THEMATIC BACKGROUND STUDY

Establishment of a Global Network for the *In Situ* Conservation of Crop Wild Relatives: Status and Needs

Nigel Maxted and Shelagh Kell

October 2009

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

By Nigel Maxted and Shelagh Kell[1]

---

[1] School of Biosciences, University of Birmingham.

Disclaimer

CONTENTS

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[2]. 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 so far some attempts by individual countries to set up *in situ* conservation areas for CWR, but no systematic effort to build up national, regional or global networks of these areas. The objective of this study is to provide sufficient baseline information for allowing decision-makers to strengthen efforts for the *in situ* conservation of CWR, including at national level, and analyzes in particular which could be 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.

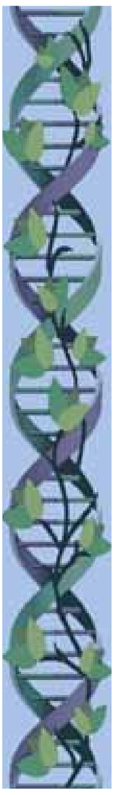
This background study addresses these issues in four parts. Part 1 is an introduction to CWR: how they are defined, global numbers of CWR, their importance to humankind as gene donors for crop improvement, threats to natural populations, how complementary conservation can be achieved and how CWR might 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.

---

[2] CPGR/89/REP, paragraphs 32-37.

PART 1: 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 for allowing 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 analyzes 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 provides further examples of the use of CWR in crop improvement programmes for 29 major crops.

1.3 Definition of a crop wild relative

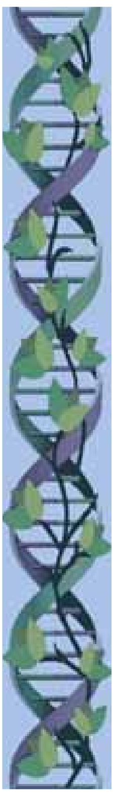
CWR are commonly defined in terms of wild species that are relatively closely related to agricultural and horticultural crops; therefore, a broad definition of a CWR would be any taxon belonging to the same genus as a crop. This definition is intuitively accurate and can be simply applied. However, application 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 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 in genus	Primary CWR species	Secondary CWR species	% Priority in genus[1]
Finger millet	*Eleusine coracana*	9	3	3	66.67
Barley	*Hordeum vulgare*	16	1	1	12.50
Sweet potato	*Ipomoea batatas*	600–700	3	11	2.00
Cassava	*Manihot esculenta*	98	3	13	16.33
Banana/plantain	*Musa acuminate*	30	10	15	83.33
Rice	*Oryza sativa*	23	8	9	73.91
Pearl millet	*Pennisetum glaucum*	80–140	1	2	2.14
Garden pea	*Pisum sativum*	3	1	2	100.00
Potato	*Solanum tuberosum*	1 000	6	24	3.00
Sorghum	*Sorghum bicolor*	25	2	2	16.00
Wheat	*Triticum aestivum*	6+22	6	12	64.29
Faba bean	*Vicia faba*	140	1	0	0.71
Cowpea	*Vigna unguiculata*	61	1	3	6.56
Maize	*Zea mays*	4	1	3	100.00
Totals		**2 117–2 277**	**47**	**100**	
%		100	2.06	4.39	6.45

[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

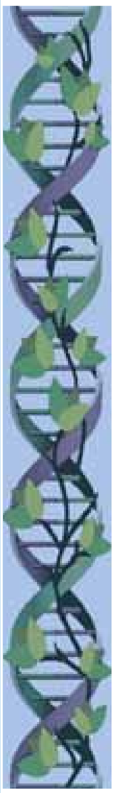
Naturally, some countries harbour greater numbers of CWR than others. In general, the greater the number of species in the country's flora, the greater the number of CWR there will be. In those countries with higher numbers of CWR, a greater injection of resources will be needed in order to secure populations *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 disproportionally 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[3]) and *ex situ* (primarily as seed in gene banks, but also as explants in tissue culture 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 bicolour*) (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.

---

[3] 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'.

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.

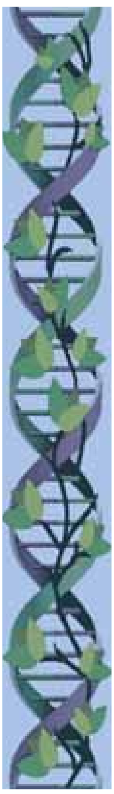
Conservation of CWR is just as feasible outside of conventional reserves as it is within fully designated genetic reserves. However, there are advantages and disadvantages to this approach. A major advantage of CWR conservation outside protected areas is that the management interventions at the site 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 2: NATIONAL CWR CONSERVATION STRATEGIES

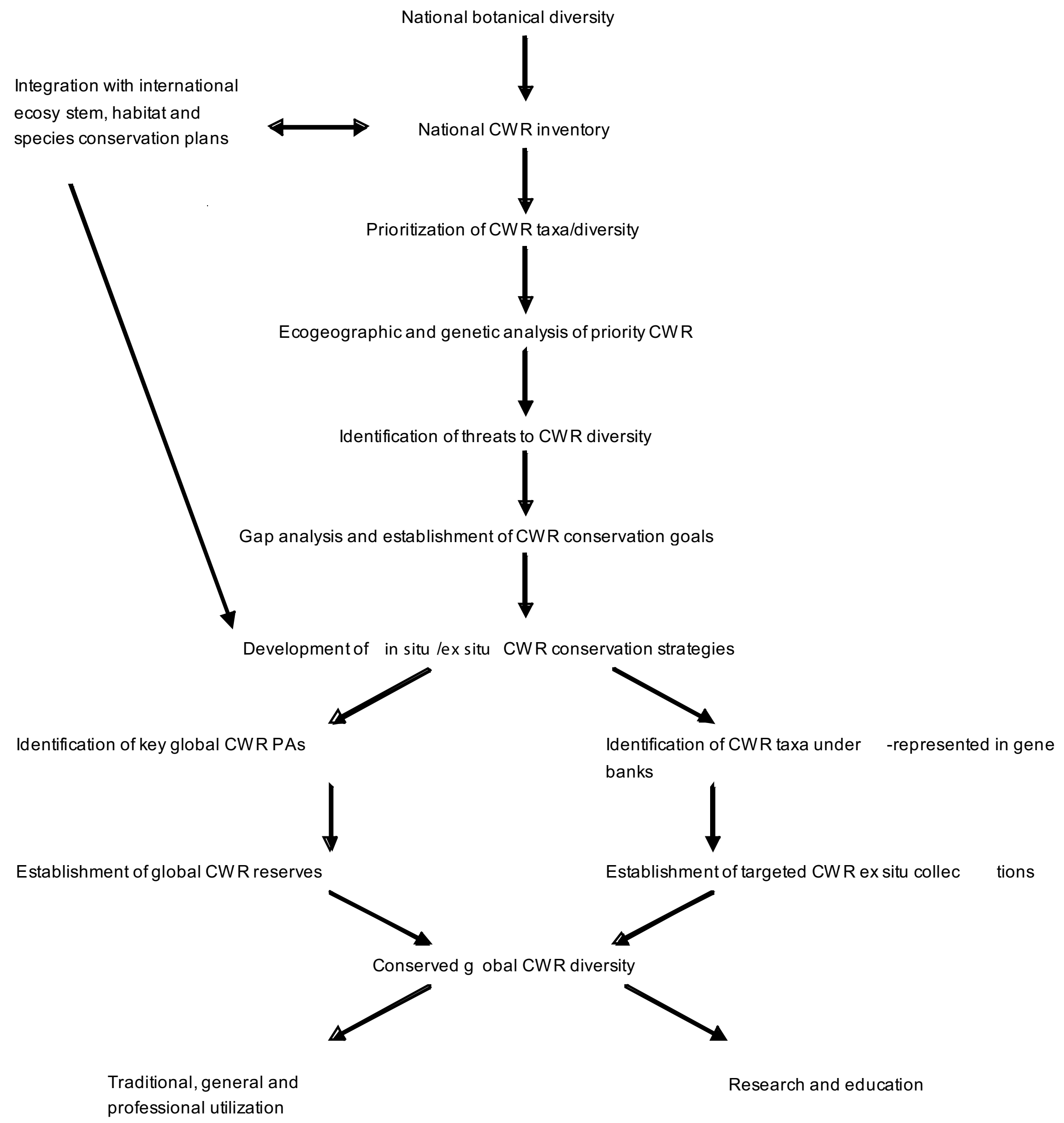
There are many potential approaches to systematic CWR conservation. But as every country contains CWR diversity, they are obliged as signatories to the CBD and ITPGRFA, or other policy instruments, to adopt a national approach to systematically conserve this diversity. This section outlines how a national 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.

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: Case study: National CWR conservation strategy for the UK, which outlines how the UK National Inventory of CWR was prepared.

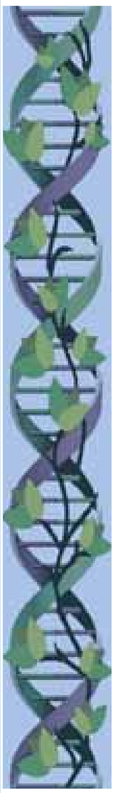
FIGURE 1

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 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

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.

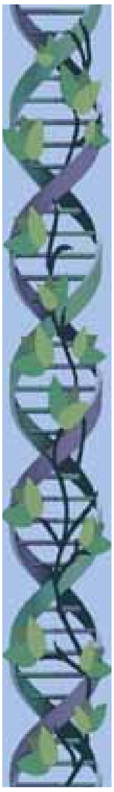
Determination of the actual number of specific CWR genetic reserves will ultimately be pragmatic—dictated by the resources available for *in situ* CWR conservation as well as the size of the country and richness of its CWR flora. For example, in UK 17 sites in existing protected areas (nine in Special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

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 how the selection of priority crop gene pools to the prioritization of taxa within these gene pools and the application of *in situ* gap analysis to identify priority sites for inclusion in a global network of CWR genetic reserves. 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.

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

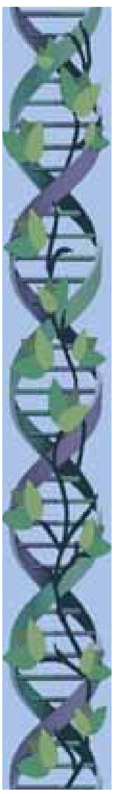
Within each crop gene pool, the wild relatives that are most closely related to the cultivated taxon are generally given priority over the more distantly related species because these are the taxa that can more easily be used in crop improvement using conventional breeding methods. However, we have also 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 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.

3.2.1 Rice

Scientific name

Oryza sativa L.

Principle synonyms

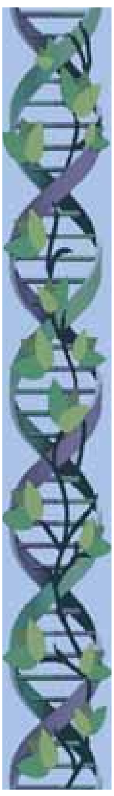
Padia meyeriana Zoll. & Moritzi, *Oryza formosana* Masamune & Suzuki

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 53ºN to 35ºS 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 previous identified by Cheng *et al*., 2002), and the third group contained the Australian species *O. meridionales* 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 & Shastry
- *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 A genome *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)

Trait	Donor species
Grassy stunt resistance	*O. nivara*
Bacterial blight resistance	*O. longistaminata* *O. officinalis* *O. minuta* *O. latifolia* *O. australiensis* *O. brachyantha*
Blast resistance	*O. minuta*
Brown plant hopper resistance	*O. officinalis* *O. minuta* *O. latifolia* *O. australiensis*
White-backed plant hopper resistance	*O. officinalis*
Cytoplasmic male sterility	*O. perennis* *O. glumaepatula*
Tungro resistance	*O. rufipogon* *O. rufipogon* *O. rufipogon*
Introgression lines under evaluation	
Yellow stem borer	*O. longistaminata* *O. rufipogon*
Sheath blight resistance	*O. minuta* *O. rufipogon*
Increased elongation ability	*O. rufipogon*
Tolerance of acidity and iron and aluminium toxicity	*O. glaberrima* *O. rufipogon* *O. rufipogon*
Resistance to nematodes	*O. glaberrima*

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*[4] and *O. schlechteri*[5]

