual taxa but noted the number of taxa and provided a reference for further information. Tertiary wild relatives are also only included to species level.

### 3.1.3. Selection of target sites

The most efficient approach to establishing CWR genetic reserves is to set them up within existing protected areas when possible (Maxted *et al.*, 2008b). Therefore, the most appropriate protected areas (e.g., national parks and heritage sites) in which to locate genetic reserves need to be identified. To achieve this, distribution data have been obtained for the target species identified within each crop gene pool and a GIS programme used to map these data along with protected area data, to ascertain whether populations of the target species are likely to occur within their boundaries. Using this method, we have identified the protected areas that are predicted to contain populations of the target CWR; however, it will be necessary to confirm or ground truth the actual existence of a target taxon population or populations within these sites.

Obviously, not all the target taxa occur within existing protected areas; therefore, we have also identified high priority sites that contain (or are likely to contain) populations of target taxa that are currently not protected.

Target taxon populations that occur within existing protected areas should be prioritized for inclusion in the CWR genetic reserve network on the basis that they have already been afforded some degree of protection, even if only by default. However, active site management and monitoring is needed to conserve the range of genetic diversity inherent in CWR populations.

If no target taxon populations occur within existing protected areas, these populations should also be immediately prioritized for inclusion in the CWR genetic reserve network on the basis that they have not already been afforded any degree of protection. Obviously, in this case, new protected areas will need to be established; which presents a greater challenge.

For some target taxa, it may be necessary to conserve populations both inside and outside existing protected areas, depending on a range of ecogeographic factors. Ideally, detailed ecogeographic surveys should be carried out for each of the target taxa. Furthermore, in the light of climate change, projections should be made when possible to assess the likelihood of the taxon's range changing significantly in the coming decades. When this type of information is available, the possibility of linking protected areas to allow for this migration and to secure suitable habitat for the continued survival of the populations, should be investigated. However, with limited resources and an urgent need to afford some degree of protection to target CWR populations, pragmatic decisions often have to be made, based on the information available to us now.

Nomination of reserves at the target locations may also be hindered by a range of socio-political and economic factors, such as land use conflicts, issues of land ownership, lack of local support, insufficient funding, or lack of infrastructure and capacity for reserve establishment. However, these issues are outside the scope of this background study and will need to be carefully investigated on a site-by-site basis.

A further important consideration is for the establishment of reserves in Vavilov's 'centres of diversity', or 'centres of origin' of crop plants, as outlined above. These are the areas of the world that are recognized as not only being the centres of diversity for crop complexes, but also the centre of domestication too. While the establishment of reserves in the Vavilov centres is desirable, this does not negate the need for genetic reserve establishment for the target taxa outside their centres of origin/diversity—this has to be considered on a case-by-case basis.

#### **3.1.4.      *Data collation and analysis***

Data were collated from a variety of sources; including peer-reviewed literature, books, the internet, databases and personal communications. National and international protected area data were downloaded from the World Database on Protected Areas (<http://www.unepwcmc.org/wdpa/index.htm>). These data are freely available for non-commercial use. Geographic data were analysed in ArcGIS 9.2 and maps produced from the same software.

### **3.2.      Crop case studies**

For each crop included in this study, taxon data sheets have been produced that provide the following information:

- **Crop common name** – primary vernacular name used
- **Crop scientific name** – the crop taxon to which the CWR are related
- **Principle synonym(s)** – commonly used synonyms

- **Global, regional and local importance** – a review of the uses of the crop and its socio-economic importance
- **Taxonomic classification** – the classification used in this study and discussion of taxonomic issues
- **Wild relatives** – a list of CWR classified according to their relative degree of relationship to the crop (primary, secondary and tertiary wild relatives)
- **Distribution and centre of diversity** – discussion of the distribution of the crop and its wild relatives, outlining the centre(s) of diversity
- **Known uses of wild relatives in crop improvement** – a review of crop breeding efforts that have utilized wild relatives
- **Priority taxa** – identification of the highest priority taxa for immediate inclusion in the CWR genetic reserve network, with supporting justification
- **Priority sites** – identification of the highest priority sites for immediate inclusion in the CWR genetic reserve network, with supporting justification
- **Recommendations** – recommended conservation actions and requirements for further research

Examples of two data sheets are presented here in abbreviated form. The full data sheets for all 14 crops are presented in Annexe 4 of the full version of the study.

### 3.2.1. *Rice*

#### Scientific name

*Oryza sativa* L.

#### Principle synonyms

*Padia meyeriana* Zoll. & Moritzi, *Oryza formosana* Masamune & Suzuki

#### Global, regional and local importance

Rice feeds half the world's people—mainly in Asia (Jackson *et al.*, 1997)—and is the crop with the second highest total production (after maize) (634.6 million t in 2006) (FAO, 2008b). It is the most important food energy source in the world—demand for rice is increasing at the rate of about 1.9% annually, the number of rice consumers is likely to increase by 50% and the food requirement by 25% during the next 20 years (Brar, 2005). The cultivated Asian rice (*O. sativa* L.) is spread worldwide and is planted on a much larger scale than African rice, *O. glaberrima* Steud., which is confined almost exclusively to West Africa and is being replaced by Asian rice (Chang, 1995). Rice is produced under a wide variety of climatic conditions, ranging from the wettest areas of the world to the driest. It is cultivated from 53°N to 35°S in latitude around the globe. China and India are the main growers, but the USA and Thailand are the main exporting countries (Chang, 1995). Highest rice yields are achieved in high latitude regions with long day length and where intensive agriculture is the norm, or in low latitude areas where there is very high solar radiation. The six countries with highest rice areas cultivated and production are China (29.4 million ha or 19.0%/184.0 million t or 29.0%), India (43.7 million ha or 28.3%/136.5 million t or 21.5%), Indonesia (11.4 million ha or 7.4%/54.4 million t or 8.6%), Bangladesh (11.2 million ha or 7.3%/43.7 million t or 6.9%), Vietnam (7.3 million ha or 4.7%/35.8 million t or 5.6%) and Thailand (10.1 million ha or 6.5%/29.2 million t or 4.6%) (FAO, 2008b).

#### Taxonomic classification

The genus *Oryza* includes two cultivated species, *O. sativa* and *O. glaberrima*, both of which are diploid and are designated as members of the A genome group (Vaughan, 1994). These two species

show relatively small morphological differences and can be hybridized, though hybrids are highly sterile (Chang, 1995). There are 21 wild species within the genus, possessing one of, or various combinations of, the 9 genomes (Aggarwal *et al.*, 1997; Kurata, 2008). There are both diploid and tetraploid species, some being allopolyploid. There remains some debate over how best to classify the infra-specific diversity of Asian rice (*O. sativa*)—the classifications produced reflect the data sources used in their construction, but the indica, japonica and javanica terminology has been extensively used within *O. sativa* by plant breeders (Chang, 1976). This concept was further developed by Glaszmann (1987), who recognized isozyme groups I to VI to describe the bulk of the primary gene pool of Asian rice, where group I corresponds to the indica rice and group VI encompasses the japonica and javanica (tropical japonica) types.

### Wild relatives

The infra-generic classification of *Oryza* is yet to be agreed and the situation is complicated by the relative success of interspecific crosses, particularly when embryo rescue is employed (Brar and Khush, 1997). This makes the application of the classic Harlan and de Wet (1971) Gene Pool concept difficult to apply (Oka, 1991). Within the primary AA genome wild relatives, Kwon *et al.* (2006) found three groupings based on Rim2/Hipa Cacta transposon display. The first group of Asian species was composed of *O. sativa*, *O. nivara* and *O. rufipogon*, the second group composed of the African species *O. glaberrima*, *O. barthii* and *O. longistaminata*, as well as the American *O. glumaepatula* (a grouping previously identified by Cheng *et al.*, 2002), and the third group contained the Australian species *O. meridionalis* alone. The two cultivated species, *O. sativa* and *O. glaberrima*, are thought to have originated from *O. rufipogon* and *O. barthii*, respectively (Bautista *et al.*, 2001); therefore, these may be regarded as the closest wild relatives. In fact, on the basis of RFLP analysis, Lu *et al.* (2002) have questioned the validity of the specific distinction between *O. sativa*, *O. nivara* and *O. rufipogon*. Overall, however, based on an extensive literature the following may be identified as primary, secondary and tertiary wild relatives:

#### Primary wild relatives

- *Oryza sativa* L. f. *spontanea* Roshev.
- *O. nivara* S.D. Sharma & Shastri
- *O. rufipogon* Griff.
- *O. glaberrima* Steud.
- *O. barthii* A. Chev.
- *O. longistaminata* A. Chev. & Roehrich
- *O. glumaepatula* Steud.
- *O. meridionalis* N.Q. Ng

#### Secondary wild relatives

- *O. officinalis* Wall.
- *O. minuta* J. Presl. & C. Presl.
- *O. rhizomatis* D. A. Vaughan
- *O. eichingeri* Peter
- *O. punctata* Kotschy ex Steud.
- *O. latifolia* Desv.
- *O. alta* Swallen
- *O. grandiglumis* Prodoehl



- *O. australiensis* Domin

### ***Tertiary wild relatives***

Other *Oryza* species and species of *Zizania*, *Porteresia* and *Leersia*.

### **Distribution and centre of diversity**

The two cultivated species, *O. sativa* and *O. glaberrima*, were domesticated independently from *Oryza* species in Asia and Africa (Ogawa, 2003). Although many authors have suggested India as the centre of domestication of Asian rice (*O. sativa*), the earliest archaeological evidence is only from 2500 BC, whereas sites in China show cultivation dated to 8500BP and there is recorded evidence of cultivation to 3000 BC in China and 4000 BC in Thailand (Solheim, 1972). Asian rice was introduced to the Mediterranean region following Alexander the Great's expedition to India between 344 and 324 BC and to the Americas with European settlers (FAO, 1998). The wild species are found almost exclusively within the boundaries of the tropics, while cultivated rice is grown as far as 50° N in China and 40° S in Argentina.

### **Known uses of wild relatives in crop improvement**

Wild species of *Oryza* are important sources of genes for resistance to major biotic and abiotic stresses (Table 2) and have been widely used in rice breeding. Introgression of genes from various wild species, such as *O. nivara*, *O. longistaminata*, *O. officinalis* and *O. rufipogon* (Xiao *et al.*, 1998) has resulted in the transfer of a range of important traits, including resistance to grassy stunt virus, bacterial blight and brown plant-hopper (Brar and Khush, 1997). Direct crosses and embryo rescue techniques have been used to successfully produce hybrids between Asian rice and all other wild species (except *O. schlechteri*). Recently, IRRI researchers have characterized five candidate genes for stress tolerance and nutritional and grain quality in the African species, *O. glaberrima*, and five candidate genes in 152 wild accessions (IRRI, 2007). *O. ridleyi*, a remote tetraploid CWR species has several useful genes for resistance to BB, tungro, yellow stem borer and leaf-folder (IRRI, 2004).

**Table 2. Progress in the transfer of agronomically important genes from wild *Oryza* species into cultivated rice at IRRI (Brar, 2005).**

<b>Trait</b>	<b>Donor species</b>
Grassy stunt resistance	<i>O. nivara</i>
Bacterial blight resistance	<i>O. longistaminata</i> <i>O. officinalis</i> <i>O. minuta</i> <i>O. latifolia</i> <i>O. australiensis</i> <i>O. brachyantha</i>
Blast resistance	<i>O. minuta</i>
Brown plant hopper resistance	<i>O. officinalis</i> <i>O. minuta</i> <i>O. latifolia</i> <i>O. australiensis</i>
White-backed plant hopper resistance	<i>O. officinalis</i>
Cytoplasmic male sterility	<i>O. perennis</i> <i>O. glumaepatula</i>
Tungro resistance	<i>O. rufipogon</i> <i>O. rufipogon</i> <i>O. rufipogon</i>

## Introgression lines under evaluation

Yellow stem borer	<i>O. longistaminata</i> <i>O. rufipogon</i>
Sheath blight resistance	<i>O. minuta</i> <i>O. rufipogon</i>
Increased elongation ability	<i>O. rufipogon</i>
Tolerance of acidity and iron and aluminium toxicity	<i>O. glaberrima</i> <i>O. rufipogon</i> <i>O. rufipogon</i>
Resistance to nematodes	<i>O. glaberrima</i>

**Priority taxa****High priority taxa**

- *O. longiglumis* – distribution: Indonesia (Irian Jaya), Papua New Guinea
- *O. minuta* – distribution: Philippines, Papua New Guinea
- *O. rhizomatis* – distribution: Sri Lanka
- *O. schlechteri* – distribution: Indonesia (Irian Jaya), Papua New Guinea