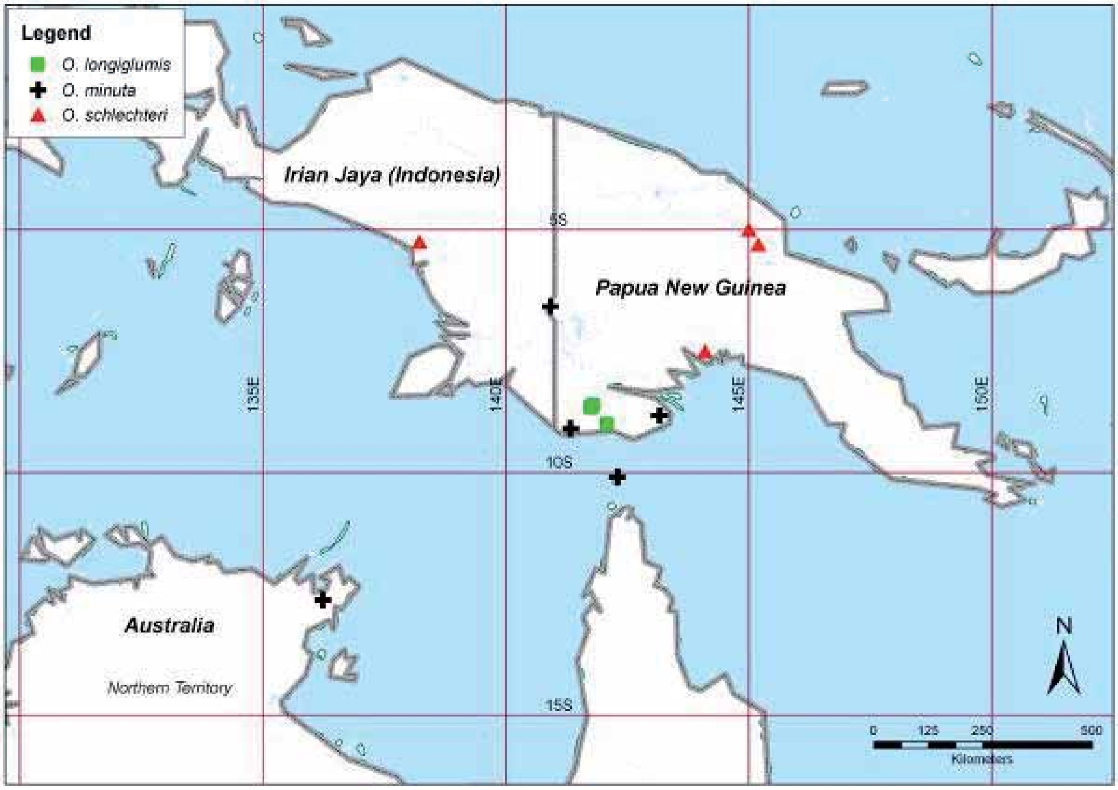
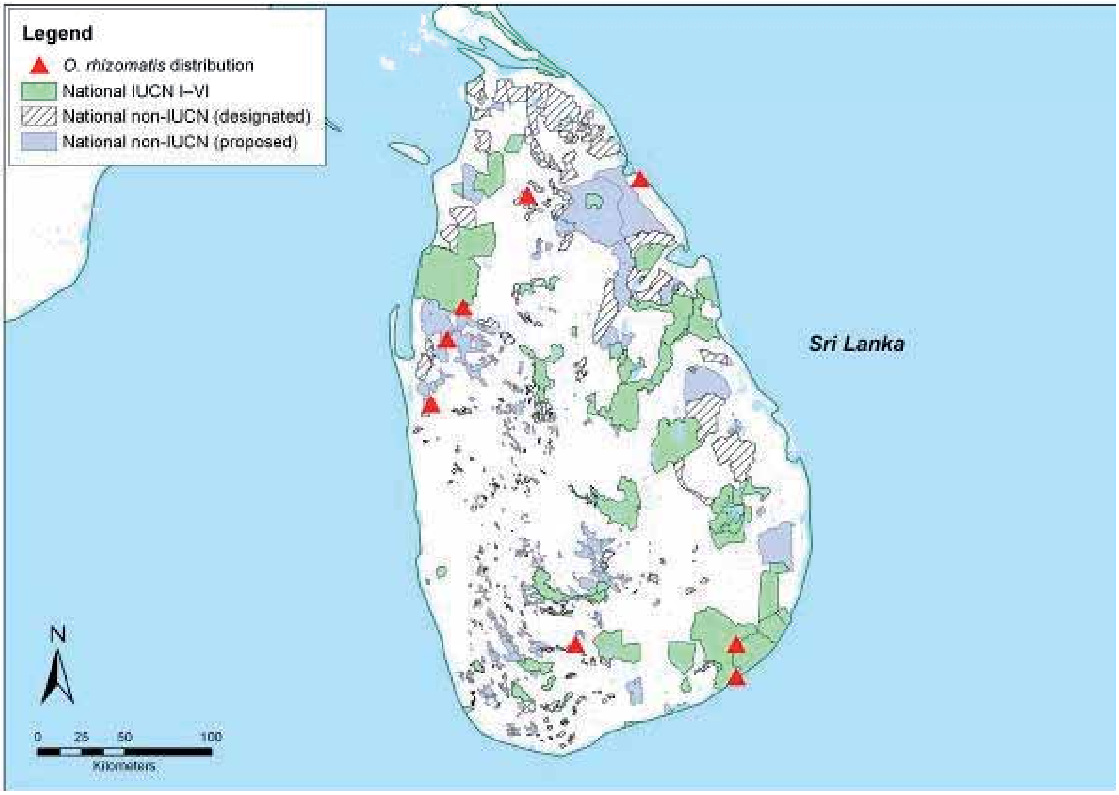


FIGURE 3

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[6].
- Wilpattu National Park (IUCN category II). *O. rhizomatis* has been recorded within the boundaries of this protected area[7].
- 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.
- Puwarasankulam Forest Reserve. *O. rhizomatis* has been recorded close to (outside) the north-eastern boundary of this protected area.

---

[4] *O. minuta* is also distributed in the Philippines, but coordinate data were not available for this study.

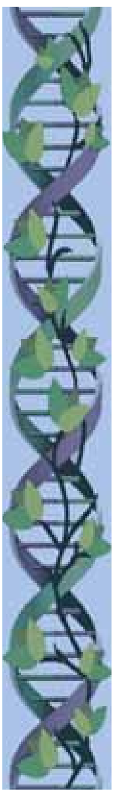
[5] Data sources – *O. longiglumis* and *O. minuta*: Plants of Papua New Guinea (accessed through GBIF data portal, http://data.gbif.org/datasets/resource/969 04/08/2008), Australian National Herbarium (CANB) (http://data.gbif.org/datasets/resource/47 04/08/2008), NSW herbarium collection (http://data.gbif.org/datasets/resource/968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

[6] *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)]

[7] *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)]

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

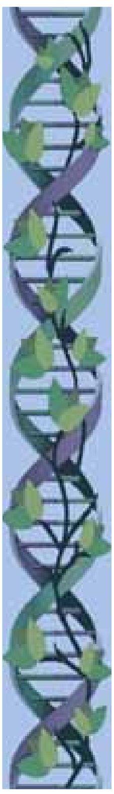
- *Triticum aestivum* subsp. *compactum*
    - subsp. *macha*
    - subsp. *spelta*
    - subsp. *sphaerococcum*

- *T. monococcum* subsp. *aegilopoides* (wild einkorn)
    - subsp. *monococcum* (cultivated einkorn)

- *T. timopheevii* subsp. *armeniacum*
    - 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; Peňa *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. *armeniacum*
- *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*

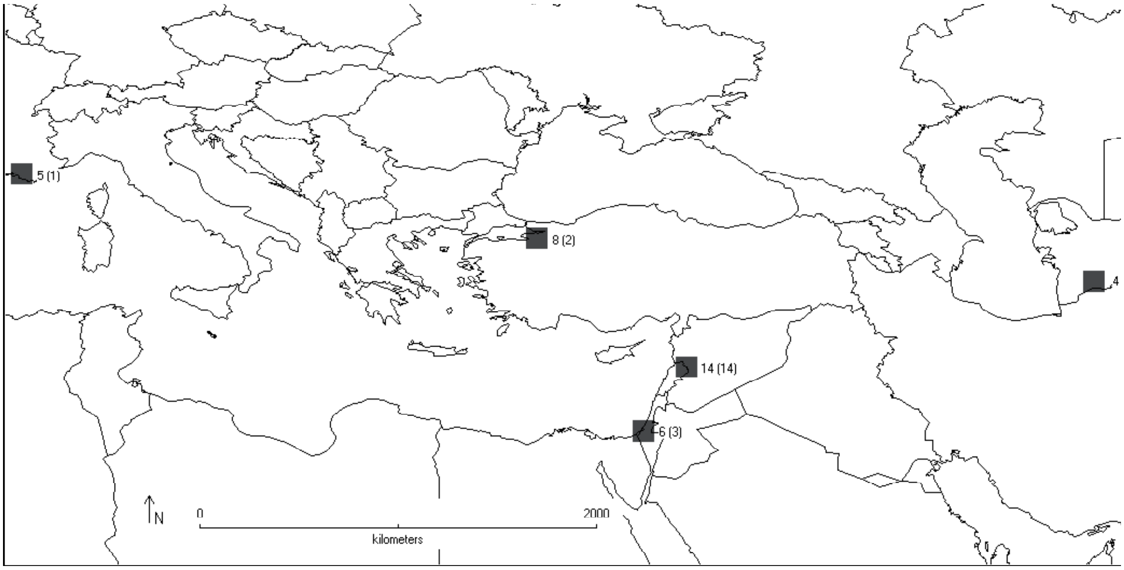
Priority sites

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 9 866 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):

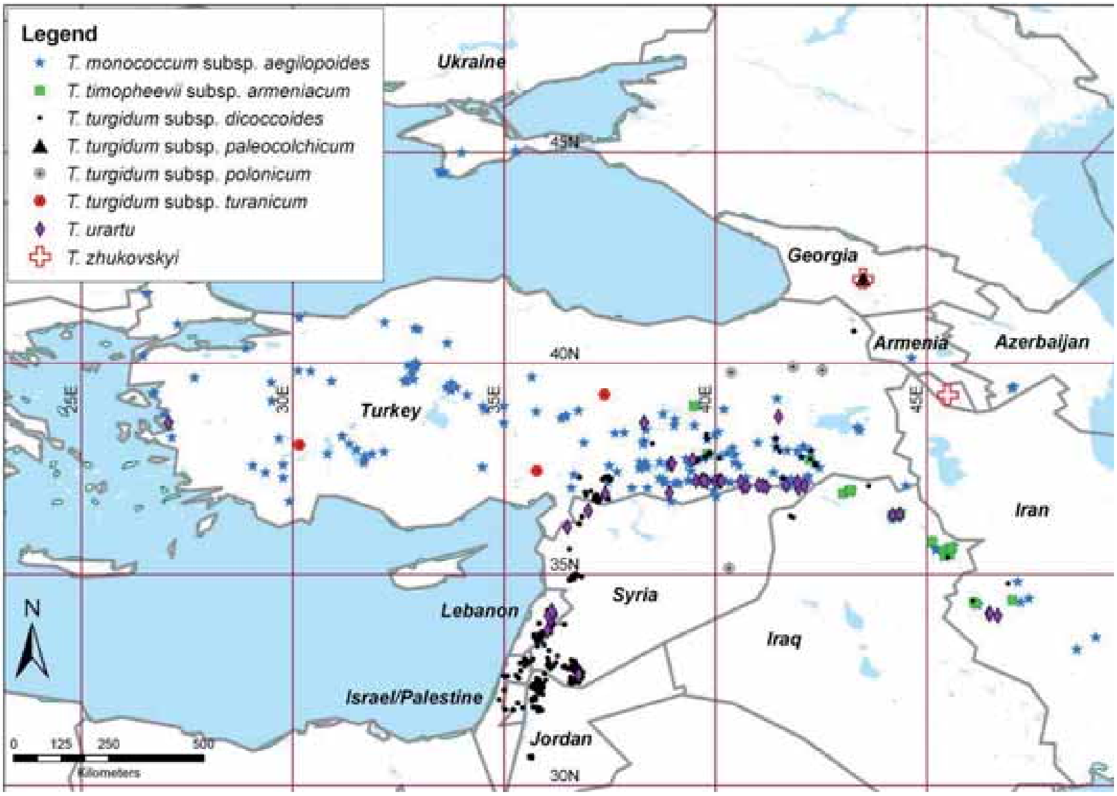
- Qal'at Al Hasn, Homs province, Syria. Maxted *et al*. (2008c) identified this location as the best option for a single reserve for *Aegilops* as it has the highest concentration of taxa (14). However, there are currently no protected areas in the vicinity and a recent study (Keisa *et al*., 2008) found 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 Qeriyyot 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. *armeniacum* and *T. urartu* have been recorded at these locations, which are currently not protected.
- Bakhtaran province, Iran. Populations of *T. timopheevii* subsp. *armeniacum, 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. *armeniacum* 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. *armeniacum* 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/1430 29/07/2008)

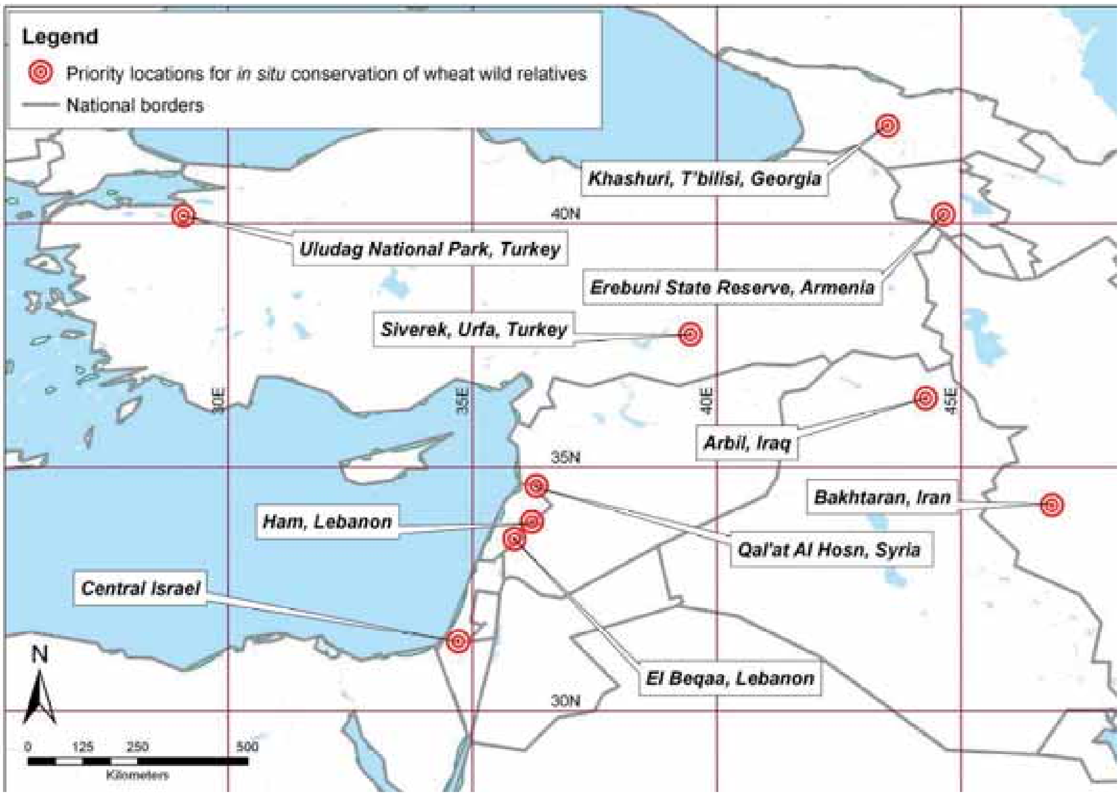


Recommendations

- Three reserves have been established in the centre of diversity specifically to conserve wild wheats—Ammiad 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 regions