**Other priority taxa**

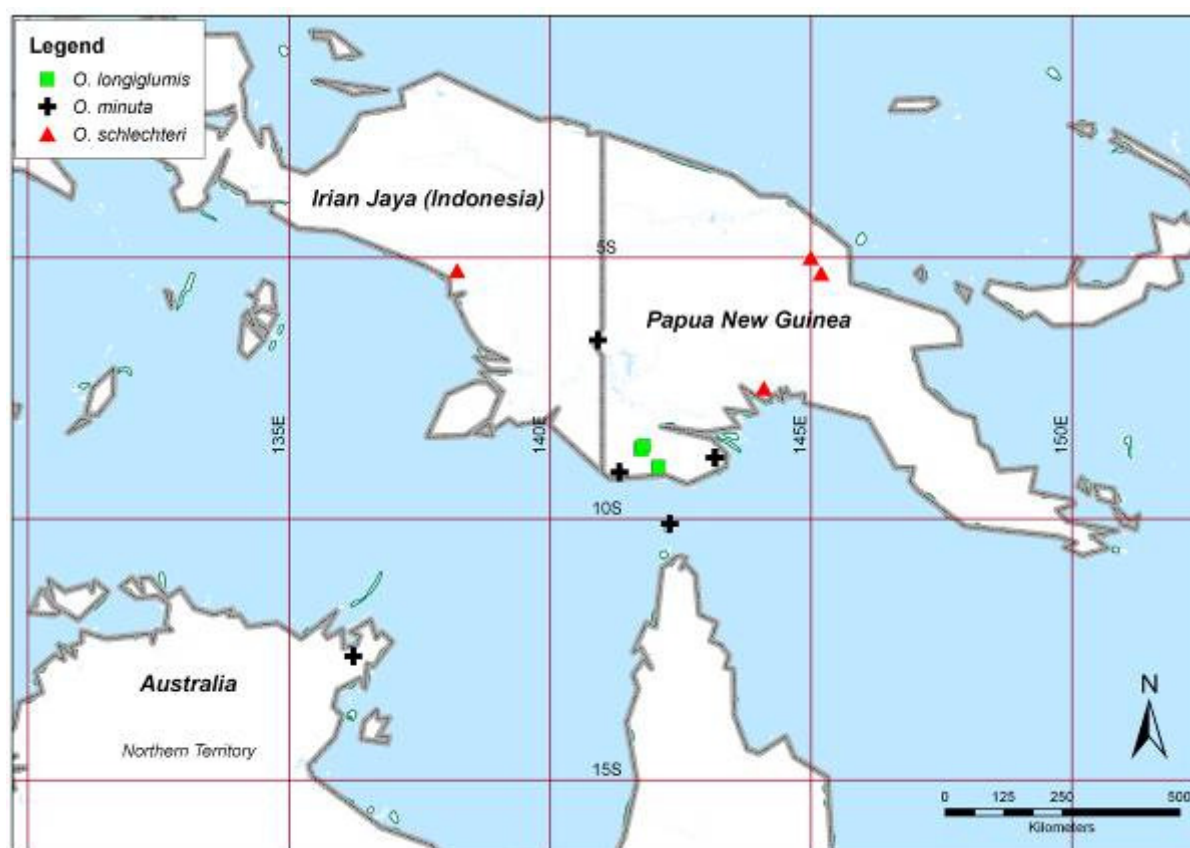
All other species in the genus (*O. alta*, *O. australiensis*, *O. barthii*, *O. brachyantha*, *O. eichingeri*, *O. glaberrima*, *O. grandiglumis*, *O. granulata*, *O. latifolia*, *O. longistaminata*, *O. meridionalis*, *O. meyeriana*, *O. nivara*, *O. officinalis*, *O. punctata*, *O. ridleyi*, *O. rufipogon*, *O. sativa*)

**Priority sites (high priority taxa)**

Based on the analysis presented in Figures 2 and 3, the following locations should be investigated further as potential sites for *in situ* conservation of the highest priority rice wild relatives:

**Papua New Guinea**

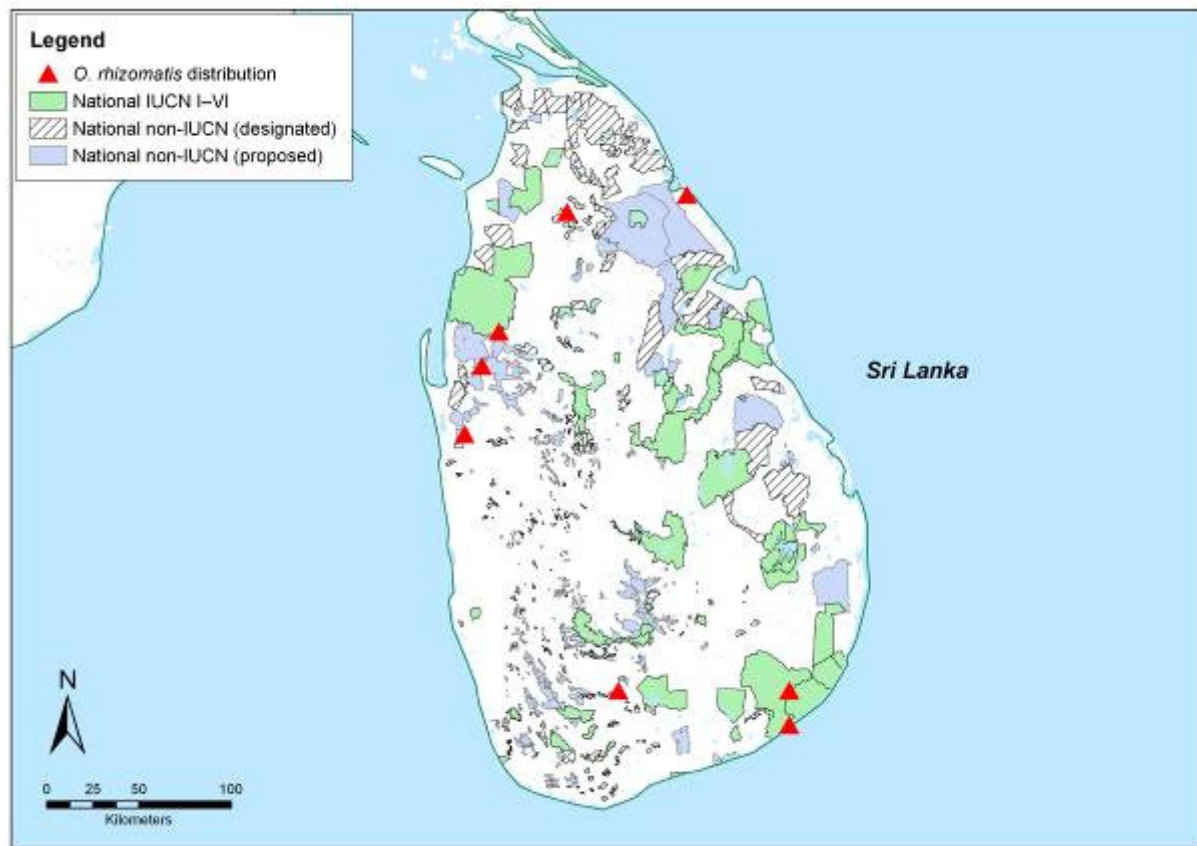
- Tonda Wildlife Management Area (IUCN category VI and Ramsar site). Data analysis indicates that *O. minuta* and *O. longiglumis* are found within the boundaries of this protected area.
- Neiru Wildlife Management Area (IUCN category VI) and Kikori Marine Park/Reserve (proposed IUCN site). *O. schlechteri* has been recorded in the near vicinity (to the west) of this site.
- Bismarck-Ramu National Park (proposed IUCN site). *O. schlechteri* has been recorded in the near vicinity (to the north and southeast) of this site.



**Figure 2.** Distribution of high priority rice wild relatives, *O. longiglumis*, *O. minuta*<sup>4</sup> and *O. schlechteri*.<sup>5</sup>

<sup>4</sup> *O. minuta* is also distributed in the Philippines, but coordinate data were not available for this study.

<sup>5</sup> Data sources – *O. longiglumis* and *O. minuta*: Plants of Papua New Guinea (accessed through GBIF data portal, <http://data.gbif.org/datasets/resource/969> 04/08/2008), Australian National Herbarium (CANB) (<http://data.gbif.org/datasets/resource/47> 04/08/2008), NSW herbarium collection (<http://data.gbif.org/datasets/resource/968> 04/08/2008); *O. schlechteri*: Vaughan (1994) (inferred from map, p. 68).



**Figure 3.** Distribution of the high priority rice wild relative, *O. rhizomatis*. Data source: SINGER (accessed through GBIF data portal, <http://data.gbif.org/datasets/resource/1430> 04/08/2008).

#### *Indonesia (Irian Jaya)*

- Gunung Lorentz National Park (ASEAN Heritage site). Although no occurrences of the high priority taxa are found within the boundaries of this protected area, *O. schlechteri* has been recorded some 30 km outside the southeast boundary.

#### *Sri Lanka*

- Yala Strict Nature Reserve (IUCN category Ia) and Yala (Ruhuna) National Park (IUCN category II). *O. rhizomatis* has been recorded within the boundaries of these two adjacent protected areas<sup>6</sup>.
- Wilpattu National Park (IUCN category II). *O. rhizomatis* has been recorded within the boundaries of this protected area<sup>7</sup>.
- Weerakulicholai-Elavankulam Forest Reserve (proposed IUCN). *O. rhizomatis* has been recorded on the southeastern boundary of this protected area. The location is also close to the neighbouring Wanniyagama Forest Reserve.
- Wilpotha Forest Reserve (proposed IUCN site). *O. rhizomatis* has been recorded close to (just outside) the eastern boundary of this protected area.

<sup>6</sup> *O. eichingeri* has also been recorded within this protected area (coordinates not available) [Data source: Australian National Herbarium (CANB) (accessed through GBIF data portal, <http://data.gbif.org/datasets/resource/47> 05/08/2008)].

<sup>7</sup> *O. eichingeri* has also been recorded within this protected area (coordinates not available) [Data source: Australian National Herbarium (CANB) (accessed through GBIF data portal, <http://data.gbif.org/datasets/resource/47> 05/08/2008)].

- Puwarasankulam Forest Reserve. *O. rhizomatis* has been recorded close to (outside) the north-eastern boundary of this protected area.

### Recommendations

- Despite warnings of the loss of wild rice diversity through habitat destruction and introgression from cultivated populations (e.g., Akimoto *et al.*, 1999; Fan *et al.*, 2000; Gao *et al.*, 2000; Gao, 2003), and the need for systematic *in situ* conservation with the establishment of protected areas (Vaughan and Chang, 1992), there remain no genetic reserves that conserve wild *Oryza* diversity. These threats are having a serious impact on the diversity of the wild rice gene pool; therefore, implementation of a network of wild rice genetic reserves is critical to global food security, particularly in Asia where the human population is dependent on rice as a staple food.
- The high priority taxa identified in this study are those that are of very limited distribution and therefore likely to be in greatest threat of genetic erosion. The locations of these taxa require verification by visiting the identified sites. Detailed ecogeographic surveys should also be carried out to identify further locations by converting existing descriptive locations to geographic coordinates.
- Based on this study, it is possible that three of the high priority taxa may already have been afforded some degree of protection (*O. minuta*, *O. longiglumis* and *O. rhizomatis*), since data analysis indicates that they are likely to be found within the boundaries of existing protected areas. These data require verification and if they are found at these sites steps should be taken to ensure that genetic management is put in place as an adjunct to the existing management plan for the sites.
- *O. schlechteri* only occurs in Irian Jaya and Papua New Guinea and this analysis indicates that none of the known locations are protected. However, some locations are in the vicinity of existing protected areas and it is therefore possible that they may also be found within the identified sites. This requires verification by visiting the sites. If none of the known locations of this taxon are found within the boundaries of existing protected areas, steps should be taken to establish new genetic reserve sites at the most suitable locations.
- In this study, we have focused only on the highest priority taxa (i.e., those with very limited distributions). This does not negate the need for active conservation of the other priority taxa. While these taxa have wider distribution ranges, this does not mean that they are not under threat of genetic erosion. Detailed studies of all the wild *Oryza* species are needed in order to identify priority locations for their conservation throughout their range. For example, in China Gao and his co-authors have been actively promoting the need for genetic reserve conservation of wild rice species, specifically to conserve populations of *O. rufipogon* in Dongxiang and Jiangxi Province (Gao, 2003) and locate additional populations in Yuanjiang, Yunnan Province.
- With such large collections as the IRRI genebank—estimated to be more than 107 000 accessions made up of mostly landrace or breeding materials of *O. sativa*, *O. glaberrima* and wild *Oryza* species, and representative species from eight genera in the tribe *Oryzeae* (IRRI, 2008)—it is not unreasonable to assume that as much diversity as can be efficiently collected is being conserved. However, as Lu *et al.* (2002) noted, geographic isolation played a significant role in the differentiation of the *Oryza* accessions; therefore, a full *ex situ* gap analysis study is needed. However, parallel to this action there is a need to streamline existing collections by identifying and removing duplicates and particularly through development of a core collection (Ford-Lloyd *et al.*, 1997; Jackson *et al.*, 1997).
- Far fewer samples of wild species are conserved *ex situ*. There are 4370 wild species in the IRRI genebank (IRRI, 2008), but several of these, including close wild relatives, are represented by only a handful of accessions. Major collections also exist in China, India, the USA, and Japan and at the Africa Rice Centre (WARDA), but the relative under-representation of wild species is duplicated in most *ex situ* gene banks worldwide. Before further collecting is planned, the priority for these species is to determine what new genetic diversity (additional alleles) might be added to existing collections by carefully planned germplasm acquisitions of different species (Hawkes *et al.*, 2000).

### 3.2.2. Wheat

#### Scientific name

*Triticum aestivum* L.

#### Principle synonyms

*T. hybernum* L., *T. macha* Dekap. & Menab., *T. sativum* Lam., *T. sphaerococcum* Percival, *T. vulgare* Vill.

#### Global, regional and local importance

Wheat is grown in almost all areas that are cropped, except the humid lowland tropics. Rain-fed winter wheat dominates agricultural production in Europe, the USA, Ukraine and southern Russia, while spring sown wheat predominates in semi-arid conditions of Canada, Kazakhstan and Siberia. Bread wheat (*Triticum aestivum* subsp. *aestivum*) forms the most widely cultivated taxon of a group of closely related cultivated wheat species, including: durum or macaroni wheat (*T. turgidum* subsp. *durum*), grown primarily in the drier areas of the Mediterranean Basin, Australia, India, the former USSR, Argentina and the central plains of the USA and Canada; the less widely cultivated emmer (*T. turgidum* subsp. *dicoccon*) which is currently cultivated in Morocco, Spain (Asturias), the Carpathian mountains on the border of the Czech and Slovak republics, Albania, Turkey, Switzerland and Italy; einkorn (*T. monococcum* subsp. *monococcum*) which is primarily cultivated in Ethiopia, but is also grown as a minor crop in India, Italy and the north-eastern parts of the eastern Mediterranean; and *T. timopheevii* which is cultivated in restricted areas of the Transcaucasia (Feldman *et al.*, 1995; Dubin *et al.*, 1997). The largest wheat-producing countries in 2006 were China (104.5 million t), India (69.4 million t), USA (57.3 million t), Russian Federation (45.0 million t), France (35.4 million t) and Canada (27.3 million t) (FAO, 2008b).

#### Taxonomic classification

The tribe Triticeae of the family Poaceae is economically the most important of the grass family, as it contains numerous important crop and forage species (wheats, barleys, ryes and others) (Feldman *et al.*, 1995). The wheat genus, *Triticum* L., comprises a series of diploid, tetraploid and hexaploid forms that have arisen by hybridization and introgression between various closely related *Triticum* and *Aegilops* L. species. For example, bread wheat is thought to have originated as a natural hybrid between the amphidiploid emmer *Triticum turgidum* (AABB genome) with *Aegilops tauschii* (syn. *Ae. squarrosa*) (DD genome) (McFadden and Sears, 1946). Linnaeus (1753) recognized both *Triticum* and *Aegilops*, which comprise the core gene pool of the wheats, as two distinct genera. Subsequent taxonomists have failed to agree on the precise distinction between the two genera, but van Slageren (1994) argued for their retention, with the cultivated taxa and their closest wild relatives in *Triticum* and the wild forms in *Aegilops*. The genus *Triticum* is composed of six species—two diploids, two tetraploids and two hexaploids (van Slageren, 1995), while *Aegilops* comprises 22 species, inclusive of ten diploids, ten tetraploids and two hexaploids (Manners and van Slageren, 1998).

#### Wild relatives

There is some disagreement between taxonomists over the precise delimitation of GP1, GP2 and GP3 in the wheat gene pool. One interpretation is that proposed by van Slageren (1994):

#### Primary wild relatives

- *Triticum aestivum* subsp. *compactum*
  - subsp. *macha*
  - subsp. *spelta*
  - subsp. *sphaerococcum*
- *T. monococcum* subsp. *aegilopoides* (wild einkorn)

- subsp. *monococcum* (cultivated einkorn)
- *T. timopheevii* subsp. *armeniicum*
  - subsp. *durum*
  - subsp. *timopheevii*
- *T. turgidum* subsp. *carthlicum*
  - subsp. *dicoccoides* (wild emmer)
  - subsp. *dicoccon* (cultivated emmer)
  - subsp. *durum*
  - subsp. *paleocolchicum*
  - subsp. *polonicum*
  - subsp. *turanicum*
  - subsp. *turgidum*
- *T. urartu*
- *T. zhukovskyi*

### **Secondary wild relatives**

All *Aegilops* species (particularly *Ae. biuncialis*, *Ae. columnaris*, *Ae. crassa*, *Ae. cylindrica*, *Ae. geniculata*, *Ae. juvenalis*, *Ae. neglecta*, *Ae. speltoides*, *Ae. tauschii*, *Ae. triuncialis*, *Ae. umbellulata*, *Ae. ventricosa*) and *Amblyopyrum muticum*.

### **Tertiary wild relatives**

Several species of *Agropyron* and *Elymus*, and other more remote members of the tribe Triticeae.

### **Distribution and centre of diversity**

The primary centre of natural distribution of *Triticum* and *Aegilops* is Transcaucasia, the Fertile Crescent and the eastern Mediterranean regions. The cultivated wheats spread from this region in Neolithic times (Zeven, 1979) and established secondary centres of variation in the Hindu Kush, China and Japan, and probably the African Sahara. The distribution of the cultivated *Triticum* species is heavily influenced by humans—the hexaploid species are found worldwide in drier and cooler regions, the tetraploid species are found throughout the Mediterranean Basin, Transcaucasia and Ethiopia, and the diploid species are more restricted to the north-eastern Mediterranean (Kimber and Feldman, 1987). *Aegilops* species have a much wider distribution, extending circum-Mediterranean and into Central Asia, as well as Transcaucasia and the Fertile Crescent (van Slageren, 1994).

Climatically, *Triticum* and *Aegilops* species are limited to areas with hot, dry summers and winter rainfall, while away from the sea they can also be found in dry continental areas with colder winters. The entire altitudinal range of the taxa is from -400 (near the Dead Sea) to 2700 m, but most species are much more specific and are most commonly found from 500–1200 m (van Slageren, 1994).

### **Known uses of wild relatives in crop improvement**

The history and extent of the use of CWR for wheat improvement is unrivalled (Hodgkin and Hajjar, 2008). McFadden (1930) was the first to transfer desirable traits via inter-specific hybridization to wheat when he introduced disease resistance from emmer wheat. Examples of beneficial traits introduced to wheat from related wild species include yellow rust resistance (McIntosh *et al.*, 1966; Peng *et al.*, 1999; Millet *et al.*, 2008), leaf rust resistance (Kerber and Dyck, 1969; Gill *et al.*, 1988; McIntosh *et al.*, 2003; Marias *et al.*, 2008), *Septoria*, stem rust, powdery mildew, eyespot and other disease resistances (Jahier *et al.*, 1979; Miller *et al.*, 1987; Lagudah and Appels, 1993; Mujeeb-Kazi and Hettel, 1995; Mujeeb Kazi *et al.*, 2001), hessian fly-resistance (Cox and Hatchett, 1994), greenbug resistance (Wells *et al.*, 1982), cyst nematode resistance (Delibes *et al.*, 1993), root knot nematode resistance (Raupp *et al.*, 1993), grain protein content (Avivi, 1978; Hoisington *et al.*, 1999), water-

logging tolerance (Villareal *et al.*, 2001), sprouting suppression (Xiu-Jin *et al.*, 1997) and quality-desirable glutenins improvement (William *et al.*, 1993; Peña *et al.*, 1995).

Wheat wild relatives still hold additional potentially useful traits for resistance to biotic and abiotic stress (the latter particularly important in times of climate change), and for technological and nutritional quality (Millet *et al.*, 2008). Many useful traits have been transferred from *Aegilops* species to wheat; however, there remains much that can be utilized, particularly in *Aegilops* species not previously evaluated and with the aid of advanced molecular characterization (Schneider *et al.*, 2008).

## Priority taxa

### High priority taxa

- *T. monococcum* subsp. *aegilopoides*
- *T. timopheevii* subsp. *armeniicum*
- *T. turgidum* subsp. *paleocolchicum*
  - subsp. *dicoccoides*
  - subsp. *polonicum*
  - subsp. *turanicum*
- *T. urartu*
- *T. zhukovskyi*

### Other priority taxa (Maxted *et al.*, 2008c)

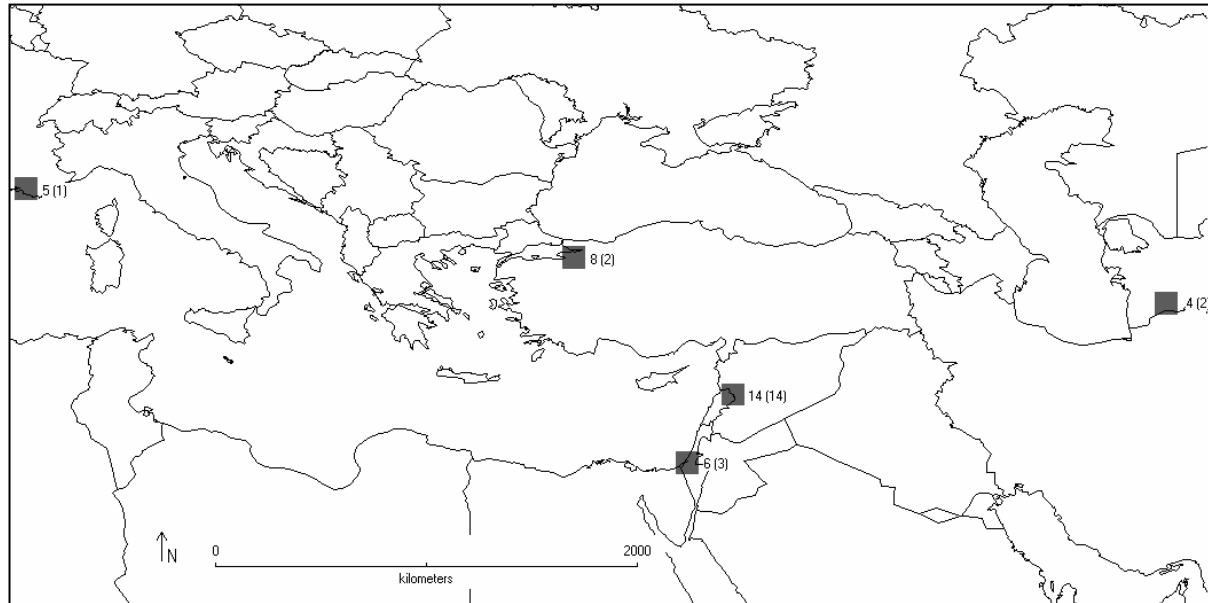
- *Ae. bicornis*
- *Ae. comosa*
- *Ae. juvenialis*
- *Ae. kotschyi*
- *Ae. peregrine*
- *Ae. sharonensis*
- *Ae. speltoides*
- *Ae. uniaristata*
- *Ae. vavilovii*

## Priority sites

A recent study of *Aegilops* taxa diversity (Maxted *et al.*, 2008c) identified two particular hotspots containing between 12 and 14 *Aegilops* species—the first in western Syria (covering Damascus, Homs, Hama, Idlib and Halab provinces) and Northeast Lebanon (North, Central and East Bekaa Valley), and the second in northern Iraq (Ninawa and Arbil provinces). The same study undertook complementarity analysis on an *Aegilops* dataset of 9866 records and identified the five 100 × 100 km grid cells required to capture all 22 species in the *Aegilops* genus (Figure 4), giving the most suitable sites to implement complementary genetic reserve conservation for the *Aegilops* gene pool.

In the current study, distribution data for high priority *Triticum* species obtained from NPGS and GBIF were plotted (see Figure 5), showing Turkey as the main centre of diversity of the taxa, with Iraq, Iran, Georgia, Azerbaijan, Syria, Lebanon, Israel and Palestine also containing populations of high priority taxa. A more complete data set obtained through a detailed ecogeographic survey would most likely reveal further locations of high priority taxa; for example, Armenia and central Israel are known centres of wild wheat diversity, but this is not reflected in these data sets.





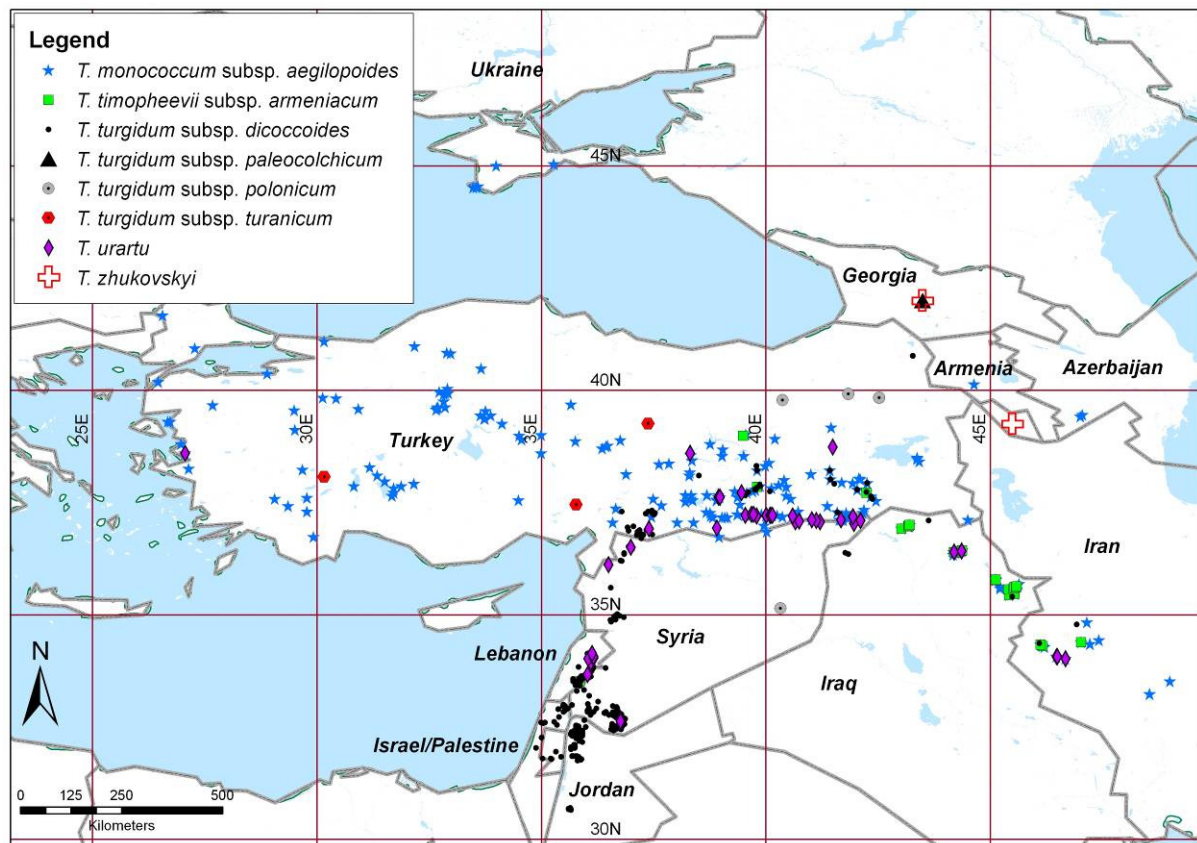
**Figure 4.** Location of five complementary *Aegilops* species diversity hotspots (Maxted *et al.*, 2008c). Total numbers of *Aegilops* species present in each shown, as well as additional *Aegilops* species not found at other sites in brackets.

Based on the data presented in Figures 4 and 5, the following sites/locations are important for the *in situ* conservation of wheat wild relatives (see Figure 6):

- Qal'at Al Hasn, Homs province, Syria. Maxted *et al.* (2008c) identified this location as the best option for a single reserve for *Aegilops* as it has the highest concentration of taxa (14). However, there are currently no protected areas in the vicinity and a recent study (Keisa *et al.*, 2008) found that this area is being developed for tourism very rapidly and is highly threatened. Designation and site protection is a priority.
- Ham, Baalbek-Hermel province, Lebanon. The site was established as a genetic reserve under the recent Global Environment Facility funded regional project on: 'Conservation and Sustainable Use of Dryland Agrobiodiversity in West Asia' (<http://www.icarda.cgiar.org/gef.html>) though the current level of active conservation is unknown.
- Central Israel, possibly within Eshqol (Habsor) National Park (IUCN category V), Ha Besor Nature Reserve, Karmiyya Nature Reserve, Kurkar Gervar'am Nature Reserve, Lahav Darom Nature Reserve, Lahav Zafon Nature Reserve or Tel Qeriyot Nature Reserve (all IUCN category IV). Although these sites have fewer total *Aegilops* species, they do contain additional endemic species.
- Uludag National Park, Bursa province. There are 8 *Aegilops* species present and two additional species to those found in West Asia.
- Erebuni State Reserve, Yerevan, Armenia. The 89 ha reserve was established in 1981 near Yerevan in the foothills of the Ararat concavity and the south-western slope of Voghjaberd upland, specifically to protect wild cereals (Avagyan, 2008). The site was also included as a genetic reserve within the recent Global Environment Facility funded regional project on: 'In Situ Conservation of Crop Wild Relatives Through Enhanced Information Management and Field Application' (<http://www.cwr.am>) though the current level of active conservation is unknown.
- Khashuri near Tbilisi, Georgia. Data analysis indicates that *T. turgidum* subsp. *paleocolchicum* and *T. zhukovskyi* both occur at this location. This is the only location of *T. zhukovskyi* showing in this analysis and one of two locations of wild *T. turgidum* subsp. *paleocolchicum* (the other location is in Azerbaijan). The location does not appear to be protected, though it could fall within the

unknown boundaries of Nezdi Nature Sanctuary (IUCN category IV) and the Borjomi Nature Reserve (IUCN category Ia) is also close by to the southwest.