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 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

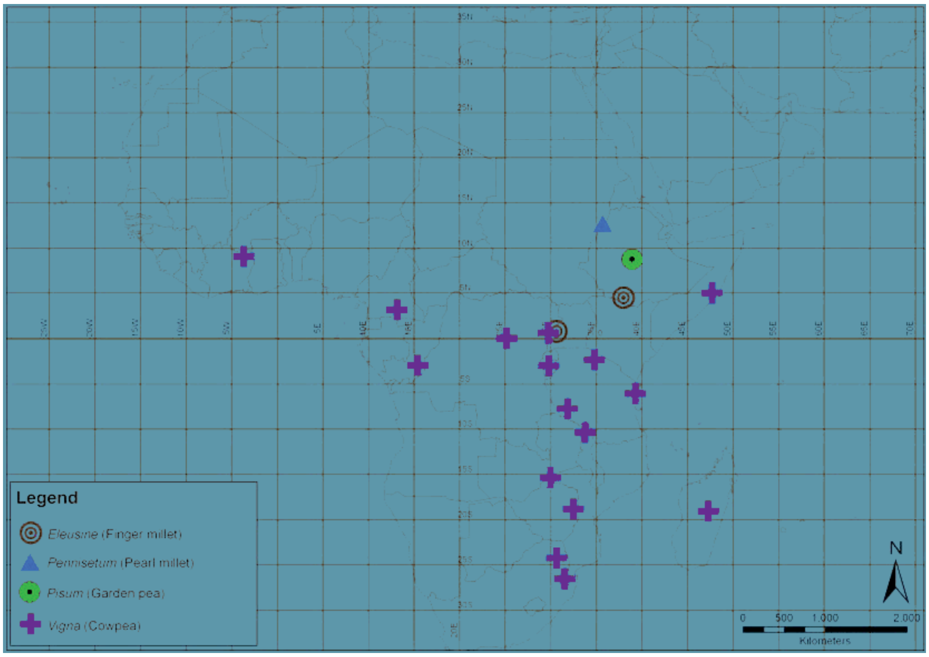


FIGURE 8

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

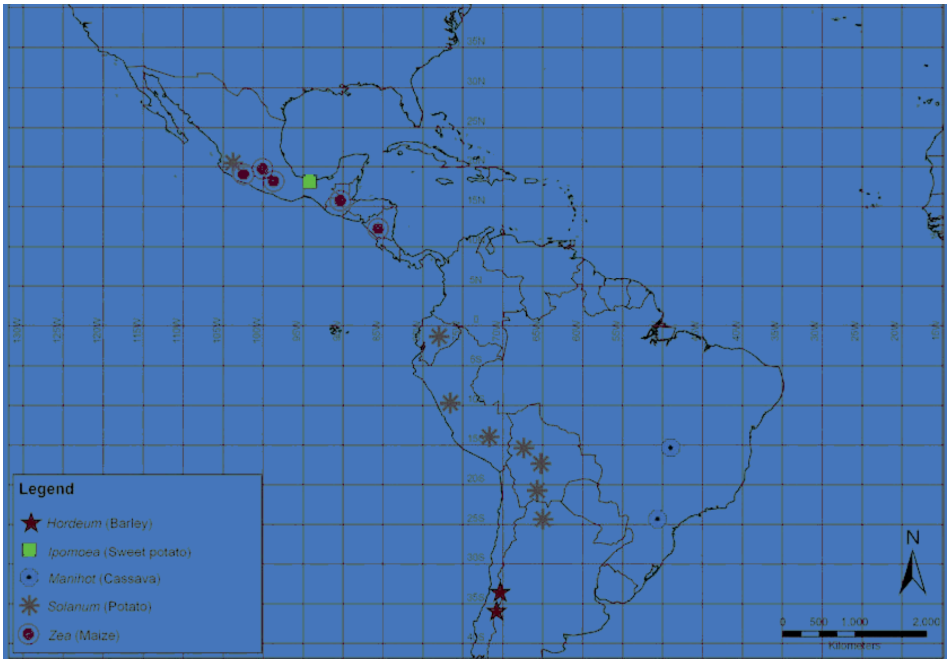
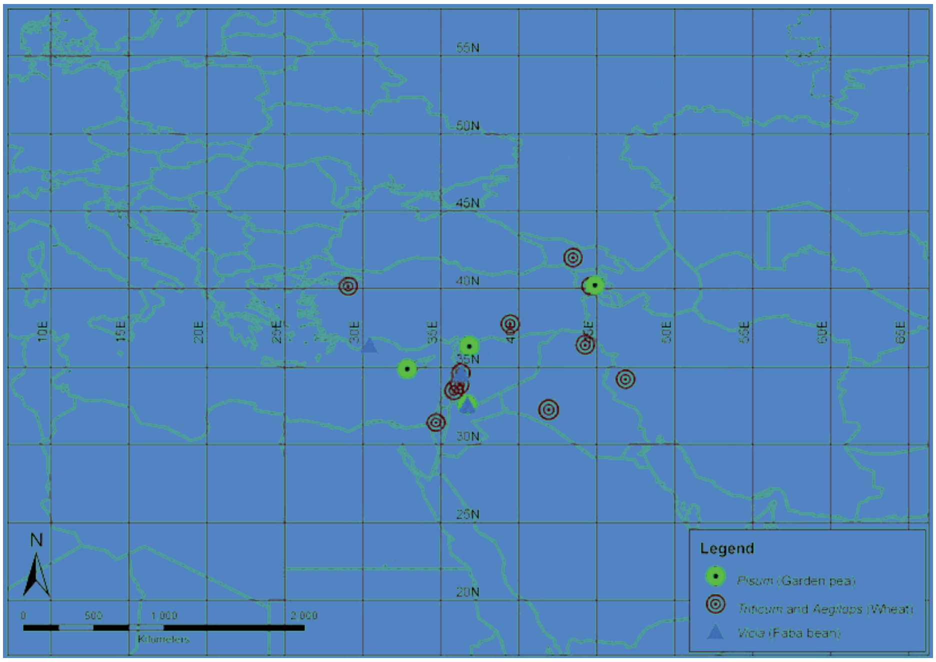


FIGURE 9

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



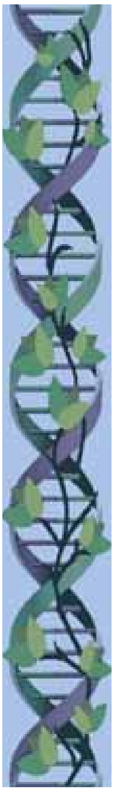
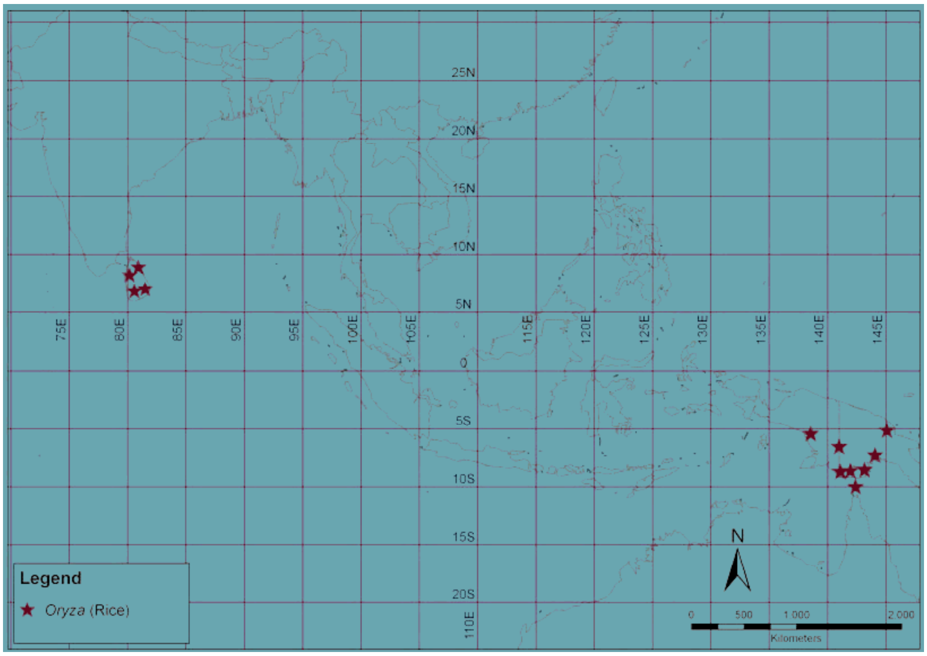


FIGURE 10

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



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* conservation CWR 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). 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.

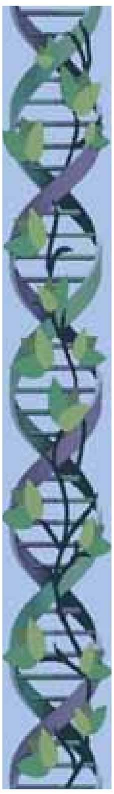
There are several high priority CWR taxa in the *Vigna* gene pool and they are widespread throughout sub-Saharan Africa. The taxa have restricted distributions and there is little overlap between them; therefore, opportunities for multi-taxon reserves for high priority *Vigna* wild relatives are limited. 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. tabascana* 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 Goias 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:

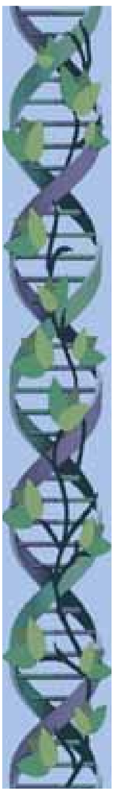
- Identification of the agency that will be responsible for developing and overseeing a global network once established, including on-going monitoring of the effectiveness of the individual sites;
- Negotiation with national protected area agencies to include their site in a global network and to ensure 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.

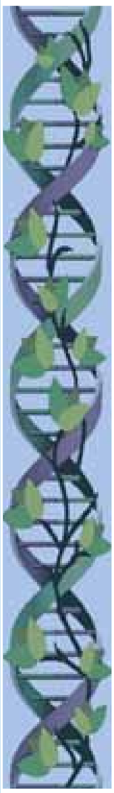
4.6 Improve information dissemination

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/cwris/cwris.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 5th 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 SSLP 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.

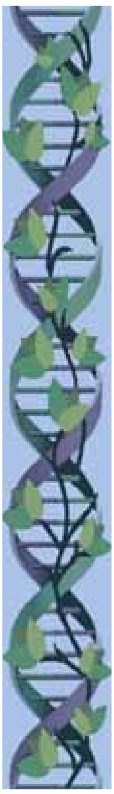
Bradshaw, J.E. and Ramsey, G. (2005). Utilization of the Commonwealth Potato Collection in Potato Breeding. *Euphytica* 146, 9–19.

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-Sanchez, 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]. [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 *Criteriia*: Version 3.1. IUCN Species Survival Commission. IUCN, Gland, Switzerland and Cambridge, UK. 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.

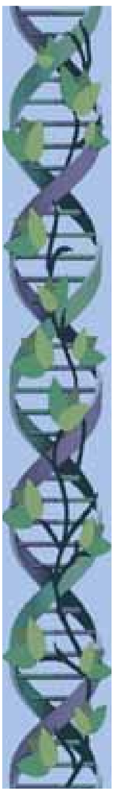
Jahier, J., Doussinault, G, Dosba, F. and Bourgeois, F. (1979), Monosomic analysis of resistance to eyespot in the variety "Roazon". In: Ramanujam S (ed.) Proceedings of 5th International Wheat Genetic Symposium. pp 437–440. Indian Society of Genetics and Plant Breeding, IARI, New Delhi, India.

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., Knüpffer, 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., Knüpffer, 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.

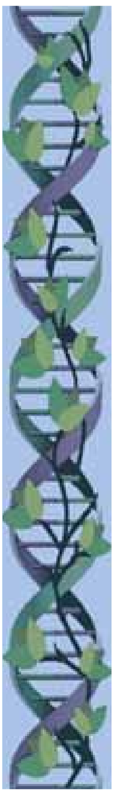
Linnaeus, C. (1753). Species Plantarum, edn. 1. 2: 996, 1050–1051. Salvius, Stockholm.

Lovisolo, 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 10th 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 [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.

Peňa, 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.

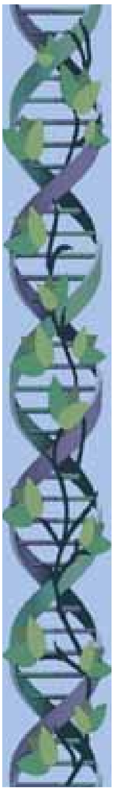
Phillips, S.M. (1972). A survey of the *Eleusine* Gaertn. (Gramineae) in Africa. Kew Bulletin, 27: 251–270.

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.

Rebelo, 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.

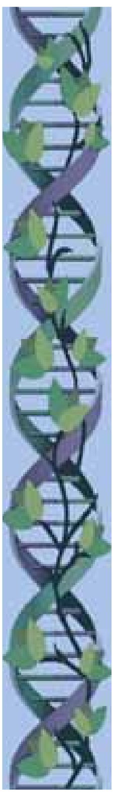
William, M.D.H.M., Peňa, R.J. and Mujeeb-Kazi, A. (1993). Seed protein and isozyme variations in Triticum tauschii (*Aegilops squarrosa*). Theoretical and Applied Genetics, 87: 257–263.

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.