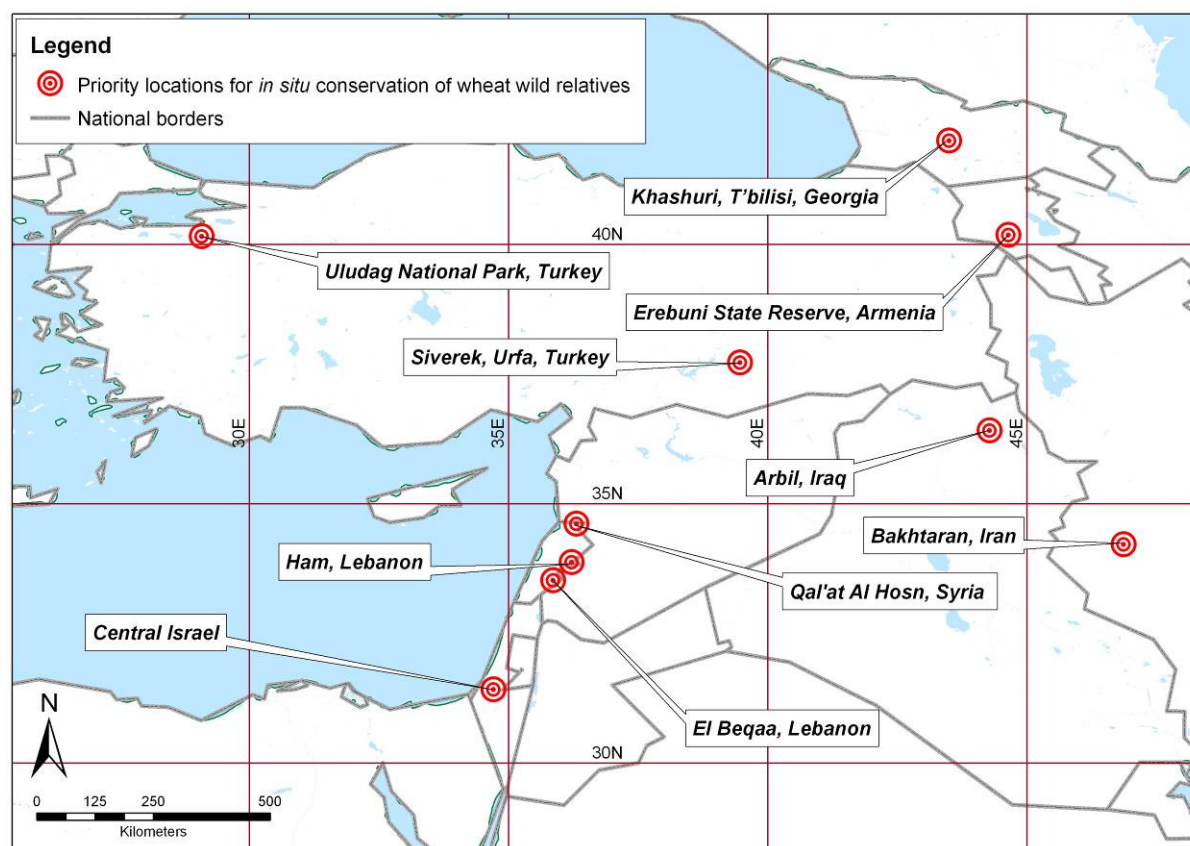
- Urfa, Turkey, 16–18 km east of Siverek. Data analysis shows this location to contain populations of *T. monococcum* subsp. *aegilopoides*, *T. turgidum* subsp. *dicoccoides* and *T. urartu*. This area is not currently protected but the relatively geographically close Ceylanpinar State Farm on the Syrian border was designated as a genetic reserve by the Global Environment Facility funded Turkish *In situ* Conservation of Genetic Diversity Project, which following a detailed survey was found to contain *T. monococcum*, *T. dicoccoides*, *Ae. speltoides* var. *speltoides*, *Ae. speltoides* var. *ligustica*, *Ae. tauschii*, *Ae. crassa*, *Ae. juvenalis*, *Ae. vavilovii*, *Ae. triuncialis*, *Ae. biuncialis*, *Ae. triaristata*, *Ae. caudata*, *Ae. columnaris*, *Ae. umhellulata*, *Ae. ovata*, *Ae. cylindrica*, along with *Hordeum spontaneum*, *H. bulbosum*, other *Hordeum* spp. and *Avena* spp. (Karagöz, 1998). The current level of active conservation within the site is unknown.
- Arbil, Iraq, 1 km northeast of Salahadin and 4 km northeast of Shaqlawa. *T. monococcum* subsp. *aegilopoides*, *T. timopheevii* subsp. *armeniicum* and *T. urartu* have been recorded at these locations, which are currently not protected.
- Bakhtaran province, Iran. Populations of *T. timopheevii* subsp. *armeniicum*, *T. urartu*, *T. monococcum* subsp. *aegilopoides* and *T. turgidum* subsp. *dicoccoides* have been recorded in this province. Data analysis indicates that none of these taxa are currently protected *in situ*, except perhaps for *T. monococcum* subsp. *aegilopoides*, which is on the edge of Bisotun Protected Area (IUCN category V and World Heritage Convention). This site and the neighbouring Bisotun (Varmangeh) Wildlife Refuge could however contain populations of all these taxa. Searches are required. To the southwest, searches in Ghalajeh Protected Area (IUCN category V) should also be carried out. Critically, populations of *T. timopheevii* subsp. *armeniicum* and *T. urartu* appear not to be protected in this vicinity.
- El Beqaa, Lebanon, between Kfarkouk and Aiha. *T. monococcum* subsp. *aegilopoides*, *T. timopheevii* subsp. *armeniicum* and *T. turgidum* subsp. *dicoccoides* have been recorded at this site, which is currently not protected.



**Figure 5.** Distribution of high priority wheat wild relatives (*Triticum* spp.). Data sources: *T. monococcum* subsp. *aegilopoides*, *T. timopheevii* subsp. *armeniacum*, *T. turgidum* subsp. *dicoccoides*, subsp. *paleocolchicum*, *T. urartu* and *T. zhukovskyi* – USDA, ARS, National Genetic Resources Program. pcGRIN. National Germplasm Resources Laboratory, Beltsville, Maryland; *T. turgidum* subsp. *dicoccoides*, subsp. *polonicum*, subsp. *turanicum* – SINGER (accessed through GBIF data portal, <http://data.gbif.org/datasets/resource/143029/07/2008>).

## Recommendations

- Three reserves have been established in the centre of diversity specifically to conserve wild wheats—Amiad in Israel (Anikster *et al.*, 1997), Ceylanpinar in Turkey (Ertug Firat and Tan, 1997) and Erebuni in Armenia (Avagyan, 2008). There is a need to complement these existing reserves by establishing additional genetic reserves in the sites with the highest *Triticum* and *Aegilops* taxon richness. Iran has significant unique *Triticum* and *Aegilops* taxa and as it is at the eastern extreme of the centre of diversity, further study should be devoted to establishing an appropriate site to conserve this diversity *in situ*. The results presented in this study should be backed up with further detailed ecogeographic surveys of the priority taxa. It is not clear from this analysis whether records of *T. turgidum* subsp. *polonicum* and subsp. *turanicum* are cultivated or wild. Further research is needed to ascertain locations of wild populations of these taxa.
- Wheat species have been relatively comprehensively surveyed and collected for *ex situ* conservation by the CGIAR centres, which have ensured that the cultivated wheats are systematically conserved *ex situ* with approximately 850 000 accessions stored, mainly of *Triticum* species (FAO, 1998). However, van Slageren (1994) comments that there is a conspicuous absence of collections from central and eastern Iran and western Afghanistan, and that it seems likely that the areas to the north of this area (Turkmenistan and Uzbekistan) are also under-collected.



**Figure 6.** Priority locations for wheat wild relative genetic reserve conservation.

### 3.3. Important areas and conservation gaps: synthesis

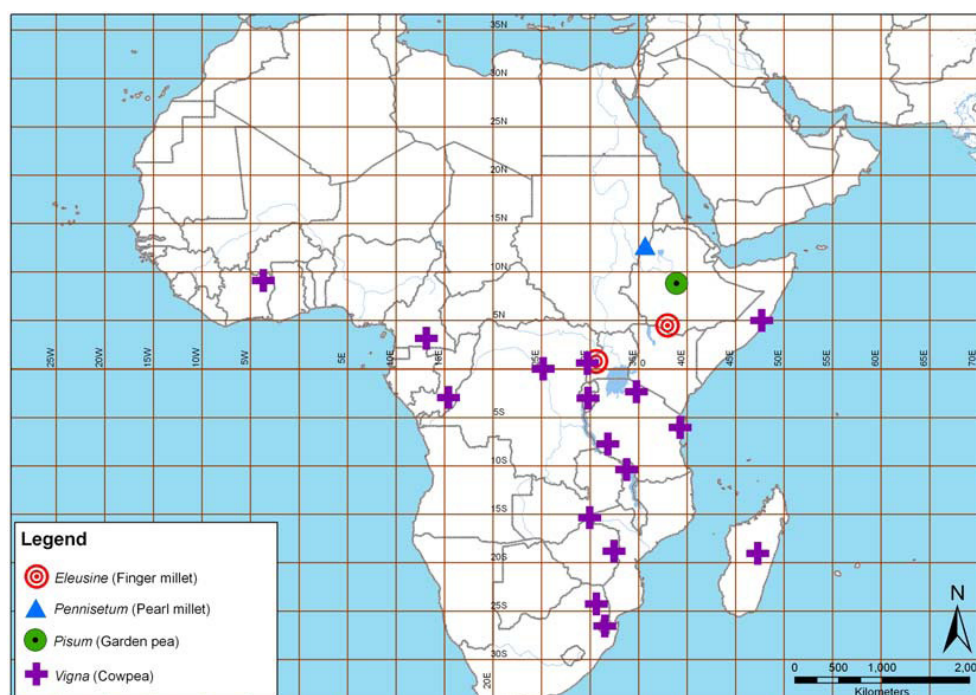
#### 3.3.1. Overview of selected crop gene pools by region

Figures 7–10 show the priority locations for CWR genetic reserve establishment identified in this study in each of four regions: Africa, the Americas, the Middle East, and Asia and the Far East. The symbols shown on the maps indicate the highest priority locations for *in situ* conservation of the wild relatives within each of the 14 crop case studies.

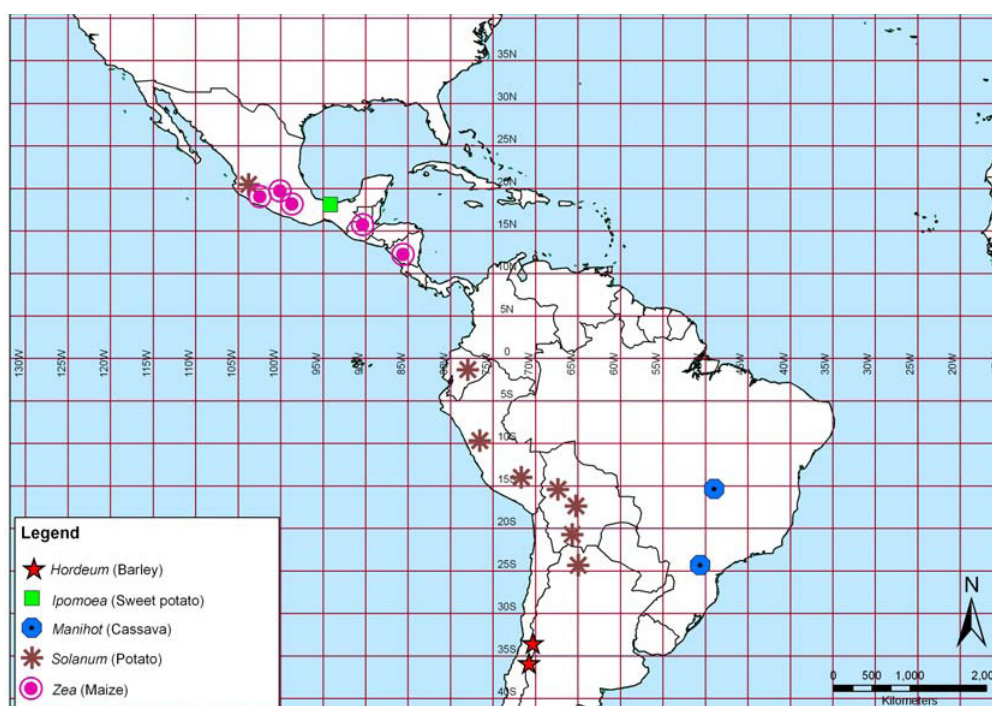
It is important to stress that the potential genetic reserve locations shown in Figures 7–10 are for a limited number of crop complexes and within these, for the highest priority CWR taxa only. Therefore, the results of this analysis should be considered as a first step in the process of establishing a global network with a view to carrying out further research in the future.

Because of the limited number of crop gene pools included and the fact that only the highest priority taxa have been taken into consideration, the recommended sites are not evenly spread throughout the regions and many countries are shown as not containing high priority CWR genetic reserve locations. However, this does not mean that there are not high priority CWR genetic reserve locations within these countries. On the contrary, as stated in Part 1 of this report, a holistic approach to the *in situ* conservation of CWR is needed that involves a three-pronged geographical approach: local (individual protected area managers actively conserving CWR within existing sites), national (each country implementing a national CWR conservation strategy) and global (establishment of global CWR conservation priorities). Therefore, it is vital that individual countries take steps to initiate national CWR conservation strategies (see Annexe 2 of the full version of the study for details), to ensure that the widest range of CWR taxa are actively conserved as quickly as possible. In particular, they should

take into account species-rich areas and the establishment of multi-taxon genetic reserves where possible.