ANNEXE 1: INTRODUCTION TO CROP WILD RELATIVES



1.1 Background and scope

Natural ecosystems hold important plant genetic resources for food and agriculture (PGRFA), including populations of crop wild relatives (CWR)—species that have particular value because of their potential to contribute beneficial traits to crops, such as pest or disease resistance, yield improvement or stability (Maxted *et al*., 2006). CWR species tend to contain greater genetic variation than crops themselves because they have not passed through the genetic bottleneck of domestication severely limiting the diversity available to breeders in crops such as maize, cassava, potato and banana/plantain and so present a reservoir of useful variation for crops (Vollbrecht and Sigmon, 2005). Feuillet *et al*. (2008) question the ability of breeders to increase or simply sustain crop yield and quality in the face of dynamic biotic and abiotic threats. They suggest that the increasing ease of gene discovery, the development of enabling genetic and breeding techniques and a better understanding of the previous limitations on exotic germplasm make CWR the obvious choice for meeting contemporary food security demands. Dwivedi *et al*. (2008) review the barriers to the use of CWR and how those barriers are being systematically overcome by technological advances.

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.

Climate change is predicted to increase average temperatures by 2–4°C over the next 50 years and cause considerable changes in regional and seasonal patterns of precipitation (IPCC, 2007). Within Europe, Thuiller *et al*. (2005) predict that by 2080 climate change will result in a 27–42% loss of species, with potential extremes ranging from 2.5–86% loss of current floristic diversity. The authors also predict immigration or emigration per 50 km^2 of between 45–63% (with extreme ranges of 17–86%). Further, they concluded that the greatest changes are expected in the transition between the Mediterranean and Euro-Siberian regions—the very region that contains the highest proportion of agronomically important taxa. There have been few studies of the likely impact 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. Interestingly, they also found that the results varied significantly between the three crop complexes, with the most deleterious impact on *Arachis* in which 24–31 (out of 50) species are predicted to go extinct and of the remaining species, their ranges are likely to decrease by 85–94% (Jarvis *et al*., 2008). The authors note that *Arachis* species are predicted to suffer higher extinction rates because they are predominantly distributed in flat regions where the horizontal displacement of climate is fastest and that this is further compounded by a slow potential migrational rate of 1 m per year. Looking at these figures, the loss of such a high number of species is extremely disturbing; however, the potential range decreases of 85–94% for extant *Arachis* spp. are also a grave concern because although it is unlikely that range loss is directly correlated to genetic diversity, range loss of this magnitude must question the viability of populations in terms of retaining sufficient genetic diversity to maintain the long-term survival of the species.

Climate change will undoubtedly alter the environmental conditions under which our crops grow, dramatically impacting agriculture and horticulture and leading to a critical demand for abiotic adaptive genes. 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. Failure to meet this challenge will have a devastating impact on the global economy and social well-being. Genetic diversity offers an insurance against the devastating impact of climate change and CWR are particularly 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, 2008).

However, the study and conservation of CWR diversity has yet to be addressed systematically; a position little changed since Darwin (1868) observed "*… it appears strange to me that so many of our cultivated plants should still be unknown or only doubtfully known in the wild state*".

It is estimated that between 2–6% of global genebank *ex situ* collections are CWR and of the total number of CWR species, only about 6% have any accessions conserved *ex situ*. Apart from a few notable exceptions, such as the activities of 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 because most of the world's national parks and other protected areas were not established to conserve PGRFA, but to conserve particular habitats or charismatic species. Therefore, CWR populations have rarely received specific attention in protected area management plans unless their conservation is coincident with other protected area priorities; for example, when they are valued because they are recognized as a nationally important rare or threatened species. Yet CWR species, like any other group of wild species, are subject to an increasing range of threats in their host habitats, and in many countries their conservation tends to fall between two conservation sectors—ecological conservation efforts are focused on rare or threatened wild species, while agricultural conservationists focus on crops; as a result, their conservation has been neglected. The time is now right to redress this neglect and implement systematic CWR conservation at the global, national and individual protected area levels.

In response to this issue, the Commission on Genetic Resources for Food and Agriculture has called for the development of a network of *in situ* conservation areas for CWR. The rolling *Global Plan of Action* for the conservation and sustainable utilization of plant genetic resources for food and agriculture includes conservation of CWR as a priority area, and Article 5 of the International Treaty on Plant Genetic Resources for Food and Agriculture (ITPGRFA) also promotes *in situ* conservation of CWR, including in protected areas. Moreover, the Commission has approved, with priority, a thematic background study on 'The conservation of crop wild relatives' to support the preparation of the Second Report of the *State of the World's Plant Genetic Resources for Food and Agriculture*, as a basis for updating the *Global Plan of Action*.

The Commission is now establishing a Multi-Year Programme of Work, which represents a unique opportunity for the Commission to plan for the establishment, development and monitoring of a network of *in situ* conservation areas for CWR. The objective of this study is to provide sufficient baseline information for planning future work of the Commission, in particular:

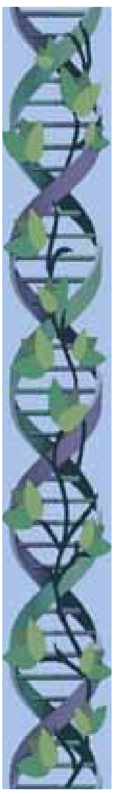
- Identify which important areas for CWR are already part of existing protected areas, in particular in the centres of origin or diversification;
- Pinpoint existing conservation gaps, in order to assess which important areas for CWR are yet to be protected within and outside existing protected areas;
- 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 and how complementary conservation can be achieved. Part 2 provides elements for 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 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 reviews current initiatives and future needs for CWR conservation, stressing the need for a coordinated and collaborative approach; in particular, at regional level. In this context, the recently proposed Global Strategy for Crop Wild Conservation and Use is introduced, which will underpin regional and national efforts to promote both the conservation and sustainable utilization of CWR diversity.

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. It outlines the basis for action at national, regional and global levels, but also for further research where needed. In Part III of this report, which addresses 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. The information presented is based on scientific data only—individual nations have not been taken into account; therefore, not all countries will be highlighted. However, this does not negate the need for those countries that do not feature in this report to develop national CWR strategies.

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 step in initiating further research and formulating detailed action plans for their conservation. The case studies presented can also be used as templates for investigations into further crop groups.

Finally, 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 are species closely related to crops, including crop progenitors, and are defined by their potential ability to contribute beneficial traits to crops such as pest or disease resistance, yield improvement or stability. Almost all modern varieties of crops contain some genes derived from a CWR. Notably, De Candolle (1855) and Darwin (1868) discussed the origin of cultivated plants and recommended the study of related CWR species, but it was the Russian botanist Nikolai Ivanovich Vavilov who fully recognized and championed the potential of CWR for crop improvement in the 1920s and 30s, referring to the use of wild *Aegilops, Secale, Haynaldia* and *Agropyron* species in wheat breeding for example (Vavilov, 1949). Subsequently, CWR were first routinely used by agricultural scientists to improve major crops in the 1940s and 50s, and by the 1960s and 70s this practice was leading to some major breeding improvements (Meilleur and Hodgkin, 2004). CWR are now identified 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, 1986; Hoyt, 1988; Maxted *et al*., 1997a; Meilleur and Hodgkin, 2004; Stolten *et al*., 2006). However, CWR, like any other group of wild species, are subject to an increasing range of threats in their host habitats and more systematic attention to their conservation is required (FAO, 1996; 1998).

It is clear that there has been increasing interest in CWR conservation and use in recent years and it seems likely that this has arisen from increased valuation associated with the recognition that:

1. CWR themselves are increasingly threatened by the loss, degradation and fragmentation of their natural habitats;
2. CWR are often associated with disturbed habitats and these habitats are not being adequately conserved by ecosystem conservation agencies;
3. Both CWR taxonomic and genetic diversity is likely be particularly threatened by climate change due to their common reliance on disturbed habitats and the lack of resilience of these habitats;
4. If crops are to maintain or increase production levels there is a need for new trait diversity outside that which has been historically used by farmers and plant breeders—CWR offer the necessary, novel genetic diversity that can enhance crop productivity or commodity improvement, promote disease and pest resistance and increase tolerance of adverse or marginal environments;
5. Globally, agriculture is being practiced in more adverse or marginal environments, whether due to human degradation of habitats or the demand for food forcing the expansion of agricultural lands—the desired traits to grow crops in these environments are found in CWR species;
6. The conservation of CWR in existing protected areas offers an additional ecosystem service to the protected areas themselves, so for limited additional resource commitment the perceived value of the protected areas can be significantly enhanced;
7. There is a continuous and growing demand for novel diversity by breeders to be used in the development of new varieties due to the relatively short-term commercial lifespan of modern cultivars (usually 5–10 years);
8. Conventional and biotechnological breeding techniques have improved dramatically in recent years enabling more precise targeting of desirable traits, relatively easy transfer to the crop and less problems with the transfer of unwanted characteristics.

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

Development in the biotechnology industries has also allowed the transfer of genes from more distantly related species, further enhancing the value of CWR—both those closely and more distantly related (see Hajjar and Hodgkin, 2007; Hodgkin and Hajjar, 2008). CWR have contributed significantly to improving food production; for example, Prescott-Allen and Prescott Allen (1986) calculated that the yield and quality contribution to US grown or imported crops was over US$ 350 million a year. Phillips and Meilleur (1998) noted that losses of rare wild plants represent a substantial economic loss to agriculture, estimating that the endangered food crop relatives have a worth of about US$ 10 billion annually in wholesale farm values. Further, Pimentel *et al*. (1997) estimated that if the contribution of genetic resources to yield increase is about 30% of production and that a significant amount of this is due to wide crosses with wild accessions, then the introduction of new genes from wild relatives contributes approximately US$ 20 billion toward increased crop yields per year in the United States and US $115 billion worldwide. As a specific crop-based 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 wild varieties of Mexican maize (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, 2007). 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).

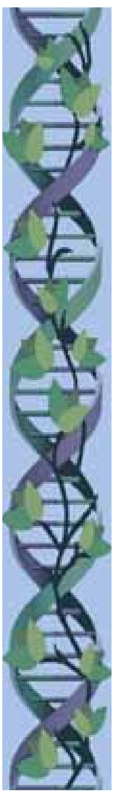
Gene introductions have tended to be most effective when the wild species are close relatives of the crop, or are even direct ancestors of it. Although historically trait transfer from CWR to crops has often been seen as difficult due to cross incompatibility, hybrid sterility and linkage drag (Stebbins, 1958; Zeven *et al*., 1983), recent technological advances have improved the ease of transfer of traits between distantly related species and expanded the value of CWR by increasing their usefulness into the secondary and tertiary crop gene pools (Meilleur and Hodgkin, 2004). Tanksely and McCouch (1997) argued that breeders were not fully exploiting the potential of CWR. Historically, breeders relied on searching for specific beneficial traits associated with particular CWR taxa rather than searching more generally for beneficial genes, and they avoided transfer into polyploid crops where transfer was more difficult (e.g., rice, sorghum and sweet potato). Hodgkin and Hajjar (2008) surveyed the use of CWR in crop improvement in the last 20 years and found that approximately 80% of all beneficial traits introduced from CWR were for pest or disease resistance and the remaining 20% were made up by abiotic stress tolerance, improvement of quality (e.g., colour, size and protein content), cytoplasmic male sterility/fertility and to a far lesser degree, yield improvements. Hajjar and Hodgkin (2007) comment that although quantitative trait loci have been identified in many CWR species, the potential to exploit them as a breeding resource using new molecular technologies has yet to be fully realized. Although this is likely to improve with time, it does underpin the need for the continued availability of a broad range of CWR diversity, also emphasizing the conservation–use linkage and the need for the conservation community to meet the evolving needs of CWR user groups.

Table 1 provides further examples of the use of CWR in crop improvement programmes for 29 major crops. Based on this sample of CWR use, which is not in itself comprehensive, it is interesting to note:

- The extent of CWR use: for the 29 crop species included, there are 234 references that report the identification of useful traits in 183 CWR taxa.
- Although 234 references are cited in Table 1, these are primarily published journal papers and we do not know how close a correlation there is between the data presented in journal papers and actual use of CWR in commercial crop breeding (just because we know a useful trait is present in a CWR and it can be transferred to a crop it does not mean that this exercise resulted in a novel variety). It would also be very difficult to give a precise estimate of CWR use by breeders because the data are likely to be commercially sensitive and therefore not readily available; however, it is thought to be significant (see Table 2).
- The degree to which breeders use CWR species varies between crops. CWR use is particularly prominent in barley, cassava, potato, rice, tomato and wheat, but rice and wheat are the crops in which CWR have been most widely used, both in terms of number of CWR taxa used and successful attempts to introgress traits from the CWR to the crop.
- The exploitation of the potential diversity contained in CWR species remains hit and miss as the approach by breeders to CWR use has not been systematic or comprehensive; therefore, the vast majority of CWR diversity remains untapped for utilization.
- The number of publications for the papers detailing use of CWR in breeding has increased gradually over time, presumably as a result of technological developments for trait transfer, with 2% of citations recorded prior to 1970, 13% in the 1970s, 15% in the 1980s, 32% in the 1990s and 38% after 1999.
- The most widespread CWR use has been and remains in the development of disease and pest resistance, with the references citing disease resistance objectives accounting for 39%, pest and disease resistance 17%, abiotic stress

13%, yield increase 10%, cytoplasmic male sterility and fertility restorers 4%, quality improvers 11% and husbandry improvement 6% of the reported inter-specific trait transfers.

- It can also be seen that since the year 2000 the number of attempts to improve quality, husbandry and end-product commodities has increased substantially.



1.3 Definition of a crop wild relative

CWR are wild plant species related to a crop, but what actually constitutes a CWR and how closely related to a crop does a taxon have to be to be considered a CWR? 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. Therefore, within the utilitarian sense of global conservation in relation to meeting requirements for food and agriculture it seems likely that inter-species exploitation will remain primarily focused on CWR for the majority of national breeding programmes. It is therefore important that we apply an accurate definition of the relationship between a crop and its close wild relatives, so that conservationists competing for limited resources may objectively prioritize taxa for study (Kell *et al*., 2003; Meilleur and Hodgkin, 2004; Maxted *et al*., 2006).