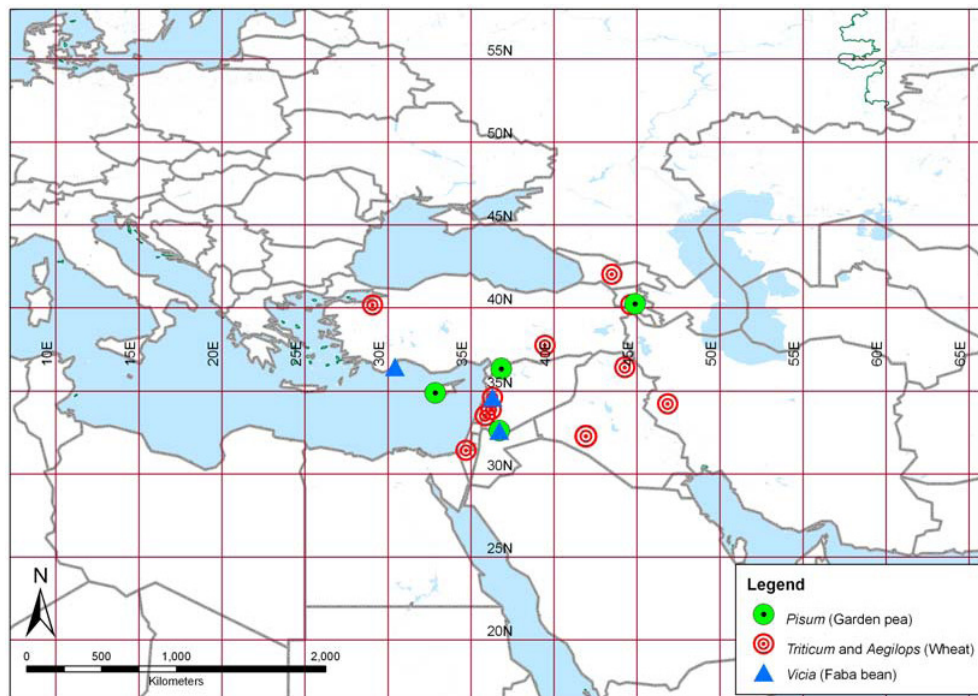


**Figure 7.** Priority CWR genetic reserve network locations in Africa. For a detailed list of taxa and sites, refer to the crop case studies in Annexe 4 of the full version of the study.

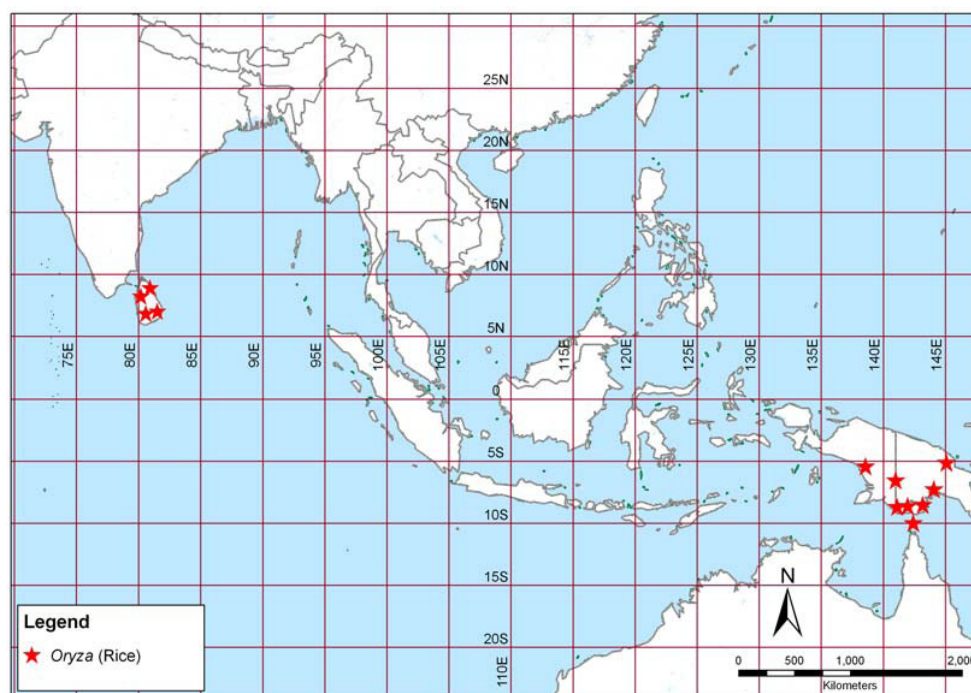


**Figure 8.** Priority CWR genetic reserve network locations in the Americas. For a detailed list of taxa and sites, refer to the crop case studies in Annexe 4 of the full version of the study.





**Figure 9.** Priority CWR genetic reserve network locations in the Middle East. For a detailed list of taxa and sites, refer to the crop case studies in Annexe 4 of the full version of the study.



**Figure 10.** Priority CWR genetic reserve network locations in Asia and the Far East. For a detailed list of taxa and sites, refer to the taxon data sheets in Annexe 4 of the full version of the study.

The sites identified are almost exclusively located in developing countries, many of which may have limited technical and financial resources to take responsibility for maintaining a global network of CWR genetic reserves. As acknowledged in the ITPGRFA (FAO, 2001), the capacity of developing countries to effectively implement their commitments on *in situ* CWR conservation will depend on the effective allocation, particularly by developed countries, of the financial resources needed.

There are relatively few options for the establishment of multi-crop-complex genetic reserves for the highest priority taxa treated in this study, probably because these taxa are of restricted distribution range and adapted to specific ecological conditions and therefore less likely to overlap. However, multi-taxon sites within crop gene pools have been identified where possible (for details, refer to the taxon data sheets in Annexe 4 of the full version of the study). To maximize the efficiency of the global *in situ* network, the establishment of genetic reserves for the high priority taxa treated in this study should also be supported with further research to investigate whether other CWR occur at the same locations, which would give greater weight to justification for reserve establishment. These additional CWR taxa may be more common and widespread but their conservation *in situ* is also necessary to ensure that the widest pool of genetic diversity of CWR is protected and as a buffer for the impact of climate change. Here, we briefly summarize the genetic reserve locations for high priority CWR taxa for the 14 crop gene pools treated in this study, on a regional basis.

## Africa

Figure 7 shows priority genetic reserve locations for finger millet (*Eleusine* spp.), pearl millet (*Pennisetum* spp.), garden pea (*Pisum* spp.) and cowpea (*Vigna* spp.) wild relatives in Africa.

High priority locations for *in situ* conservation of the wild relatives of both finger millet and pearl millet are found in East Africa—the mountainous border area between Kivu Province in the Democratic Republic of Congo, Rwanda and Burundi for finger millet and southern Ethiopia and the Sudan–Ethiopia border for pearl millet.

The high priority garden pea wild relative, *Pisum abyssinicum* has been recorded in Ethiopia and Yemen, but we only found occurrence records for Ethiopia.

There are several high priority CWR taxa in the *Vigna* gene pool and they are widespread throughout sub-Saharan Africa. The taxa have restricted distributions and there is little overlap between them; therefore, opportunities for multi-taxon reserves for high priority *Vigna* wild relatives are limited. However, lower priority *Vigna* CWR may be present at the same sites, as well as CWR of other crops not included in this study; therefore, opportunities for the establishment of multi-species reserves may arise upon further investigation.

## The Americas

Figure 8 shows priority genetic reserve locations for barley (*Hordeum* spp.), sweet potato (*Ipomoea* spp.), cassava (*Manihot* spp.), potato (*Solanum* spp.) and maize (*Zea* spp.) wild relatives in the Americas.

The highest priority barley wild relative, *Hordeum chilense* occurs in central–south-west Chile and western Argentina. The close sweet potato wild relatives, *Ipomoea batatas* var. *apiculata* and *I. tabascanana* are both of very restricted distribution and endemic to the coast of Veracruz and neighbouring Tabasco (Mexico), respectively. Several cassava wild relatives warrant conservation action, but the highest priority taxa occur only in the states of Goiás and Paraná, Brazil. Four high priority wild relatives of maize are concentrated mainly in south–central Mexico. All of the highest priority CWR taxa found in the Americas in these four crop gene pools have very restricted distributions and warrant urgent conservation action, both *in situ* and *ex situ*.

Identification of specific sites for the conservation of potato wild relatives will involve further research. Several species-rich areas have been identified in Mexico, Ecuador, Peru, Bolivia and Argentina, and the identification of suitable genetic reserve sites in these areas is recommended. However, the majority of potato wild relatives have very restricted distributions, many of which do not overlap, and this presents a major challenge in terms of *in situ* conservation. However, it is possible that many of these species have already been afforded some degree of protection if they are within the boundaries of existing protected areas. A detailed comparison of distribution data with current

protected areas is needed to begin to formulate an appropriate *in situ* conservation strategy for this group.

### The Middle East

Figure 9 shows priority genetic reserve locations for garden pea (*Pisum* spp.), wheat (*Triticum* spp. and *Aegilops* spp.) and faba bean (*Vicia* spp.) wild relatives in the Middle East.

Four priority wild relatives of garden pea are distributed in Turkey, Cyprus, Syria, Lebanon, Israel, Palestine, Jordan, Iraq, Iran, Armenia, Azerbaijan and Georgia. Four priority genetic reserve sites have been identified in this study, in Armenia, Syria and Cyprus. However, other wild *Pisum* populations, of both higher and lower priority taxa, should be included in national CWR genetic reserve networks as part of national CWR strategies for individual countries.

Eight high priority wheat wild relatives (*Triticum* spp.) are distributed in Turkey, Syria, Lebanon, Israel, Palestine, Jordan, Iraq, Iran, Armenia, Azerbaijan and Georgia, with some additional populations of the more widespread taxon, *T. monococcum* subsp. *aegilopoides* found in Ukraine and Serbia and Montenegro. Ten priority genetic reserve sites are recommended for immediate establishment for the conservation of wheat wild relatives (*Triticum* spp. and *Aegilops* spp.). Most of the selected sites contain multiple species—some have already been afforded some degree of protection as they fall within the boundaries of existing protected areas, but many currently have no known level of protection.

The high priority wild relatives of faba bean have a wider overall distribution, extending west into continental Europe and the UK. However, the main centre of diversity is concentrated in Turkey, Cyprus, Syria, Lebanon, Israel and Palestine. Two high priority genetic reserve sites have been recommended for immediate establishment in southern Syria and eastern Syria, close to the Lebanese border.

### Asia and the Far East

Figure 10 shows high priority genetic reserve locations for rice (*Oryza* spp.). The four highest priority taxa, which are of extremely restricted distributions, are found in Sri Lanka, Indonesia (Irian Jaya) and Papua New Guinea and all require urgent conservation attention.

In this study, we have focussed only on the highest priority rice wild relatives (i.e., those with very limited distributions). Further research is needed to look in detail at the distributions of other priority taxa in the genus. While these other taxa have wider distribution ranges, this does not mean that they are not under threat of genetic erosion. On the contrary, it is widely accepted that wild rice genetic diversity is being lost through habitat destruction and introgression from cultivated populations. Therefore, detailed studies of all the wild *Oryza* species are needed in order to identify priority locations for their conservation throughout their range.

Asia and the Far East is also the centre of distribution of banana/plantain wild relatives in the genus *Musa*. Priority locations for *in situ* conservation of this genus are not shown in Figure 10 because distribution data were not readily available for analysis. However, ten priority banana/plantain wild relatives have been identified in this study. They occur in India, Bhutan, China, Myanmar, Thailand, Vietnam, Sumatra, Papua New Guinea and the Philippines. The highest priority areas for *in situ* conservation based on the known distribution ranges of the priority species are Assam (India), Bhutan, Papua New Guinea, Sumatra and the Philippines. Further research is needed on the priority taxa to order to ascertain their *in situ* conservation status and identify genetic reserve sites for inclusion in the network.



### 3.3.2. *Strengthening cooperation for the in situ conservation of CWR*

The systematic establishment of networks of CWR genetic reserves will require the strengthening of international cooperation in order to be effective and efficient. There are a few generic recommendations that need to be considered in this regard:

- *Consultation with crop-based experts* – It would be wise to engage in a dialogue with crop-based specialists for each of the 14 crop case studies prepared to confirm that they support the sites/areas recommended for the establishment of CWR genetic reserves. This is necessary because of the variability in the quantity and quality of information available when preparing the case studies. For some case studies, such as finger millet (*Eleusine* spp.), cassava (*Manihot* spp.) and pearl millet (*Pennisetum* spp.), limited data were available, while for others, such as wheat (*Triticum* and *Aegilops* spp.), faba bean (*Vicia* spp.), cowpea (*Vigna* spp.) and maize (*Zea* spp.), significant data sets were available.
- *Crop case study extension* – The crop case studies provided in this study could be used as a template for other crops, including each of the ITPGRFA Annex I list of Crops Covered Under the Multilateral System, so that over time a global network could be extended from those sites identified in this study to provide a comprehensive network of *in situ* genetic reserves that conserve the world's CWR diversity.
- *Financing genetic reserve location and implementation* – As already noted, global network sites are almost exclusively likely to be located in developing countries, many of which may have limited technical and financial resources to take responsibility for maintaining the genetic reserves. As acknowledged in the ITPGRFA (FAO, 2001), the onus is on developed countries to work with developing countries to help conserve CWR diversity. Therefore, a funding mechanism should be put in place to help meet the cost of genetic reserve location and implementation, so that the additional cost does not fall solely on developing country economies.
- *Harmonization of crop case studies with national CWR conservation strategies* – As already stressed in this study, the effective global complementary conservation of CWR diversity must involve efforts at national level, both to effect the conservation of the priority CWR taxa identified in the global crop case studies but also to implement national CWR strategies, which will take a floristic approach and consider national priorities. The publication of the current study and subsequent inclusion of *in situ* conservation of CWR in the *Second Report on the State of the World's PGRFA* and *Global Plan of Action* should go a long way towards meeting this need; however, there is a need to plan ahead for the provision of arenas for specific dialogue between those involved in the establishment and management of networks, both through face to face communication at meetings and via electronic means. Web tools dedicated to providing such an arena, as well as access to guidance documents and contacts could be made available.
- *Protected area manager dialogue* – To avoid the substantial costs of purchasing new sites, genetic reserves should be established within the boundaries of existing protected areas where possible. However, existing protected area management plans will need to be amended to permit the *in situ* genetic conservation of CWR diversity; therefore, there will be a need for a dialogue between those with overall responsibility for managing a global network of CWR genetic reserves and individual protected area managers. It is likely that this dialogue will need to involve or be mediated by the National PGRFA Coordinators.
- *Guidelines for in situ genetic conservation of CWR diversity* – To ensure the efficient and effective *in situ* genetic conservation of CWR diversity, genetic reserve managers will need to be supplied with guidelines on how to adapt current management plans to allow for genetic conservation of CWR. Iriondo *et al.* (2008a) already offers such generic guidance but it may be thought appropriate to supply more specific guidelines to meet the specific needs of CWR genetic reserve managers. A practical manual providing the minimum guidance needed would be beneficial.
- *Training for CWR genetic reserve managers* – Whether the reserves are established within or outside of existing protected areas, training of reserve managers and staff will be beneficial, in

addition to the provision of the guidelines suggested above. Genetic reserve management training will be a particular requirement in developing countries where the bulk of a global network is likely to be located.