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 wide range 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*., 2008). Therefore, there is a need to estimate the degree of CWR relatedness to enable limited conservation resources to be focused on priority species—those most closely related to the crop.

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). Interestingly, Harlan and de Wet (1971) in fact commented in their paper that GP2 may be equated to the whole genus of the crop. This simple application of the Gene Pool concept is applicable to crop complexes where hybridization experiments have been performed and the pattern of genetic diversity within the gene pool is well understood, so that the gene pools can be clearly defined. However, for the majority of crop complexes, particularly those in the tropics, the wild species related to crops have been described and classified using a combination of morphological characteristics; therefore, the degree of reproductive differentiation among species remains unknown, making application of the Gene Pool concept *sensu* Harlan and de Wet (1971) impossible.

TABLE 1

Examples of the transfer of CWR traits to crops [8,9]

Crop	CWR	Application(s)	Reference(s)
Peanut (*Arachis hypogaea*)	*A. appressipila, A. paraguariensis*	Early leaf spot resistance	ICRISAT (1995), Stalker *et al.* (2002a)
	A. cardenasii	Multiple disease and insect resistance	Reddy *et al.* (1996)
		Root knot nematode resistance	Simpson and Starr (2001), Stalker *et al.* (2002b)
		Corn earworm, potato leaf hopper and southern corn rootworm	Stalker and Lynch (2002)
	A. kempff-mercadoi	Multiple disease and insect resistance	Mallikarjuna *et al.* (2004)
Oat (*Avena sativa*)	*A. sterilis*	Rust resistance	Prescott-Allen and Prescott-Allen (1986)
	A. sterilis	Yield improvement	Frey (1976), Takeda and Frey (1976)
	A. macrostachya	Powdery mildew resistance	Herrmann (2006)

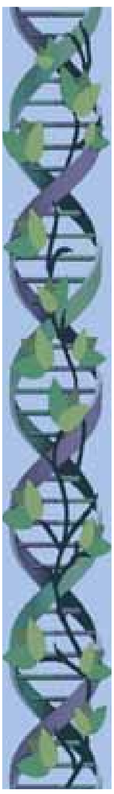
---

[8] Further discussion of CWR use is included in the individual CWR crop case studies presented in Part 3.

[9] This table incorporates citations previously included in Prescott-Allen and Prescott-Allen (1986), Kameswara Rao et al. (2003), Hajjar and Hodgkin (2007), Hodgkin and Hajjar (2008), Dwivedi et al. (2008), and from personal study.

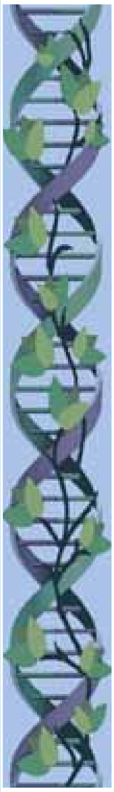
Crop	**CWR**	**Application(s)**	**Reference(s)**
Beets (*Beta vulgaris*)	*B. maritima*	Leaf spot resistance	Prescott-Allen and Prescott-Allen (1986)
	B. patellaris, B. procumbens, B. webbiana	Sugar beet nematode resistance	Prescott-Allen and Prescott-Allen (1986)
Oil-seed rape (*Brassica napus*)	*B. rapa, B. oleracea*	Seed yield	Osborn *et al*. (2007)
Pigeon pea (*Cajanus cajan*)	*Atylosia scarabaeoides*	Protein improvement	Reddy *et al.* (1979)
	C. cajanifolious	Nuclear male sterility	Mallikarjuna and Saxena (2005)
Pigeon pea (*Cajanus cajan*)	*C. cajanifolious, C. scarabaeoides, C. sericeus, C. volubilis*	Cytoplasmic male sterility	Ariyanayagam *et al*. (1995), Wanjari et al. (2001), Saxena and Kumar (2003), Saxena *et al*. (2005)
	C. lineatus	Cleistogamy	Saxena *et al*. (1998)
	C. scarabaeoides	Dwarfism	Reddy (1990)
Pepper (*Capsicum annuum*)	*C. frutescens*	Yield improvement	Rao *et al*. (2003)
Chickpea (*Cicer arientinum*)	*C. echinospermum, C. reticulatum*	Yield improvement	Singh and Ocampo (1997), Malhotra *et al*. (2003), Singh *et al.* (2005)
	C. echinospermum, C. reticulatum	Cyst nematodes, drought and cold tolerance	Malhotra *et al.* (2003)
	C. judaicum	Fusarium wilt	Prescott-Allen and Prescott-Allen (1986)
	C. pinnatifidum	Ascochyta blight resistance	Mallikarjuna (1999)
	C. reticulatum	Ascochyta blight resistance	Hawtin (1979), van der Maesen (1979), Singh *et al.* (2005)
		Drought and temperature tolerance	Hajjar and Hodgkin (2007)
Coffee (*Coffea arabica*)	*C. canephora, C. liberica*	Coffee rust resistance	Prescott-Allen and Prescott-Allen (1988)
Soyabean (*Glycine max*)	*G. soja*	Cold tolerance and early ripening	Budin (1973), Sun *et al.* (1997), Zhao and Gai (2006)
	G. soja	Protein content	Diers *et al*. (1992), Sebolt *et al.* (2000)
	G. soja	Yield improvement	Concibido *et al.* (2003)
	G. tomentella	Soybean cyst nematode resistance	Riggs *et al.* (1998)
Cotton (*Gossypium barbadense*)	*G. anomalum*	Bacterial blight resistance	Williams *et al.* (1975)
Sunflower (*Helianthus annuus*)	*H. paradoxus*	Salt tolerance	Lexer *et al.* (2004)
Sunflower (*Helianthus annuus*)	*H. petiolaris*	Cytoplasmic male sterility	Prescott-Allen and Prescott-Allen (1986)
	H. praecox	Downy mildew, rust, verticillium wilt and broomrape resistance	Hajjar and Hodgkin (2007)
	H. tuberosus	Broomrape resistance	Putt (1978)
Barley (*Hordeum vulgare*)	*H. bulbosum*	Powdery mildew resistance	Jones and Pickering (1978), Szigat and Pohler (1982), Gustafsson and Claësson (1988), Xu and Snape (1989), Xu and Kasha (1992), Pickering *et al.* (1995), Pickering and Johnston (2005),
	H. bulbosum	Mosaic virus resistance	Walther *et al.* (2000), Ruge *et al.* (2003), Ruge-Wehling *et al*. (2006)
	H. bulbosum	Leaf rust resistance	Walther *et al.* (2000), Zhang *et al*. (2001)
	H. bulbosum	Septoria resistance	Toubia-Rahme *et al.* (2003)
	H. bulbosum, H. brevisubulatum	Russian wheat aphid	Kindler and Springer (1991)
	H. chilense	Leaf rust	Patto *et al*. (2001), Martín and Cabrera (2005)
	H. spontaneum	Powdery mildew resistance	Fischbeck *et al*. (1976), Russell (1978), Moseman *et al*. (1983), Lehmann and von Bothmer (1988), von Korff *et al.* (2005)
	H. spontaneum	Yield improvement	Vega and Frey (1980), Matus *et al*. (2003), Pillen *et al*. (2003), von Korff *et al*. (2006)
	H. spontaneum	Drought and temperature tolerance	Hadjichristodoulow (1993), Eglinton *et al*. (2001), Baum *et al*. (2003), Talame *et al*. (2004), Hajjar and Hodgkin (2007), Chen *et al*. (2008)
Sweet potato (*Ipomoea batatas*)	*I. trifida*	Root knot nematode and root lesion nematode resistance	Sakamoto (1976)
Lettuce (*Lactuca sativa*)	*L. serriola*	Downy mildew resistance	Hooftman *et al*. (2007)
Lettuce (*Lactuca sativa*)	*L. virosa*	Leaf aphid resistance	Eenink *et al*. (1992)

Crop	CWR	Application(s)	Reference(s)
Tomato (*Lycopersicon esculentum*)	*L. cheesmanii, L. pennellii, L. peruvianum*	Various forms of resistance, drought and salinity tolerance, soluble solids, insect resistance	Stevens and Rick (1986), Rick and Chetelat (1995)
	L. chilense	Tomato yellow leaf curl virus	Zamir *et al*. (1994)
	L. chmielewskii	Soluble solids	Stevens and Rick (1986)
	L. hirsutum, L. pimpinellifolium	Improved processing ability	Tanksley *et al*. (1996), Bernacchi *et al*. (1998)
	L. pimpinellifolium	Wilt causing fungus	Porte and Walker (1945)
		Quality control characters	Tanksley and McCouch (1997)
	L. pimpinellifolium	Fruit size and shape	Tanksley *et al*. (1996)
	L. pimpinellifolium	Disease resistance, early maturity, determinate growth habit, parthenocarpy, soluble solids	Stevens and Rick (1986)
Cassava (*Manihot esculenta*)	*M. aesculifolia*	Robustness	Jennings (1995)
	M. angustiloba	Drought tolerance	Jennings (1995)
	M. caerulescens, M. catingae, M. dichotoma, M. epruinosa, M. esculenta var. flabellifolia, M. esculenta var. peruviana, M. glaziovii, M. pseudoglaziovii, M. tristis	Cassava mosaic disease resistance	Unnikrishnan *et al*. (2007), Nair and Unnikrishnan (2007)
	M. carthagenensis	Improved protein content	Lopez and Herrera (1970)
	M. davisiae	Drought tolerance	Jennings (1995)
	M. glaziovii	Improved protein content	Prescott-Allen and Prescott-Allen (1988)
	M. glaziovii	Cassava mosaic disease and cassava bacterial blight resistance	Akano *et al*. (2002), Nweke (2004), Nassar (2007)
	M. neusana	Apomixis	Nassar (2000), Nassar *et al*. (2000)
Cassava (*Manihot esculenta*)	*M. oligantha*	Quality control characters, improved protein content	Nassar and Dorea (1982), Nassar (2003)
	M. rubricaulis	Adaptation to high altitudes and cool temperatures	Jennings (1995)
	M. saxicola, M. tristis	Cassava mosaic disease resistance, cassava bacterial blight resistance and decreased cyanide content	Hanh *et al*. (1980)
	M. tristis	Improved protein content	Asiedu *et al*. (1992)
	M. walkerae	Post-harvest physiological deterioration tolerance	CIAT (2006)
Apple (*Malus domestica*)	*M. baccata*	Cold tolerance	Cummins and Aldwinckle (1979)
	M. baccata, M. zumi	Podaspaera leucotricha resistance	Alston (1977)
	M. floribunda	Apple scab resistance	Brown (1975)
Tobacco (*Nicotiana tabacum*)	*N. debneyi*	Black root rot resistance	Prescott-Allen and Prescott-Allen (1986)
	N. glutinosa	Tobacco mosaic virus resistance	Prescott-Allen and Prescott-Allen (1986)
	N. longiflora	Angular leaf spot, black shank and wildfire resistance	Prescott-Allen and Prescott-Allen (1986)
	N. longiflora	Tobacco mosaic virus resistance	Prescott-Allen and Prescott-Allen (1986)
	N. plumbaginifolia	Wildfire and black shank resistance	Russell (1978)
Banana and plantain (*Musa acuminata, Musa balbisiana*)	*M. acuminate subsp. malaccensis, subsp. banksii, subsp. errans, subsp. burmannica*	Bacterial and fusarial wilt, sigatoka, and burrowing nematode resistance	Novak (1992), Vuylsteke *et al*. (1993)
	M. balbisiana, M. nagensium	Drought resistance	INIBAP/IPGRI (2006)
	M. basjoo, M. sikkimensis	Abiotic stress (such as cold tolerance) resistance	INIBAP/IPGRI (2006)
	M. itinerans	Water-logging resistance	INIBAP/IPGRI (2006)
Rice (*Oryza sativa*)	*O. australiensis*	Brown plant-hopper resistance, bacterial blight	Ishii *et al*. (1993), Multani *et al*. (1994)
	O. brachyantha	Bacterial blight	Khush *et al*. (1990), Brar *et al*. (1996)
	O. glaberrima	Stress tolerance, nutritional and grain quality improvement	IRRI (2007)
	O. grandiglumis	Grain quality improvement	Yoon *et al*. (2005)



Crop	CWR	Application(s)	Reference(s)
Rice (*Oryza sativa*)	*O. glumaepatula*	Yield improvement	Brondani and Ferreira (2002)
	O. glumaepatula, O. parennis	Cytoplasmic male sterility	Dalmacio *et al*. (1995), Dalmacio *et al*. (1996)
	O. longistaminata	Drought resistance and yield increase	Brar (2005)
	O. longistaminata, O. nivara,		
O. officinalis, O. rufipogon	*Grassy stunt virus, bacterial blight, brown plant-hopper resistance, white-backed plant hopper*	Jena and Khush (1990), Khush *et al*. (1990), Brar *et al*. (1996), Brar and Khush (1997), Xiao *et al*. (1998)	
	O. minuta	Bacterial blight	Amante-Bordeos *et al*. (1992)
	O. minuta	Improved agronomic traits	Xing *et al*. (2004)
	O. nivara	Grassy stunt virus resistance	Khush *et al*. (1977), Barclay (2004)
	O. nivara, O. rufipogon	Grassy stunt virus resistance	Prescott-Allen and Prescott-Allen (1988)
	O. nivara, O. rufipogon	Cytoplasmic male sterility	Hoan *et al*. (1997)
	O. ridleyi	Bacterial blight, tungro, yellow stem borer and leaf-folder resistance	IRRI (2004)
	O. rufipogon	High acidic-sulphate content soil tolerance	Brar and Khush (1997), Nguyen *et al*. (2003)
	O. rufipogon	Yield improvement	Xiao *et al*. (1996), Xiao *et al*. (1998), Brar and Khush (1997), Moncada *et al*. (2001), Septiningsih *et al*. (2003), Thomson *et al*. (2003), Lee *et al*. (2004), Lee *et al*. (2005), Liang *et al*. (2004), Marri *et al*. (2005), Tian *et al*. (2006)
	O. rufipogon	Rice stripe necrosis virus, soil-borne diseases	Martinez *et al*. (2002)
	O. rufipogon	Aluminium toxicity tolerance	Nguyen *et al*. (2003)
	O. rufipogon	Drought resistance	Zhang *et al*. (2006)
	O. sativa f. spontanea	Cytoplasmic male sterility	Lin and Yuan (1980), Virmani and Shinjyo (1988)
Finger millet (*Pennisetum glaucum*)	*P. glaucum subsp. monodii*	Rust and leaf spot resistance via Pyricularia grisea resistance	Hammons (1970), Wilson *et al*. (1991), Hanna (1992), Wilson and Gates (1993)
	P. glaucum subsp. monodii	Male sterility	Hanna (1989)
	P. glaucum subsp. monodii	Dry matter improvement	Bramel-Cox *et al*. (1986), Hanna (1997), Hanna (2007)
	P. glaucum subsp. monodii	Extend the growing period	Hanna (2007)
	P. glaucum subsp. monodii, subsp. stenostachyum	Striga resistance	Wilson *et al*. (2000)
	P. orientate, P. squamulatum	Earliness, long inflorescence, leaf size and male fertility improvement	Dujardin and Hanna (1989)
	P. purpureum	Pest resistance, vigorous growth and forage yield	Hanna (1997)
Common bean (*Phaseolus vulgaris*)	*P. coccineus, P. costaricensis, P. polyanthus*	Angular leaf spot, ascochyta blight, bean green mosaic virus, bean yellow mosaic virus, root rots, white moulds and cold resistance	
	Singh (2001)		
	Phaseolus vulgaris var. aborigineus	Yield and yield components	Blair *et al*. (2003), Blair *et al*. (2006)
Pea (*Pisum sativum*)	*P. abyssinicum*	Pea bacterial blight resistance	Elvira-Recuenco (2000), Elvira-Recuenco *et al*. (2003), Hollaway *et al*. (2007)
	P. fulvum	Yield improvement	Prescott-Allen and Prescott-Allen (1988)
	P. fulvum	Improved freezing ability, disease (Ascocyta pisi and Erysipi pisi) and pest resistance (bruchids)	Forster *et al*. (1999)
	P. fulvum	Powdery mildew resistance	Fondevilla *et al*. (2007)
	P. fulvum	Pea weevil resistance	Clement *et al*. (2002)
	P. fulvum	Ascochyta blight resistance	Wroth (1998)

Crop	CWR	Application(s)	Reference(s)
Sugar cane (*Saccharum officinarum*)	*S. robustum*	Plant vigour and stalk thickness	Prescott-Allen and Prescott-Allen (1986)
	S. spontaneum	Red rot, smut and sugarcane mosaic virus resistance	Prescott-Allen and Prescott-Allen (1986)
Potato (*Solanum tuberosum*)	*S. acaule*	Potato X virus resistance and potato leaf roll virus resistance	Ross (1979), Bradshaw *et al.* (2006)
	S. acaule	Frost resistance	Hawkes *et al.* (2000)
	S. acaule, S. chacoense, S. spegazzinii, S. vernei	Virus and pest resistance	Ross (1986)
	S. bulbocastanum	Late blight resistance	Hodgkin and Hajjar, 2008
	S. chacoense	Virus resistance	Bradshaw *et al.* (2006)
	S. demissum	Late blight resistance	Ross (1986), Löve (1999), Bradshaw *et al.* (2006)
	S. demissum, S. edinese	Late blight resistance	Hawkes (1979)
	S. kurtzianum, S. multidissectum, S. oplocense, S. spegazzinii, S. vernei	Cyst nematode resistance	Simmond (1995), Bradshaw and Ramsey (2005)
	S. megistacrolobum	Frost resistance	Hawkes *et al.* (2000)
	S. spegazzinii, S. vernei	Cyst nematode resistance	Ross (1979)
	S. pennellii	Yield improvement	Gur and Zamir (2004)
	S. stoloniferum	Potato Y virus resistance	Ross (1979)
	S. stoloniferum	Late blight resistance	Ross (1986), Bradshaw *et al.* (2006)
	S. tarnii	PVY, Colorado potato beetle and late blight resistance	Thieme *et al.*, 2008
	S. brevidens	Potato leaf roll virus resistance	Hawkes (1947), Estrada-Ramos (1991)
Sorghum (*Sorghum bicolor*)	*S. arundinaceum*	Yield improvement	Jordan *et al.* (2004)
	S. macrospermum	Sorghum midge resistance	Sharma and Franzmann (2001)
Sorghum (*Sorghum bicolor*)	*S. propinquum*	Yield improvement and early maturity	Hajjar and Hodgkin (2007)
	S. purpureosericeum subsp. dimidiatum	Sorghum shoot-fly resistance	Nwanze *et al.* (1990)
	S. verticilliflorum, S. virgatum	Yield improvement	Cox *et al.* (1984)
Wheat (*Triticum aestivum*)	*Ae. comosa, Ae. elongatum, Ae. speltoides, Ae. squarrosa, Ae. umbellulata, T. monococcum, T. timopheevii*	Yellow rust, stripe rust, stem rust, leaf rust	Goodman *et al.* (1987)
	Ae. cylindrica, Thinopyrum junceum	Salt tolerance	Farooq *et al.* (1992), Farooq *et al.* (1995), Wang *et al.* (2003)
	Aegilops spp., Thinopyrum spp., Elytrigia elongata, Hordeum spp.	Salt tolerance	Colmer *et al.* (2006)
	Ae. geniculata, Ae. squarrosa, Ae. Triaristata, Ae. ventricosa	Hessian fly	El Khlifi *et al.* (2004)
	Aegilops ovata	Common root rot	Bailey *et al.* (1993)
	Ae. sharonensis	Yellow rust resistance	Millet *et al.* (2008)
	Ae. speltoides	Leaf rust resistance	Millet *et al.* (2008)
	Ae. speltoides, Ae. tauschii	Septoria, stem rust, powdery mildew, eyespot and other disease resistances	Miller *et al.* (1987), Jahier *et al.* (1979), Lagudah and Appels (1993), Mujeeb-Kazi and Hettel (1995), Mujeeb-Kazi *et al.* (2001)
	Ae. speltoides, T. turgidum	Salt tolerance	Noori (2005)
	Ae. speltoides, T. turgidum subsp. dicoccoides	Superior quality, disease resistance and yield improvement	Mujeeb-Kazi *et al.* (1996)
	Ae. speltoides, T. turgidum subsp. dicoccoides	Yellow rust resistance	McIntosh *et al.* (1966), Dvorak (1977), Peng *et al.* (1999), Millet *et al.* (2008)
	Ae. speltoides, T. baeoticum	Yellow rust and leaf rust resistance, drought tolerance	Valkoun (2001),
	Ae. squarrosa	Hessian fly, green bug and rust resistance	Gill and Raupp (1987)

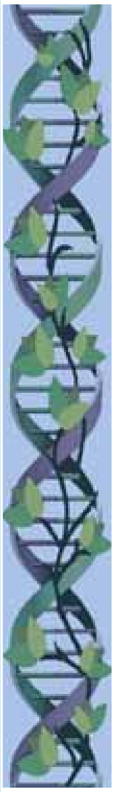


Crop	CWR	Application(s)	Reference(s)
Wheat (*Triticum aestivum*)	*Ae. squarrosa*	Hessian fly, leaf rust and soil-borne-mosaic virus resistance	Cox *et al.* (1990)
	Ae. tauschii	Drought tolerance	Gororo *et al.* (2002)
	Ae. tauschii	Hessian fly resistance	Cox and Hatchett (1994), Suszkiw (2005)
	Ae. tauschii	Karnal bunt	Villareal *et al.* (1996)
	Ae. tauschii	Quality-desirable glutenins improvement	William *et al.* (1993), Peňa *et al.* (1995)
	Ae. tauschii	Root knot nematode resistance	Raupp *et al.* (1993)
	Ae. tauschii	Rust	Kerber (1987), Cox *et al.* (1994), Cox *et al.* (1995)
	Ae. tauschii	Sprouting suppression	Xiu-Jin *et al.* (1997)
	Ae. tauschii	Wheat soil-borne mosaic virus, wheat spindle-streak mosaic virus	Cox *et al.* (1995)
	Ae. tauschii	Agronomic traits, yield improvement	Valkoun (2001), Pestsova *et al.* (2006)
	Ae. tauschii, T. turgidum	Yellow rust and leaf rust	Ma *et al.* (1995)
	Ae. tauschii, T. turgidum	Water-logging tolerance	Villareal *et al.* (2001)
	Ae. variabilis	Powdery mildew resistance	Spetsov *et al.* (1997)
	Ae. variabilis	Root-knot nematode resistance	Yu *et al.* (1990), Barloy *et al.* (2000)
	Ae. ventricosa	Cyst nematode resistance	Delibes *et al.* (1993)
	Ae. ventricosa	Eye spot resistance	Prescott-Allen and Prescott-Allen (1988)
	Agropyron elongatum, Ae. umbellulata	Leaf and stem rust resistance	Kerber and Dyck (1969), Prescott-Allen and Prescott-Allen (1986), Gill *et al.* (1988), McIntosh *et al.* (2003), Marias *et al.* (2008)
	Ag. elongatum	Drought tolerance	Goodman *et al.* (1987)
	Agropyron sp.	Frost resistance	Budin (1973)
	Secale cereale	Yield improvement	Budin (1973)
Wheat (*Triticum aestivum*)	*T. dicoccoides, T. timopheevii, T. monococcum, Ae. speltoides*	Fusarium head blight	Cai *et al.* (2005)
	T. monococcum	Stem rust	Kerber and Dyck (1973)
	T. turgidum subsp. dicoccoides	Protein quality improvement	Avivi (1978), Kushnir and Holloran (1984), Prescott-Allen and Prescott-Allen (1988), Hoisington *et al.* (1999), Mesfin *et al.* (1999), Mesfin *et al.* (2000), Khan *et al.* (2000)
	T. turgidum subsp. dicoccoides	Powdery mildew	Rong *et al.* (2000)
	T. turgidum subsp. dicoccoides	Stem rust	McFadden (1930)
	T. urartu	Powdery mildew	Qiu *et al.* (2005)
	Thinopyrum bessarabicum	Salt resistance	King *et al.* (1997a), King *et al.* (1997b)
	Th. intermedium, Th. ponticum	Barley yellow dwarf virus, wheat streak mosaic virus	Sharma *et al.* (1995), Fedak *et al.* (2001), Jiang *et al.* (2005)
	Th. ponticum	Fusarium head blight resistance	Shen and Ohm (2007)
	Thinopyrum sp.	Greenbug resistance	Wells *et al.* (1982)
Grape vine (*Vitis vinifera*)	*V. amurensis*	Cold resistance	Golodriga and Souyatinou (1981)
	V. berlandieri, V. riparia, V. rupestris	Phylloxera vitifoliae resistance	Prescott-Allen and Prescott-Allen (1988)
Maize (*Zea mays*)	*Tripsacum dactyloides*	Yield improvement and top firing resistance	Prescott-Allen and Prescott-Allen (1986)
	T. dactyloides	Corn leaf blight resistance	Goodman *et al.* (1987)
	Z. diploperennis	Increased tillering	Sondahl *et al.* (1984)
	Z. diploperennis , Z. perennis	Viral resistance	Nault *et al.* (1982)
	Z. diploperennis , Z. perennis	Yield improvement	Cohen and Galinat (1984)

TABLE 2

Examples of the use of CWR in crop improvement (adapted from Dwivedi *et al*., 2008)

Crop	Elite germplasm/ cultivar	CWR	Country of release	Application(s)	Reference(s)
Peanut (*Arachis hypogaea*)	Spancross and Tamnut 74	*A. cardenasii*	USA	Yield and pod/ seed characteristic improvement	Hammons (1970), Simpson and Smith (1975)
	ICGV 86699 and ICGV87165	*A. cardenasii*	USA	Rust and late leaf spot resistance	Reddy *et al*. (1996), Moss *et al*. (1997)
	ICGV SM 86715	*A. cardenasii*	Mauritius	Foliar disease resistance	Moss *et al*. (1998)
	Coan and NemaTAM	*A. cardenasii, A. batizocoi, A. diogoi*	USA	Nematode resistance	Simpson and Starr (2001), Simpson *et al*. (2003)
	11 interspecific derivatives	*A. cardenasii*	USA	Early leaf spot, root-knot nematode, southern com rootworm, corn earworm, fell armyworm, and velvet bean caterpillar resistance	Stalker and Lynch (2002), Stalker *et al*. (2002a,b)
	Advanced lines	*A. hypogaea*	USA	root-knot nematode and tomato spotted wilt virus resistance	Holbrook *et al*. (2003)
	Advanced lines	*A. batizocoi,* *A. cardenasii,* *A. duranensis,* *A. stenosperma,* *A. villosa*	India	*Rust and late leaf spot resistant*	Singh *et al*. (2003)
Oat (*Avena sativa*)	Rapida and Sierra	*A. fatua*	USA	Drought resistance	Suneson (1967a,b)
Chickpea (*Cicer arietinum*)	BG 1100, BG 1101, and BG 1103	*C. reticulatum*	–	Yield improvement and fusarium wilt resistance	Yadav *et al*. (2004)
Soybean (*Glycine max*)	SS201 and SS202	*G. soja*	Japan	Specific variety for production of soy sprouts and fermented natto	Fehr *et al*. (1990a,b)
Soybean (*Glycine max*)	13	–	Korea	Drought tolerance and improved root development	Li (1990)
	Pearl	–	Japan	Specific variety for production of fermented natto	Carter *et al*. (1995)
Barley (*Hordeum vulgare*)	North Dakota (ND) 497 and ND 586	*H. bulbosum, H. brachyantherum, H. bogdanii*	USA	Yellow dwarf virus tolerance	Schooler and Franckowiak (1981)
	Athene and Birgit	*H. vulgare subsp. spontaneum*	Germany	Yield improvement	Arias *et al*. (1983)
	81882	*H. bulbosum*	USA	Powdery mildew and leaf rust resistance	Pickering *et al*. (1998)
	72 recombinant lines	*H. bulbosum*	–	Leaf disease resistance	Pickering and Johnston (2005)
Common bean (*Phaseolus vulgaris*)	Tara and Jules	*P. acutifolius*	USA	Drought, salinity or high temperature tolerance	Munoz *et al*. (2004)
	XAN159 and HR67, OAC Rex and HR45	*P. acutifolius*	USA	Bacterial blight resistance	Liu *et al*. (2004/2005)
Rice (*Oryza sativa*)	IR28, IR29, IR30, IR32, IR34, and IR36	*O. nivara*	Asia	*Grassy stunt virus resistance*	Brar and Khush (1997)
	IR2701-625-3	*O. longistaminata*	India	Grassy stunt virus resistance	Brar and Khush (1997)
	MTL98, MTL103, and MTL105	*O. officinalis*	Vietnam	Brown plan hopper resistance	Brar and Khush (1997)
	Tong 31 and Tong 35	*Zizania latifolia*	China	Improved grain quality and resistance to blast and sheath blight	Liu *et al*. (1999)