## PART 4: CONCLUSIONS AND RECOMMENDATIONS

CWR genetic diversity is currently far from secure. If this critically important group of plants is to provide the basis for future exploitation, the immediate issue that must be addressed is the development of a systematic CWR conservation strategy. This strategy needs to encompass both *in situ* and *ex situ* techniques, link the conserved diversity to actual or potential utilization to ensure its sustainability, and include an element of awareness-raising (among both the public and professional stakeholders) to ensure the profile of CWR is raised and their conservation is no longer neglected. The strategy will require coordinated efforts at national, regional and global levels and will need a coordinated approach between the professional PGRFA and nature conservation communities.

Critically, because the *raison d'être* for CWR conservation is primarily actual or potential use in crop enhancement, the utilization of CWR diversity is as fundamental as the maintenance of the genetic diversity itself. Therefore, the onus is on the conservation community to ensure that when CWR diversity is conserved, it is also available for use; CWR diversity needs to be characterized and evaluated and its availability promoted to the stakeholder community.

Although a systematic approach to global CWR conservation has not yet been widely adopted, the importance of CWR has been recognized in a number of international policy and legislative instruments—most notably, the Global Plan of Action for the Conservation and Sustainable Utilization of Plant Genetic Resources for Food and Agriculture (GPA), the ITPGRFA and the CBD Global Strategy for Plant Conservation (GSPC)—as well as regional policy instruments such as the European Strategy for Plant Conservation (ESPC).

These instruments provide the formal policy framework for action, but a commitment from individual nations to act both at the country level and collectively at regional and global levels is now urgently needed to put in place practical measures to secure CWR diversity. Some key recommendations for action follow. This report has highlighted specific sites or areas where genetic reserves need to be established for the highest priority wild relatives of the 14 crops treated in this study and could form the initial basis for developing a global network of CWR genetic reserves. However, after selecting the best sites in terms of taxon and genetic diversity representation, there are many factors that will require resolution, such as:

- Identification of the agency that will be responsible for developing and overseeing a global network once established, including on-going monitoring of the effectiveness of the individual sites;
- Negotiation with national protected area agencies to include their site in a global network and to ensure that CWR genetic diversity is appropriately managed within these sites;
- Investigation of the best options for conserving CWR taxa outside of protected areas, either by establishing new genetic reserves or encouraging their conservation in an on-farm context, as appropriate.

The analysis and efforts should be expanded to include the wild relatives of other major and minor food crops, focusing first on crops that are most significant in terms of global food security and those that are particularly critical on a local level to some of the poorest sectors of society. We recommend that a full analysis of the kind undertaken for the case studies undertaken for this study is undertaken for all ITPGRFA Annex 1 crop complexes to ensure that a global network encompasses the wild relatives of the full range of global priority food and agricultural crops. However, given that the global estimate for the number of highest priority CWR species may be as low as 700, there is an imperative to identify and effectively conserve these critical species to underpin future world food security and to ensure that the conserved diversity is made available globally for use in crop improvement programmes. In the long term, a global network should aim to conserve multiple taxa in the same sites where possible. Even if a more common and widespread taxon is found at a site

identified for the conservation of a less common taxon, the value of the site will be vastly increased if both taxa can be actively conserved. It is important not to lose sight of the fact that many of the more common and widespread taxa may become more restricted in future; particularly in response to climate change.

The success of a global network of CWR genetic reserves will depend on a number of parallel and supporting activities to ensure that full and complementary conservation of high priority CWR is effected. Some key recommendations in this respect are highlighted below.

#### **4.1 Establish national CWR conservation strategies for individual countries**

Each country should be encouraged to systematically address conservation of their native CWR resources, with establishment of priority genetic reserves and *ex situ* duplication of CWR diversity put in place (see Part 2).

#### **4.2 Effect back-up duplication of CWR diversity ex situ**

Complementary conservation (i.e., conservation using both *in situ* and *ex situ* techniques) is perhaps more critical now in the face of climate change, shifting ecosystems and habitat loss than ever before. There is an urgent need to ensure *ex situ* back-up duplication of the conserved *in situ* diversity in appropriate national, regional and global gene banks. The ancillary benefit of establishing systematic collections will be the improved availability of CWR diversity for utilization.

#### **4.3 Improve consensus-building between the biodiversity and agrobiodiversity communities**

As any attempt to implement a global network of CWR genetic reserves is likely to be focused on existing protected areas, the biodiversity and agrobiodiversity communities will need to work much more closely together. Therefore, we strongly recommend that consensus-building activities be undertaken between the two communities, such as organization of joint conferences, collaboration in research and conservation projects, working on joint publications and establishment of joint national, regional and global conservation committees.

#### **4.4 Enhance CWR availability for breeders' use**

There is an urgent need to ensure that information concerning CWR diversity, its conservation and actual or potential utilization is made readily available to the widest stakeholder community.

Specifically, to help improve access to CWR diversity for breeders' use, there is a need to: promote the use of CWR diversity for crop improvement; develop strategies to ensure more reliable identification of wild species in gene banks; improve CWR characterization and evaluation; employ virtual or predictive characterization of CWR accessions using ecogeographic data and GIS techniques; build genomic databases of known useful genes in the range of CWR; and improve techniques for transferring traits between species.

#### **4.5 Address the sustainability of CWR conservation**

Greater efforts are needed to ensure that CWR are recognized as a distinct component of national, regional and global genetic resources in PGR conservation policy, as well as in both agrobiodiversity and biodiversity conservation and utilization strategies.

It is critical that specific provision for the conservation of CWR diversity is made by national, regional and international funding bodies, linked to the conservation of both PGRFA and wild species and habitats in general. Given that most of the sites identified as part of a global network are in developing countries, there is a need for developed countries to establish a funding mechanism to provide support to developing countries to assist them in the location and establishment of genetic reserve sites and in managing the sites. Developing countries also require financial support to study, describe, conserve

and utilize their CWR diversity. Linked to the financing of CWR diversity conservation, there is a requirement to ensure the equitable sharing of the benefits that arise from CWR diversity exploitation.

To promote sustainable *in situ* CWR conservation there is a need to encourage and facilitate stronger legislative protection of protected areas. This is particularly important for protected areas in Vavilov Centre's of Origin/CWR hotspots or those that belong to a global network of CWR genetic reserves.

There is also a need to increase professional and public awareness of the importance of conserving CWR diversity and of the direct link between CWR diversity maintenance and food security.

#### **4.6. Improve information dissemination**

There is an urgent need to ensure that information concerning CWR diversity, its conservation and actual or potential utilization is made readily available to the widest stakeholder community. Providing access to such information is critical, both for supporting effective and sustainable complementary CWR conservation, and to encourage and facilitate the use of CWR genetic diversity for crop improvement.

There have been some recent notable initiatives aimed at improving the management of and access to CWR information. These include the Crop Wild Relative Information System (CWRIS – <http://www.pgrforum.org/cwr/cwrinfo.asp>) (Kell *et al.*, 2008b) and the CWR Global Portal (<http://www.cropwildrelatives.org/>). However, limited financial resources means that the sustainability of such systems is not guaranteed. This reinforces the need for sufficient financial support to be available for the full range of CWR conservation activities, including the provision of information management systems that lie at the heart of all conservation and use activities.

#### **4.7. Conduct priority CWR research activities**

There are a number of particular areas of research that are needed to improve our knowledge of where to target CWR conservation efforts, how to conserve CWR that are found outside of protected areas, the causes of loss of CWR diversity, how climate change is likely to impact on CWR populations, how to involve local communities in the conservation and use of CWR, and addressing the taxonomic issues that underpin CWR conservation and use initiatives. The methods and tools are widely available to undertake such research (e.g., gap analysis, Red List assessment, climate change modelling); however, there is a need for greater injection of resources to implement these research methods for the benefit of CWR conservation and use.

## CONCLUDING REMARK

Climate change presents a new degree of threat to global food security. CWR contain the genetic diversity that can at least partially mitigate this threat, yet CWR themselves are in turn threatened. Knowledge, experience and techniques are available to adequately conserve and use CWR diversity for the benefit of humankind—all that is required now is the will to act.

## REFERENCES

- Aggarwal, P.K., Kropff, M.J., Cassman, K.G. and ten Berge, H.F.M. (1997). Simulating genetic strategies for increased rice yield potential in irrigated, tropical environments. *Field Crops Research*, 51: 5–17.
- Akimoto, M., Shimamoto, Y. and Morishima, H. (1999). The extinction of genetic resources of Asian wild rice, *Oryza rufipogon* Griff.: a case study in Thailand. *Genetic resources and Crop Evolution*, 46: 419–425.
- Al-Atawneh, N., Amri, A., Assi, R. and Maxted N. (2008). Management plans for promoting *in situ* conservation of local agrobiodiversity in the West Asia centre of plant diversity. In: *Crop Wild Relative Conservation and Use* (eds. Maxted, N., Ford-Lloyd, B.V., Kell, S.P., Iriondo, J., Dulloo, E. and Turok, J.). Pp. 338–361. CABI Publishing, Wallingford.
- Anikster, Y., Feldman, M. and Horovitz, A. (1997). The Ammiad experiment. In: *Plant genetic conservation: the in situ approach* (eds. Maxted, N., Ford-Lloyd, B.V. and Hawkes, J.G.). Pp. 239–253. Chapman and Hall, London.
- Avagyan, A. (2008). Crop wild relatives in Armenia: diversity, legislation and conservation issues. In: Maxted, N., Ford-Lloyd, B.V., Kell, S.P., Iriondo, J., Dulloo, E. and Turok, J. (eds.) *Crop Wild Relative Conservation and Use*. Pp. 58–68. CABI Publishing, Wallingford.
- Avivi, L. (1978). High grain protein content in wild tetraploid wheat *Triticum dicoccoides* Körn. *Proceedings of 5<sup>th</sup> international Wheat Genetic Symposium, New Delhi*. 372–380.
- Barazani, O., Perevolotsky, A., and Hadas, R. (2008). A problem of the rich: prioritizing local plant genetic resources for *ex situ* conservation in Israel. *Biological Conservation*, 141(2): 596–600.
- Bautista, N.S., Solis, R., Kamijima, O. and Ishii, T. (2001). RAPD, RFLP and SSCP analyses of phylogenetic relationships between cultivated and wild species of rice. *Genes, Genetics and Systematics*, 76: 71–79
- Bisht, M.S. and Mukai, Y. (2002). Genome organization and polyploid evolution in the genus *Eleusine* (Poaceae) *Plant Systematics and Evolution*, 233: 243–258.
- Bradshaw, J.E. and Ramsey, G. (2005). Utilization of the Commonwealth Potato Collection in Potato Breeding. *Euphytica* 146, 9–19.
- Bradshaw, J.E., Bryan, G.J. and Ramsay, G. (2006). Genetic resources (including wild and cultivated *Solanum* species) and progress in their utilization in potato breeding. *Potato Research*, 49, 49–65.
- Brar, D.S. (2005). Broadening the gene pool of rice through introgression from wild species. In: *Rice is life: scientific perspectives for the 21st century*. Proceedings of the World Rice Research Conference held in Tsukuba, Japan, 4–7 November 2004 (eds. Toriyama, K., Heong, K.L. and Hardy, B.). Pp. 157–160. International Rice Research Institute, Philippines.

- Brar, D.S. and Khush, G.S. (1997). Alien introgression in rice. *Plant Molecular Biology*, 35: 35–47.
- CBD (1992). *Convention on Biological Diversity*. Secretariat of the Convention on Biological Diversity, Montreal, Quebec, Canada.
- CBD (2002). *Strategic Plan for the Convention on Biological Diversity*. Secretariat of the Convention on Biological Diversity, Montreal, Quebec, Canada.
- Chang, T.T. (1976). The origin, evolution, cultivation, dissemination, and diversification of Asian and African rices. *Euphytica*, 25: 425–441.
- Chang, T.T. (1995). Rice. In: *Evolution of Crop Plants* (eds. Smartt, J. and Simmonds, N.W.). Pp. 147–155. Longman, Harlow, UK.
- Cheng, C., Tsuchimoto, S., Ohtsubo, H. and Ohtsubo, E. (2002). Evolutionary relationships among rice species with AA genome based on SINE insertion analysis. *Genes, Genetics and Systematics*, 77: 323–334.
- Cox, T.S. and Hatchett, J.H. (1994). Hessian Fly-Resistance Gene H26 Transferred from *Triticum tauschii* to Common Wheat. *Crop Science*, 34: 958–960.
- D'Arcy, W.G. (ed.) (1986). *Solanaceae: Biology and Systematics*. Columbia University Press, New York.
- D'Arcy, W.G. (1991). The Solanaceae since 1976, with a review of its bibliography. In: *Solanaceae III: Taxonomy, Chemistry and Evolution* (eds. Hawkes, J.G., Lester, R.N., Nee, M. and Estrada-R., N.). pp 75–138. Royal Botanic Gardens, Kew, London.
- Delibes, A., Romero, D., Aguaded, S., Duce, A., Mena, M., López-Braña, I., Andrés, M.F., Martín-Sánchez, J.A. and García-Olmedo, F. (1993). Resistance to cereal cyst nematode (*Heterodera avenae* Woll.) transferred from the wild grass *Aegilops ventricosa* to hexaploid wheat by a ‘stepping stone’ procedure. *Theoretical and Applied Genetics*, 87: 402–408.
- Dubin, H.J., Gilchrist, L., Reeves, L. and McNab, A. (1997). *Fusarium head blight: global status and prospects*. CIMMYT, Mexico City.
- Ertug Firat, A. and Tan, A. (1997). *In situ* conservation of genetic diversity in Turkey. In: *Plant genetic conservation: the in situ approach* (eds. Maxted, N., Ford-Lloyd, B.V. and Hawkes, J.G.). Pp. 254–262. Chapman and Hall, London.
- Fan S-G., Zhang Z-J., Liu L., Liu H-X. and Liang C-Y. (2000). Conservation of wild rice genetic resources in China and their utilization in breeding. *Biodiversity Science*, 8(2): 198–207.
- FAO (1997). *The State of the World's Plant Genetic Resources for Food and Agriculture*. Food and Agriculture Organization of the United Nations. Available at: <http://www.fao.org/WAICENT/FAOINFO/AGRICULT/AGP/AGPS/Pgrfa/pdf/swrfull.pdf> [Accessed 21 October 2008].
- FAO (1998). *The State of the World's Plant Genetic Resources for Food and Agriculture*. FAO, Rome, Italy.
- FAO (2001). *International Treaty on Plant Genetic Resources for Food and Agriculture*. Food and Agriculture Organization of the United Nations. Available at: <http://www.fao.org/ag/cgrfa/itpgr.htm> [Accessed 21 October 2008].

- FAO (2005). *Harvesting Nature's Diversity*.  
<http://www.fao.org/DOCREP/004/V1430E/V1430E00.htm#TOC> [Accessed 03 March 2009].
- FAO (2008a). *Climate Change and Biodiversity for Food and Agriculture*. FAO, Rome.
- FAO (2008b). *FAOSTAT* website [<http://faostat.fao.org/site/567/DesktopDefault.aspx?PageID=567>]. [Accessed 07 April, 2008].
- FAO/CIP (1995). *Potatoes in the 1990s: Situation and Prospects of the World Potato Economy*. FAO, Rome, Italy.
- Feldman, M., Lupton, F.G.H. and Miller, T.E. (1995). Wheats. In: *Evolution of crop plants, 2nd edn.* (eds. Smartt, J. and Simmonds, N.W). Pp. 184–192. Longman Scientific, London.
- Feuillet, C., Langridge, P. and Waugh, R. (2008). Cereal breeding takes a walk on the wild side. *Trends in Genetics*, 24: 24–32.
- Ford-Lloyd, B.V., Jackson, M.T. and Newbury, H.J. (1997). Molecular markers and the management of genetic resources in seed genebanks: a case study of rice. In: *Biotechnology and Plant Genetic Resources: Conservation and Use* (eds. Callow, J.A., Ford-Lloyd, B.V. and Newbury, H.J.). Pp. 103–118. CAB International, Wallingford.
- Ford-Lloyd, B.V., Maxted, N., Kell, S.P., Mitchell, M., Scholten, M., Magos Brehm, J. (2008). Establishing conservation priorities for crop wild relatives, in: Maxted, N., Dulloo, E., Ford-Lloyd, B., Kell, S.P., Iriondo, J.M. (Eds.), *Crop Wild Relatives Conservation and Use*. Pp. 110–119. CAB International Publishing, Wallingford.
- Frankel, O. (1970). Genetic conservation of plants useful to man, *Botanical Conservation*, 2: 162–169.
- Gao, L.Z. (2003). The conservation of rice biodiversity in China: significance, genetic erosion, ethnobotany and prospect. *Genetic Resources and Crop Evolution*, 50: 17–32.
- Gao, L.Z., Chen, W., Jiang, W., Ge, S., Hong, D. and Wang, X. (2000). Genetic erosion in northern marginal population of the common wild rice *Oryza rufipogon* Griff. and its conservation, revealed by the change of population genetic structure. *Hereditas*, 133: 47–53.
- Gill, B.S., Raupp, W.J., Browder, L.E. and Cox, T.S. (1988). Registration of KS86WGR02 Leaf rust resistant hard red wheat germplasm. *Crop Science*, 28: 207.
- Glaszmann, J.C. (1987). Isozymes and classification of ancient rice varieties. *Theoretical and Applied Genetics*, 74: 21–30.
- Groombridge, B. and Jenkins, M.D. (2002). *World Atlas of Biodiversity*. Prepared by the UNEP World Conservation Monitoring Centre. University of California Press, Berkeley, California.
- Hajjar, R. and Hodgkin, T. (2007). The use of wild relatives in crop improvement: a survey of developments over the last 20 years. *Euphytica*, 156: 1–13.
- Harlan, J.R. and de Wet, J.M.J. (1971). Towards a rational classification of cultivated plants. *Taxon*, 20, 509–517.
- Hawkes, J.G. (1958). Significance of wild species and primitive forms for potato breeding. *Euphytica*, 7: 257–270.
- Hawkes, J.G. (1990). *The potato: evolution, biodiversity and genetic resources*. Belhaven Press, London.



- Hawkes, J.G., Maxted, N. and Ford-Lloyd, B.V. (2000). *The ex situ conservation of plant genetic resources*. Pp. 1–250. Kluwer, Dordrecht, The Netherlands.
- Heywood, V.H. and Dulloo, M.E. (2006). In *Situ Conservation of Wild Plant Species – a Critical Global Review of Good Practices*. IPGRI Technical Bulletin No. 11. IPGRI, Rome.
- Hijmans, R.J., Spooner, D.M., Salas, A.R., Guarino, L. and de la Cruz, J. (2002). Atlas of wild potatoes. Systematic and Ecogeographic Studies in Crop Genepools 8. IPGRI, Rome.
- Hodgkin, T. and Hajjar, R. (2008). Using crop wild relatives for crop improvement: trends and perspectives. In: Maxted, N., Ford-Lloyd, B.V., Kell, S.P., Iriondo, J., Dulloo, E. and Turok, J. (eds.) *Crop Wild Relative Conservation and Use*. Pp. 535–548. CABI Publishing, Wallingford, UK.
- Hoegh-Guldberg, O., Hughes, L., McIntyre, S., Lindenmayer, D.B., Parmesan, C., Possingham, H.P. and Thomas, C.D. (2008). Assisted colonization and rapid climate change. *Science*, 321: 345–346.
- Hoisington, D., Khairallah, M., Ribaut, J.M., Skovmand, B., Taba, S. and Warburton, M. (1999). Plant genetic resources: what can they contribute toward increased crop productivity? *Proceedings of the National Academy of Science, USA*, 99: 8133–8138.
- Hoyt, E. (1988). *Conserving the Wild Relatives of Crops*. IBPGR, IUCN, WWF, Rome and Gland.
- Hunter, M.L. (2007). Climate change and moving species: furthering the debate on assisted colonization. *Conservation Biology*, 21: 1356–1358.
- ICRISAT (2008). *ICRISAT Website*. International Crops Research Institute for the Semi-Arid Tropics, <http://www.icrisat.org/index.htm> [Accessed 21 October 2008].
- Iriondo, J.M., Dulloo, E., Maxted, N. (Eds.) (2008a). *Conserving Plant Genetic Diversity in Protected Areas: Population Management of Crop Wild Relatives*. CAB International Publishing, Wallingford.
- IRRI (2004). *2003 Annual Report. Plant Breeding, Genetics, and Biochemistry Division*. International Rice Research Institute, Manila, Philippines. Available at: <http://www.irri.org/publications/techbulletin/pdfs/TB%2011.pdf> [Accessed 21 October 2008]
- IRRI (2007). *Annual Report of the Director General, 2006–07. Project 1, Germplasm conservation, characterization, documentation, and exchange*. International Rice Research Institute, Manila, Philippines. Available at: <http://www.irri.org/science/progsum/pdfs/DGReport2007/Project-1.pdf> [Accessed 21 October 2008]
- IRRI (2008). *Genebank* [[http://www.knowledgebank.irri.org/GRCManuals/The\\_genebank.htm](http://www.knowledgebank.irri.org/GRCManuals/The_genebank.htm)]. [Accessed 01 May 2008].
- IUCN (1995). *Guidelines for Protected Area Management Categories*, IUCN Commission on National Parks and Protected Areas with the World Conservation Monitoring Centre, Gland, Switzerland.
- IUCN (2001). *IUCN Red List Categories and Criteria: Version 3.1*. IUCN Species Survival Commission. IUCN, Gland, Switzerland and Cambridge, UK. [http://www.iucnredlist.org/static/categories\\_criteria\\_3\\_1](http://www.iucnredlist.org/static/categories_criteria_3_1) [Accessed 21 October 2008].
- Jackson, M.T., Loresto, G.C., Appa Rao, S., Jones, M., Guimaraes, E.P. and Ng, N.Q. (1997). Rice. In: *Biodiversity in trust* (eds. Fuccillo, D., Sears, L. and Stapleton, P.). Pp. 271–291.
- Jahier, J., Doussinault, G., Dosba, F. and Bourgeois, F. (1979), Monosomic analysis of resistance to eyespot in the variety “Roazon”. In: Ramanujam S (ed.) *Proceedings of 5th International Wheat*

*Genetic Symposium*. pp 437–440. Indian Society of Genetics and Plant Breeding, IARI, New Delhi, India.

Jain, S.K. (1975). Genetic reserves. In: Frankel, O.H., Hawkes, J.G. (Eds.), *Crop genetic resources for today and tomorrow*. Pp. 379–396. Cambridge University Press. Cambridge, UK.

Jarvis, A., Lane, A. and Hijmans, R.J. (2008). The effect of climate change on crop wild relatives. *Agriculture, Ecosystems and Environment*, 126 (1): 13–23.

Karagöz, A. (1998). In situ conservation of plant genetic resources in the Ceylan State Farm. In: *The proceedings of international symposium on in situ conservation of plant diversity* (eds. Zencirci, N., Kaya, Z., Anikster, Y. and Adams, W.T.), Pp. 87–92. Central Research Institute for Field Crops, Ankara, Turkey.

Keisa, A., Maxted, N. and Ford-Lloyd, B.V. (2008). The assessment of biodiversity loss over time: wild legumes in Syria. *Genetic Resources and Crop Evolution*, 603–612.

Kell, S.P. and Maxted, N. (compilers) (2003). *European Crop Wild Relative Diversity Assessment and Conservation Forum. Report of Workshop 1: European crop wild relative assessment, 5–7 February, 2003, Véria, Greece*. University of Birmingham. 79 pp. Available at: <http://www.pgrforum.org/Publications.htm> [Accessed 09 October 2009].

Kell, S.P., Knüpfner, H., Jury, S.L., Maxted, N. and Ford-Lloyd, B.V. (2005). *Catalogue of Crop Wild Relatives for Europe and the Mediterranean*. University of Birmingham, Birmingham, UK. Available at: <http://www.pgrforum.org/cwris/cwris.asp> and on CD-ROM.

Kell, S.P., Knüpfner, H., Jury, S.L., Ford-Lloyd, B.V. and Maxted, N. (2008a). Crops and wild relatives of the Euro-Mediterranean region: making and using a conservation catalogue. In: Maxted, N., Ford-Lloyd, B.V., Kell, S.P., Iriondo, J., Dulloo, E. and Turok, J. (eds) *Crop Wild Relative Conservation and Use*. Pp. 69–109. CAB International, Wallingford, UK.

Kell, S.P., Moore, J.D., Iriondo, J.M., Scholten, M.A., Ford-Lloyd, B.V. and Maxted, N. (2008b). CWRIS: an information management system to aid crop wild relative conservation and sustainable use. In Maxted, N., Ford-Lloyd, B.V., Kell, S.P., Iriondo, J., Dulloo, E. and Turok, J. (eds.) *Crop Wild Relative Conservation and Use*. Pp. 469–489. CABI Publishing, Wallingford.

Kerber, E.R. and Dyck, P.L. (1969). Inheritance in Hexaploid Wheat of Leaf rust resistance and other characters derived from *Aegilops squarrosa*. *Canadian Journal of Genetics and Cytology*, 11: 639–647.

Kimber, G. and Feldman, M. (1987). *Wild wheat: an introduction*. Special Report 353. College of Agriculture, University of Missouri, Columbia, U.S.A.

Kurata, N. (2008). Chromosome and genome evolution in rice. In: *Rice biology in the genomics era* (eds. Hirano, H-Y., Sano, Y., Hirai, A. and Sasaki, T.). Pp. 235–245. Springer Berlin Heidelberg.

Kwon, S-J. Lee, J.K., Hong, S-W., Park, Y-J., McNally, K.L. and Kim, N-S. (2006). Genetic diversity and phylogenetic relationship in AA *Oryza* species as revealed by Rim2/Hipa CACTA transposon display. *Genes Genetics and Systematics*, 81: 93–101.

Lagudah, E.S. and Appels, R. (1993). Wild Relatives as a Source of New Germplasm for Cereal Improvement. In: Imrie B.C. and Hacker J.B. (eds.) *Focused Plant Improvement: Towards Responsible and Sustainable Agriculture*. Proceedings Tenth Australian Plant Breeding Conference, Gold Coast, Australia. 18–23 April 1993. Organizing Committee, Australian Convention and Travel Service, Canberra. Pp. 10–21.