Crop	Elite germplasm/ cultivar	CWR	Country of release	Application(s)	Reference(s)
Rice (*Oryza sativa*)	Zhongshan 1	*O. rufipogon*	China	Cold tolerance and other abiotic stress resistance	Song *et al.* (2005)
	IL23	*O. rufipogon*	–	Drought tolerance	Zhang *et al.* (2006)
	HG101	*O. grandiglumis*	China	Improved grain characteristics	Yoon *et al.* (2006)
	AS996	*O. rufipogon*	Vietnam	Acid sulphate soil tolerance	IRRI (2003), Barclay (2004)
	Matatag 9	–	Philippines	Tungro virus resistance	Barclay (2004)
Wheat (*Triticum aestivum*)	Hope	*Triticum turgidum subsp. dicoccon*	USA	Sr 2 stem rust resistance	McFadden (1930)
	Plainsman V	*Aegilops ovata*	USA	Improved protein content	Sharma and Gill (1983)
	Amigo	*Ae. elongate*	China	Greenbug, powdery mildew and leaf rust resistance	Cai (1994)
	4 breeders lines	*Ae. tauschii, T. turgidum*	–	Karnul bunt immunity	Villareal *et al.* (1996)
	Breeder's line	*Thinopyrum bessarabicum*	UK	Salt tolerance	King *et al.* (1997a,b)
	OK 7211542	*Th. intermedium, Th. ponticum*	Global	Barley yellow dwarf virus immunity	Ayala *et al.* (2001)
	Sunnan	*Th. ponticum*	Sweden	Leaf rust resistance (Lr19)	Bartos *et al.* (2002)
	Marquillo and H 44-24	*T. dicoccoides*	USA	Leaf rust resistance	Bartos *et al.* (2002)
	Breeder's line 2K-11-1	*Ae. geniculata*	USA	Leaf and stripe rust resistance	Aghaee-Sarbarzeh *et al.* (2002)
	4 breeders lines	*Ae. tauschii*	USA	Fusarium head blight resistance	Berzonsky *et al.* (2004)
Wheat (*Triticum aestivum*)	Sumani 3	*Ae. tauschii, Roegneria kamoji, R. ciliaris, Leymus racemosus, Thinopyrum ponticum, Th. elongatum, Th. junceum, Th. intermedium, Dasypyrum villosa, Secale cereale*	USA	Fusarium head blight resistance	Oliver *et al.* (2005)
	30 hard red winter wheats	*Ae. tauschii*	USA	Hessian fly; green bug; soil-borne mosaic and spindle streak mosaic virus; leaf, stem, and stripe rust; powdery mildew; tan spot; and fusarium head blight resistance	Kansas State University (2006)
	Plainsman V, Agent	*Ae. ovata, Agropyron elongatum*	USA	Improved protein content	Paulsen (2000)
	Chuanmai 42, Carmona	–	China, Spain	Large kernels, heavy spikes, Chinese stripe rust resistance Foliar disease resistance, improved grain quality, adaptation to zero tillage	CIMMYT (2004)

– = data not available

As a pragmatic solution to the lack of crossing and genetic diversity data for the majority of crops and related taxa, an alternative solution using the existing taxonomic hierarchy has been proposed (Maxted *et al*., 2006). 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 crop, Taxon Group 3 – same subgenus as crop, Taxon Group 4 – same genus, and Taxon Group 5 – same tribe but different genus to 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.

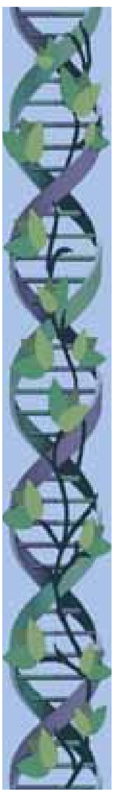
The Taxon Group concept assumes that taxonomic distance is positively correlated to genetic distance. Flint (1991), Heywood (1994), Johnson (1995) and Maxted *et al*. (2006) (among others) have drawn attention to the fact that this relationship may not always hold because of inconsistencies amongst taxonomists when describing species and gaps in the knowledge base used to define taxa (i.e., species are not all separated by the same amount of genetic isolation). Nevertheless, the taxonomic hierarchy is likely to be a reasonable approximation of the degree of genetic diversity; therefore, for practical purposes, classical taxonomy remains an extremely useful means of estimating genetic relationships. The Taxon Group concept can be applied to all crop and CWR taxa and can be used to define relative CWR relatedness for the approximate 80% of crop and CWR taxa where the Gene Pool concept is not understood (Maxted *et al*., 2006), as long as the existing classification of the genus contains an infra-generic structure.

Application of the Gene Pool and Taxon Group concepts to a crop and its wild relatives would ideally be expected to be congruent, but as discussed above and acknowledged by Harlan (1992), inconsistencies among taxonomists will mean that where both taxonomic and genetic information is available, the two concepts may not match perfectly. However, Maxted *et al*. (2006) provided the example of the Gene Pool and Taxon Group concepts applied to Narbon vetch (*Vicia narbonensis* L.) and its wild relatives, which show a close correlation between the applications of the two concepts. By combined use of the Gene Pool and Taxon Group concepts provide the best pragmatic means available to determine whether a species is a CWR and how closely related the wild relative is to the associated crop.

Based on the above arguments, a working definition of a crop wild relative was 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."

Therefore, taxa which belong to GP1B or TG1b and TG2 may be considered close CWR and demand higher conservation priority, while those in GP2 or TG3 and TG4 are more remote and may be afforded lower priority. Those in GP3 and TG5 would be excluded from being considered wild relatives of that particular crop, but of course this does not mean that these species may not posses' useful traits that could be introduced to the crop using biotechnological techniques. On this premise, the Gene Pool and Taxon Group concepts can be used together to define the degree of CWR relatedness and thus assist in establishing conservation priorities.



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[10], 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*., 2008). 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. These figures include the wild relatives of a wide range of crops (i.e., those included in Mansfeld's World Database of Agricultural and Horticultural Crops, and forestry and ornamental crops), as well as species within genera containing wild-harvested medicinal and aromatic plants. However, a high percentage of the total number of crop and CWR species in the Euro-Mediterranean (92%) are coincident with species found in genera containing agricultural and horticultural crops cultivated worldwide, as defined by Hanelt and IPK Gatersleben (2001).[11]

There have previously been no global estimates for the numbers of crop and CWR species but there are various ways in which these figures might be calculated:

a. Taking a lead from the analysis of CWR data for the Euro-Mediterranean region (Kell *et al*., 2008), nearly 51% of the genera in the Euro-Mediterranean region contain crops (based on the 2 437 plant genera in the region and 1 239 of these that are known to contain crops) and almost 83% of the species in the region are crop and CWR species (Kell *et al*., 2008). However, globally it is estimated that there are 14 500 plant genera (Brummitt, 1992) and that there are 2 539 of these that contain crops (Kell *et al*., 2008), giving a significantly lower figure of 17.5% of vascular plant genera containing crops worldwide. The precise number of species in these 2539 genera and therefore the global number of CWR species is unknown, but we can estimate this number of species by calculating and using the average number of species per genus. Based on the estimated number of accepted vascular plant genera (14 500; Brummitt, 1992) and total number of vascular plant species (283 846; Groombridge and Jenkins, 2002), there is an average of 19.57 species per genus for all plant species. If the number of genera containing crops is

---

[10] Available online via the Crop Wild Relative Information System (CWRIS) (PGR Forum, 2005)

[11] Mansfeld's Database is inclusive of a wide range of cultivated species. For example, in addition to food, fodder, forage, medicinal, aromatic and industrial crops, plants cultivated for soil improvement, sand dune fixation, hedging, grafting stock, shade and support are included. However, forestry, ornamental and wild-harvested medicinal and aromatic plants are not included.

multiplied by the average number species per genus (2 539 × 19.57), this results in a global estimate of 49 688 crop and CWR species.

b. A more precise but narrower estimate can be obtained by focusing only on those genera containing the major and minor food crops. Groombridge and Jenkins (2002) list 28 genera containing major food crops and 51 genera containing minor food crops worldwide (77 genera in total). Mabberley (1997) cites the actual number of species within these 77 genera and when these are added up, we have a global estimate of 10 739 crop and CWR species that are of direct value for food security (i.e., food crops and food CWR).

c. It can be argued that even this number is inflated by the inclusion of remote as well as closely related CWR, necessitated by the application of the broad genus-wide definition of a CWR. Ideally, it would be more effective to apply the more precise definition proposed by Maxted *et al*. (2006) and base the estimate only on GP1B or TG1b and TG2, but the data necessary to calculate this number for all food crops are not available. However, if we look at a sample of food crop groups (e.g., the 14 included in the current study), we can estimate the proportion of species that are the closest wild relatives of food crops in general (i.e., those thought to be in GP1B, TG1b or TG2) (see Table 3). Taking the total number of CWR species within these 14 crop groups (as an average across all groups), we find that an average of 2.06% of species are primary wild relatives and 4.39% are secondary wild relatives. Therefore, as a crude estimate, there are 221 species (i.e., 2.06% of 10 739) worldwide that are very close wild relatives of the major and minor food crops (i.e., those in the primary wild relative group) and 471 (i.e., 4.39% of 10 739) that are close wild relatives (i.e., those in the secondary wild relative group). Thus, as a rough estimate, we may be dealing globally with around 700 close CWR species worldwide (i.e., less than 0.26% of the world flora) in order to ensure that the highest priority genetic diversity is conserved and made available for use in crop improvement programmes as a contribution to future worldwide food security.

d. Finally, we can refine the global estimate by combining the results of a. and b. If we multiply the number of genera known to contain crops worldwide (2 539; Kell *et al*., 2008) after deducting the 77 genera containing major and minor food crops (=2 462 genera) by the average of 19.57 species per genus for all plant species, we have a total of 48 181 species. Adding the 10 739 species that are found in the 77 major and minor food crops results in a more precise global estimate of 58 920 crop and CWR species.

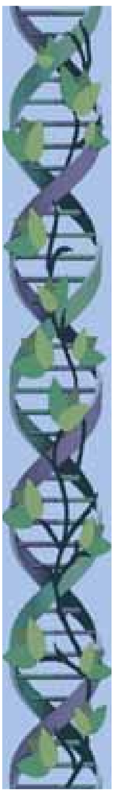
TABLE 3

Numbers of primary and secondary CWR species

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

---

[11] 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 (see Section 3.0).



The figures quoted in this section should be taken as rough estimates only. However, based on these calculations, we estimate that there are 50–60 000 CWR species worldwide and that around 700 of these are of the highest priority for immediate conservation action. The intention of providing these estimates is to give an idea of the number of species that we may be dealing with as a priority on a global scale, based on their degree of relatedness to the crop species. Of course, priorities will vary from one nation to another and from one crop group to another. For example, within some crop complexes, tertiary wild relatives may also be important gene donors for crop improvement (e.g., see the *Hordeum* case study in Section 3.0), though on the whole, the primary and secondary wild relatives are likely to be of greatest importance due to the fact that they can be more easily used in conventional breeding programmes.

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

CWR are intrinsically no different to other wild plant species, and, like them, many CWR are currently threatened with loss of diversity and/or extinction (Maxted *et al*., 1997b; Stolten *et al*., 2006). It is recognized worldwide that a catastrophic loss of plant diversity is currently occurring, both in terms of the loss of species, and the genetic diversity within species. 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 these species was an escalating problem. It is now generally acknowledged that the natural diversity inherent in CWR populations is a finite world resource that is being eroded or lost, in part by careless, unsustainable human practices (Maxted *et al*., 2007). This loss of CWR diversity can occur at both taxonomic (species) and genetic level.

IUCN's 1997 Red List assessment of plants concluded that 33 798 plant species were threatened or extinct (Walters and Gillett, 1998) and even this was likely to be an underestimate as not all plant species were evaluated. Subsequently, the revised and more objective IUCN Red List criteria (IUCN, 2001) were introduced, but these have not yet been applied to a significant number of plant species other than trees. The Gran Canaria Declaration (Anonymous, 2000) states that: "as many as two-thirds of the world's plant species are in danger of extinction in nature during the course of the 21st century … narrowing of the genetic basis of many species". The same declaration recognized that plants are vital globally in maintaining ecosystem stability but also in providing food, fibres, fuel, clothing and medicines for humankind.

It is difficult, if not impossible, to quantify the loss of genetic diversity within CWR species. However, it must be faster than the loss of species, because there will be some genetic erosion (loss of genetic diversity) from the species that remain extant and complete loss of genetic diversity from those species that become extinct (Maxted *et al*., 1997c). It therefore seems likely that virtually all CWR species are currently suffering loss of genetic diversity to varying degrees. 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. Loss of any genetic diversity means that plants may not be able to adapt to changing conditions quite so readily in the future—in a time of ecosystem instability this is a serious concern, since many of these species form the basis of our future food security.