- Laguna, E. (1999). The plant micro-reserves programme in the region of Valencia, Spain. In: *Second European Conference on the Conservation of Wild Plants* (eds. Synge, H. and Ackroyd, J.). Proceedings Planta Europa 1998. Pp. 181–185. The Swedish Threatened Species Unit and Plantlife, Uppsala and London.
- Linnaeus, C. (1753). *Species Plantarum*, edn. 1. 2: 996, 1050–1051. Salvius, Stockholm.
- Lovisollo, M.R. and Galat, B.G. (2007). Ultrastructure and development of the megagametophyte in *Eleusine tristachya* (Lam.) Lam. (Poaceae). *Flora–Morphology, Distribution, Functional Ecology of Plants*, 202(4): 293–301.
- Lu, B.R., Zheng, K.L., Qian, H.R. and Zhuang, J.Y. (2002). Genetic differentiation of wild relatives of rice as assessed by RFLP analysis. *Theoretical and Applied Genetics*, 106(1): 101–6.
- Mabberley, D.J. (1997). *The PlantBook. A Portable Dictionary of the Vascular Plants*. Cambridge University Press, Cambridge.
- Magos Brehm, J., Maxted, N., B. V. Ford-Lloyd B.V. and Martins-Loução, M.A. (2007). National inventories of crop wild relatives and wild harvested plants: case-study for Portugal. *Genetic Resources and Crop Evolution*, 55: 779–796.
- Manners, G.R. and van Slageren, M. (1998). Research and Production: Cereal Taxonomy Used in Rachis. *Rachis*, 17(1&2): 1–6.
- Marais, G.F., McCallum, B. and Marais, A.S. (2008). Wheat leaf rust resistance gene *Lr59* derived from *Aegilops peregrina*. *Plant Breeding*, 127(4): 340–345.
- Maxted, N. (2003). Conserving the genetic resources of crop wild relatives in European protected areas. *Biological Conservation* 113(3): 411–417.
- Maxted, N., Ford-Lloyd, B.V. and Hawkes, J.G. (1997a). *Plant genetic conservation: the in situ approach*. Chapman & Hall, London.
- Maxted, N., Hawkes, J.G., Ford-Lloyd, B.V. and Williams, J.T. (1997b). A practical model for *in situ* genetic conservation. In: *Plant genetic conservation: the in situ approach* (eds. Maxted, N., Ford-Lloyd, B.V. and Hawkes, J.G.), Pp. 339–367. Chapman & Hall, London.
- Maxted, N., Hawkes, J.G., Guarino, L. and Sawkins, M. (1997c). The selection of taxa for plant genetic conservation. *Genetic Resources and Crop Evolution*, 44: 337–348.
- Maxted, N., Ford-Lloyd, B.V., Jury, S.L., Kell, S.P. and Scholten, M.A. (2006). Towards a definition of a crop wild relative. *Biodiversity and Conservation*, 15(8): 2673–2685.
- Maxted, N., Scholten, M.A., Codd, R. and Ford-Lloyd, B.V. (2007). Creation and Use of a National Inventory of Crop Wild Relatives. *Biological Conservation*, 140: 142–159.
- Maxted, N., Dulloo, E., Ford-Lloyd, B.V., Iriondo, J. and Jarvis, A. (2008a). Genetic gap analysis: a tool for more effective genetic conservation assessment. *Diversity and Distributions*, 14: 1018–1030.
- Maxted, N., Iriondo, J.M., De Hond, L., Dulloo, M.E., Lefèvre, F., Asdal, A., Kell, S.P. and Guarino, L. (2008b). Genetic Reserve Management. In: *Conserving Plant Genetic Diversity in Protected Areas: Population Management of Crop Wild Relatives* (eds. Iriondo, J.M., Dulloo, M.E. and Maxted, N.). Pp. 65–87. CAB International Publishing, Wallingford.
- McFadden, E.S. (1930). A successful transfer of emmer characters to vulgare wheat. *Journal of the American Society of Agronomy*, 22: 1020–1034.

McFadden, E.S. and Sears, E.R. (1946). The origin of *Triticum spelta* and its free-threshing hexaploid relatives. *Journal of heredity*, 37: 81–107.

McIntosh, R.A., Silk, J. and The, T.T. (1966). Cytogenetic studies in wheat .17. monosomic analysis and linkage relationships of Gene *Yr15* for resistance to stripe rust. *Euphytica*, 89: 395–399.

McIntosh, R.A., Yamazaki, Y., Devos, K.M., Dubcovsky, J., Rogers, W.J. and Appels, R. (2003). Catalogue of Gene Symbols for Wheat. In: Pogna, N.E., Romano, M., Pogna, E.A., and Galterio, G. (eds.) *Proceedings of the 10<sup>th</sup> International Wheat Genetics Symposium*. S.I.M.I., Rome, Vol. 4 and MacGene2003 database on CD.

Mehra K.L. (1963). Differentiation of cultivated and wild *Eleusine* species. *Phyton*, 20, 189–198.

Meilleur, B.A. and Hodgkin, T. (2004). *In situ* conservation of crop wild relatives. *Biodiversity and Conservation*, 13: 663–684.

Miller, T.E., Reader, S.M., Ainsworth, C.C. and Summers, R.W. (1987). The introduction of a major gene for resistance to powdery mildew of wheat, *Erysiphe graminis* f. sp. *tritici* from *Aegilops speltoides* into wheat, *T. aestivum*. In: Jorna, M.L. and Shootmaker, L.A.J. (eds) *Cereal breeding related to integrated cereal production*. pp 179–183. Proceedings of Eucarpia Conference, Wageningen, The Netherlands.

Millet, E., Manisterski, J. and Ben-Yehuda, P. (2008). Exploitation of wild cereal for wheat improvement in the Institute for Cereal Crop improvement. In: Maxted, N., Ford-Lloyd, B.V., Kell, S.P., Iriondo, J., Dulloo, E. and Turok, J. (eds.) *Crop Wild Relative Conservation and Use*. Pp. 556–565. CAB International, Wallingford.

Mujeeb-Kazi, A. and Hettel, G.P. (1996). Utilizing wild grass biodiversity in wheat improvement: 15 years of wide cross research at CIMMYT. CIMMYT Research Report No. 2. CIMMYT, Mexico.

Mujeeb-Kazi, A., Fuentes-Davila, G., Villareal, R.L., Cortes, A., Roasas, V. and Delgado, R. (2001). Registration of 10 synthetic hexaploid wheat and six bread wheat germplasm resistant to karnal bunt. *Crop Science*, 41: 1652–1653.

Nee, M. (1999). Synopsis of *Solanum* in the New World. In: *Solanaceae IV: Advances in biology and utilization* (eds. Nee, M, Symon, D.E., Lester, R.N. and Jessop, J.P.) Pp. 285–334. Royal Botanic Gardens, Kew, London.

Neves, S.S., Swire-Clark, G., Hilu, K.W. and Baird, W.V. (2005). Phylogeny of *Eleusine* (Poaceae: Chloridoideae) based on nuclear ITS and plastid *trnF* sequences. *Molecular Phylogenetics and Evolution*, 35, 395–419.

Oduori, C.O.A. (2005). *The importance and research status of finger millet in Africa*. A Paper Presented at the McKnight Foundation Collaborative Crop Research Program Workshop on Tef and Finger Millet: Comparative Genomics of the Chloridoid Cereals at the Biosciences for East and Central Africa (BECA) ILRI, Nairobi, Kenya, 28–30 June 2005. Available at: [http://mcknight.ccrp.cornell.edu/program\\_docs/event/nairobi05/nairobi05\\_paper\\_oduori\\_jun05.pdf](http://mcknight.ccrp.cornell.edu/program_docs/event/nairobi05/nairobi05_paper_oduori_jun05.pdf) [Accessed 21 October 2008].

Ogawa, T. (2003). Genome research in genus *Oryza*. In: *Monograph on Genus Oryza* (Nanda, J.S. and Sharma, S.D.). Pp. 171–212. Science Publishers Inc., Plymouth, UK.

Oka, H.I. (1991). Genetics diversity of wild and cultivated rice. In: *Rice Biotechnology* (eds. Khush, G.S. and Toenniessen, H.). Pp. 55–81. CABI, Wallingford.

- Peña, R.J., Zarco-Hernandez, J. and Mujeeb-Kazi, A. (1995). Glutenin subunit compositions and bread-making quality characteristics of synthetic hexaploid wheats derived from *Triticum turgidum* x *Triticum tauschii* (Coss.) Schmal crosses. *Journal of Cereal Science*, 21: 15–23.
- Peng, J.H., Fahima, T., Röder, M.S., Li, Y.C., Dahan, A., Grama, A., Ronin, Y.I., Korol, A.B. and Nevo, E. (1999). Microsatellite tagging of the stripe-rust resistance gene *YrH52* derived from wild emmer wheat, *Triticum dicoccoides*, and suggestive negative crossover interference on chromosome 1B. *Theoretical and Applied Genetics*, 98: 862–872.
- Phillips, S.M. (1972). A survey of the *Eleusine* Gaertn. (Gramineae) in Africa. *Kew Bulletin*, 27: 251–270.
- Phillips, S.M. (1974). *Eleusine*. In: Polhill, R.M. (ed.) *Flora of Tropical East Africa*. Crown Agents for Overseas Governments and Administrations. Pp. 260–267.
- Pimentel, D., Wilson, C., McCullum, C., Huang, R., Dwen, P., Flack, J., Tran, Q., Saltman, T. and Cliff, B. (1997). Economic and environmental benefits of biodiversity. *BioScience*, 47: 747–757.
- Prance, G.T. (1997). The conservation of botanical diversity. In: *Plant genetic conservation: the in situ approach* (eds. Maxted, N., Ford-Lloyd, B.V. and Hawkes, J.G.), Pp. 3–14. Chapman & Hall, London.
- Prescott-Allen, R. and Prescott-Allen, C. (1983). *Genes From the Wild: Using Wild Genetic Resources for Food and Raw Materials*. 2nd edn. International Institute for Environment and Development/Earthscan Publications, London.
- Pressey, R.L. and Nicholls, A.O. (1989). Efficiency in conservation evaluation: scoring versus iterative approaches. *Biological Conservation*, 50: 199–218.
- Pressey, R.L., Humphries, C.R., Vane-Wright, R.I. and Williams, P.H. (1993). Beyond opportunism: key principles for systematic reserve selection. *Trends in Ecology and Evolution*, 8: 124–128.
- Raupp, W.J., Amri, A., Hatchett, J.H., Gill, B.S., Wilson, D.L. and Cox, T.S. (1993). Chromosomal location of Hessian fly-resistance genes H22, H23 and H24 derived from *Triticum tauschii* in the D genome of wheat. *Journal of Heredity*, 84: 142–145.
- Rebello, A.G. (1994). Iterative selection procedures: centres of endemism and optimal placement of reserves. In: *Botanical Diversity in Southern Africa* (ed. Huntley, B.J.), Pp. 231–257. National Botanical Institute, Pretoria.
- Ross, H. (1986). Potato Breeding – Problems and Perspectives. *Fortschritte der Pflanzenzüchtung* 13. Paul Parey, Berlin and Hamburg.
- Schneider, A., Molnár I. and Molnár-Láng, M. (2008). Utilization of *Aegilops* (goatgrass) species to widen the genetic diversity of cultivated wheat. *Euphytica*, 163: 1–19.
- Serra, L., Pérez-Rovira, P., Deltoro, V.I., Fabregat, C., Laguna, E. and Pérez-Botella, J. (2004). Distribution, status and conservation of rare relict plant species in the Valencian Community. *Bocconea*, 16(2), 857–863.
- Simmonds, N.W. (1995). Bananas. In: *Evolution of Crop Plants* (eds. Smartt, J. and Simmonds, N.W.). Pp. 370–375. Longman, Harlow, UK.
- Smith, R.D. and Linington, S. (1997). The management of the Kew Seed Bank for the conservation of arid land and U.K. wild species. *Bocconea*, 273–280.

- Solheim, W.G. (1972). Northern Thailand, Southeast Asia and world prehistory. *Asian Perspectives*, 13: 145–162.
- Spooner, D.M. and Hijmans, R.J. (2001). Potato systematics and germplasm collecting, 1989–2000. *American Journal of Potato Research*, 78: 237–268; 395.
- Stolton, S., Maxted, N., Ford-Lloyd, B., Kell, S.P. and Dudley, N. (2006). *Food Stores: Using Protected Areas to Secure Crop Genetic Diversity*. WWF Arguments for protection series. WWF, Gland, Switzerland.
- Van Slageren, M.W. (1994). *Wild wheats: a monograph of Aegilops L. and Amblyopyrum (Jaub. & Spach) Eig (Poaceae)*. Wageningen Agricultural University, Wageningen, Netherlands.
- Vaughan, D.A. (1994). The Wild Relatives of Rice, A genetic Resource Handbook. IRRI, Los Banos, Philippines.
- Vaughan, D.A. and Chang, T.T. (1992). *In situ* conservation of rice genetic resources, *Economic Botany*, 46(4): 368–383.
- Villareal, R.L., Sayre, K., Banuelos, O. and Mujeeb-Kazi, A. (2001). Registration of four synthetic hexaploid wheat (*Triticum turgidum/Aegilops tauschii*) germplasm lines tolerant to waterlogging. *Crop Science*, 41: 274.
- Vollbrecht, E. and Sigmon, B. (2005). Amazing grass: developmental genetics of maize domestication. *Biochemical Society Transactions*, 33: 1502–1506.
- Walters, K.S. and Gillett, H.J. (1998). 1997 IUCN Red List of Threatened Plants. Compiled by the World Conservation Monitoring Centre. Pp. 1–862. International Union for Conservation of Nature and Natural Resources, Gland, Switzerland.
- Wells, D.G., Kota, R.S., Sandhu, H.S., Gardner, W.A.S. and Finney, K.F. (1982). Registration of one disomic substitution line and five translocation lines of winter wheat germplasm resistant to wheat streak mosaic virus. *Crop Science*, 22: 1277–1278.
- William, M.D.H.M., Peña, R.J. and Mujeeb-Kazi, A. (1993). Seed protein and isozyme variations in *Triticum tauschii* (*Aegilops squarrosa*). *Theoretical and Applied Genetics*, 87: 257–263.
- Xiao, J., Li, J., Grandillo, S., Ahn, S.N., Yuan, L., Tanksley, S.D. and McCouch, S.R. (1998). Identification of trait-improving quantitative trait loci alleles from a wild rice relative, *Oryza rufipogon*. *Genetics*, 150: 899–909.
- Xiu-Jin, L., Deng-Cai, L. and Zhi-Rong, W. (1997). Inheritance in synthetic hexaploid wheat ‘RSP’ of sprouting tolerance derived from *Aegilops tauschii* Coss. *Euphytica*, 95: 321–323.
- Zeven, A.C. (1979). Polyploidy and domestication: the origin and survival of polyploids in cytotype mixtures. *Basic Life Science*, 13: 385–407.