CWR are subject to the same threats as any other wild species, which, fundamentally, are caused by the conflict between supply and demand for natural resources (Stuart and Adams, 1990) (i.e., there is a limited supply of the earth's resources and an increasing demand on them to meet the needs and aspirations of a growing human population). Therefore, the main factors causing loss of biodiversity are associated with anthropogenic influences—substantial increases in human population have a direct and inverse relationship to plant diversity. Humans have dramatically changed the natural vegetation globally, particularly since the age of European exploration and colonialization (see Richardson *et al*., 1996). In recent years, even apparently remote areas have been influenced by settlement or collection of forest products. The threats resulting from this anthropogenic pressure may be categorized as follows:

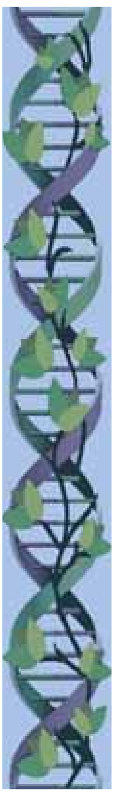
- **Deforestation** – Forest clearance and repeated burning for agriculture, as well as logging and hunting have resulted in severe degradation of natural forest communities. FAO (2007) report that during the 15 year period from 1990–2005, the world lost 3% of its total forest area. During this period, Africa has lost more than 9% of its forests and in a typical year accounts for more than half of the global forest area damaged by wildfire. FAO (2007) also report that the annual net rate of loss of forests in Latin America and the Caribbean between 2000 and 2005 (0.51%) was higher than that of the 1990s (0.46%) and that high rates of deforestation have continued in Asia and the Pacific region, particularly in Southeast Asia. It has been noted that traditional forms of shifting cultivation, which following forest clearance provides two to four years of cultivation, followed by fallow for ten to twenty years, promotes diversity (Beentje *et al*., 1994); however, cash crop production has shortened the traditional farming cycle, even eliminating the fallow period altogether, and depleted the land available for subsistence agriculture, reducing soil fertility, crop yields and natural forest diversity.

- **Logging** – Commercial logging continues on a large scale for about 15–20 species. The extraction methods employed have resulted in the extinction and genetic erosion of non-commercial tree and other plant species, along with rapid decline in soil nutrients and, often, soil erosion.
- **Plantation agriculture and forestry** – Extensive land clearance for cash crops and exotic trees leads to the fragmentation of natural habitat and a consequential reduction in size or loss of wild species' populations. For example, in 2006, the International Tropical Timber Organization concluded that only 5% of all tropical forests were managed in a sustainable manner and that unsustainable forest management was the main cause of forest degradation, particularly in terms of conversion of forests into agricultural land. The expansion of large-scale agro-industrial monocultures for food, fibre and, increasingly, energy production is both an important direct cause of deforestation and an important underlying cause of forest loss; the expansion of monocultures on existing arable land causes cattle ranching and other forms of agriculture to move towards forest areas and other natural ecosystems (ITTO, 2006). It is unquestionable that the clearance of vast areas of species-rich native forest to be replaced by monoculture plantations is resulting in significant loss of species (and genetic) diversity.
- **Industrialized agriculture** – The widespread global replacement of traditional sustainable agriculture with more industrial models has generated increased product but through the associated use of pesticides and herbicides has had a negative impact on biodiversity levels in general (Altieri, 2001) and therefore specifically it is likely to impact on the occurrence of CWR diversity.
- **Dryland destruction and desertification** – Changes in pastoralism in semi-arid regions has resulted in the exhaustion of local vegetation by domestic stock in some areas. This situation is exacerbated by increased stocking rates and prolonged droughts, resulting in overgrazing and erosion of wild plant populations, especially around permanent waterholes and wells. Desertification is the degradation of land in arid, semi-arid and dry sub-humid areas and is caused primarily by human activities and climatic variations (UNCCD, 2005). "Desertification occurs because dryland ecosystems, which cover over one third of the world's land area, are extremely vulnerable to over-exploitation and inappropriate land use. Poverty, political instability, deforestation, overgrazing, and bad irrigation practices can all undermine the productivity of the land." (UNCCD, 2005)
- **Fire** – Fire is a natural element of Mediterranean and African woodland and grassland ecosystems. In many biomes, occasional fires can enhance species diversity; however, the incidence of fire has increased along with the human population and results in restricted natural regrowth of vegetation.
- **Urbanization** – Globally, there is an ongoing mass migration to the cities, placing a heavy demand on fuelwood, charcoal, building materials, medicinal resources and easily eliminated taxa of restricted distribution. In developing countries, feeding the tourist craft market places an increasing demand on species such as African Blackwood (*Dalbergia melanoxylon*) for woodcarving, and grasses for making baskets and mats. Cunningham (1993) noted that in the vicinity of large urban centres, scarce or slow growing medicinal species are rapidly being exhausted.
- **Mining and quarrying** – The association of rare plant diversity with enclaves of extreme or otherwise distinct soils is well established—soils rich in heavy metals and certain minerals often support unique floras. The endemic vegetation found on these soils is easily threatened by mining; particularly open-cast mining that removes the entire vegetation cover.
- **Invasive species** – The problems of invasive alien species are severe and well documented. In the absence of natural pests, diseases or herbivores, monospecific stands of exotic species compete with native plant diversity and may lead to the extinction of entire populations.
- **Climate change** – Human directed climate change is predicted to increase average temperatures by 0.2°C per decade and cause considerable changes in regional and seasonal patterns of precipitation (IPCC, 2007). This will impact directly on the natural reproductive cycles of wild plant species as well as species distributions and abundance over time. It is still to be seen what the precise impact of climate change will be but many fear it will result in a step-shift in terms of extinction and genetic erosion. Thuiller *et al*. (2005) predicted that by 2080 climate change will result in 27–42% loss of all plant species in Europe, while Jarvis *et al*. (2008) predicted that 16–22% of *Arachis, Solanum* and *Vigna* species would go extinct by 2055.

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. Civil unrest and human displacement undoubtedly places further stress on natural diversity. Refugee camps are almost by definition established in areas of low human population and the often pristine vegetation is sacrificed to necessary expediency; but where the environment is fragile, recovery may take time if it is possible at all.

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 been previously known. Thus, CWR are likely to be disproportionally and adversely impacted by current ecosystem instability and changes to anthropogenic environments, at least compared to non-CWR wild species found in more stable climax communities.

It should also be noted that as a group CWR are often over-looked 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*., 2008). The same authors found that only 5% of the CWR species of Europe are found within Important Plant Areas and noted that "with only three out of the 152 species in the major food crop genera that occur in Europe included and none of the 559 species in the minor food crop genera, we might conclude that more needs to be done to ensure that CWR are represented in IPAs" (Kell *et al*., 2008). They also found that only 161 species and 23 subspecific Euro-Mediterranean CWR taxa were included in the 2004 IUCN Red List of Threatened Species—most of these taxa being trees (Kell *et al*., 2008). Therefore, it is clear that not only do CWR face a unique threat from increased habitat gross instability but as a group their conservation is being systematically under-valued.



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) and *ex situ* (primarily as seed in gene banks, but also as explants in tissue culture or cryopreserved, or as mature individuals in field collections). 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)[12]. A genetic reserve is actively managed, even if the management involves regular monitoring of the target CWR taxa alone. Importantly, conservation action is long-term because significant resources have to be invested to establish the genetic reserve. *Ex situ* seed conservation involves "the location, sampling, transfer and management of seed from its original location to a gene bank where it is dried and stored at sub-zero temperatures" (Maxted *et al*., 1997d). This technique 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*., 2008), but CWR, like any other group of wild plant species, are located both within and outside existing protected areas. 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*., 2008). Therefore, often the simplest way forward in economic and political terms is for countries to locate genetic reserves within existing protected areas (e.g., national parks, heritage sites or special areas for conservation (SACs).

The question may be asked, why do we need to establish genetic reserves when the CWR species are present in the protected area anyway? The reason is that the majority of protected areas are established to conserve specific habitats or faunal elements. 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[13]. All species in protected areas are passively conserved if the entire ecosystem or habitat is stable; however, without monitoring and active management, the genetic diversity within and between individual CWR populations could be eroded and entire populations could even go extinct. Nonetheless, Stolten *et al*. (2006) emphasize that many protected areas already play an important role in conservation of CWR species, even though many managers may be unaware that the land under their stewardship contains important crop genetic diversity. Further, 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 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 bicolour*) (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 (Box 1).

Although in each of these six categories of protected areas CWR taxa will be passively conserved, 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.

---

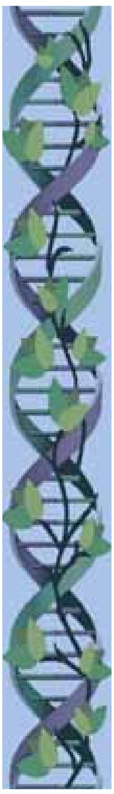
[12] Synonymous terms include 'genetic reserve management units' (GRMUs), 'gene management zones' (GMZs), 'gene sanctuaries' or 'genetic sanctuaries' and 'crop reservations'.

[13] Maxted et al. (1997a) distinguish between active and passive protected area conservation, where active management implies some form of dynamic intervention at the site and passive conservation implies that there is no management or monitoring of target populations, although there may be some general ecosystem management.

BOX 1
The IUCN Protected Area Management Categories

IUCN has developed a definition and a series of categories of protected areas, as outlined below (IUCN, 1995).

- **Category Ia: area managed mainly for science or wilderness protection** – an area of land and/or sea possessing some outstanding or representative ecosystems, geological or physiological features and/or species, available primarily for scientific research and/or environmental monitoring.
- **Category Ib: area managed mainly for wilderness protection** – large area of unmodified or slightly modified land and/or sea, retaining its natural characteristics and influence, without permanent or significant habitation, which is protected and managed to preserve its natural condition.
- **Category II: area managed mainly for ecosystem protection and recreation** – natural area of land and/or sea designated to a) protect the ecological integrity of one or more ecosystems for present and future generations, b) exclude exploitation or occupation inimical to the purposes of designation of the area, and c) provide a foundation for spiritual, scientific, educational, recreational and visitor opportunities, all of which must be environmentally and culturally compatible.
- **Category III: area managed mainly for conservation of specific natural features** – area containing specific natural or natural/cultural feature(s) of outstanding or unique value because of their inherent rarity, representativeness or aesthetic qualities or cultural significance.
- **Category IV: area managed mainly for conservation through management intervention** – area of land and/or sea subject to active intervention for management purposes so as to ensure the maintenance of habitats to meet the requirements of specific species.
- **Category V: area managed mainly for landscape/seascape conservation or recreation** – area of land, with coast or sea as appropriate, where the interaction of people and nature over time has produced an area of distinct character with significant aesthetic, ecological and/or cultural value, and often with high biological diversity. Safeguarding the integrity of this traditional interaction is vital to the area's protection, maintenance and evolution.
- **Category VI: area managed mainly for the sustainable use of natural resources** – area containing predominantly unmodified natural systems, managed to ensure long-term protection and maintenance of biological diversity, while also providing a sustainable flow of natural products and services to meet community needs.



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 the existing network does not happen to be coincident with a target taxon of restricted distribution. However, as noted by Jain (1975) and Maxted *et al*. (1997a), many CWR of major crops are commonly found in disturbed, pre-climax plant communities and as such 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. Therefore, in designing a national CWR conservation strategy, the genetic conservation of CWR outside as well as inside of protected areas needs to be considered. These areas include roadsides, field margins, orchards and even fields managed using traditional agro-silvicultural practices. Such sites are not managed for biodiversity conservation and the occurrence of CWR populations is incidental, making them particularly vulnerable to adverse management changes. However, they 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. These populations may occasionally be sampled for *ex situ* conservation but are largely ignored in terms of formal *in situ* conservation. If these sites are to be considered suitable for sustainable *in situ* conservation, the management they currently receive that has permitted the existence of healthy CWR populations in the past must be consistent and maintained in the future. The kinds of management changes that could adversely impact CWR populations in these areas are less likely to occur in protected areas because the raison d'état is already conservation, so any management change would more likely be conservative and considerate of any potential adverse impacts.

Threats faced by CWR populations outside of protected areas include the widening of roads, hedge and verge cutting, the scrubbing out of hedgerows or orchards, the introduction of herbicides rather than physical weed control, or even the physical control of weeds earlier in the season. Therefore, there is a need to establish some level of protection for these sites and consistency in management, otherwise conservation will be unsustainable. It is essential to reach a management agreement with the site owner and/or manager to ensure that current site management is not adversely changed and CWR diversity impacted. The management agreement needs to be predicated on an understanding of the conservation context, site characteristics, the target taxon population and the existing management practices that have facilitated a viable population that can be formalized into a site prescription. The prescription will then form the basis of the management agreement between the conservation agency and the landowner. Examples of this form of agreement and prescription are now commonplace in many North American and European countries along rural roadsides, but there are no known agreements yet in place in the centres of CWR diversity where *in situ* conservation is a priority. A well documented example of these kinds of local management agreements are those used in the establishment of micro-reserves in the Valencia region of Spain (see Laguna, 1999; Serra *et al*., 2004).

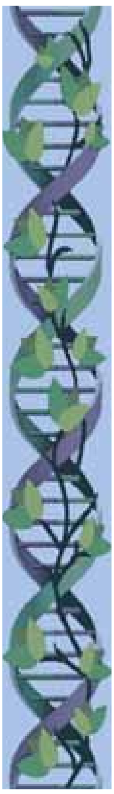
Many CWR species are also found growing as weeds in agricultural, horticultural and silvicultural systems—particularly those associated with traditional cultural practices or marginal environments. In many areas of the world this group of weedy CWR species is particularly threatened because of the widespread 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. However, the provision of government incentives must be linked to some form of guarantee from the landowner to ensure wild species thrive, so again a management agreement including a conservation prescription is required. The provision of such grants is unlikely to be a practical option in many developing countries where CWR diversity is largely located and where resources are more limited; however, there is an opportunity for the integration of on-farm landrace conservation with that of CWR diversity in these and other countries.

As a specific example of CWR conservation outside of protected areas, 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. Al-Atawneh *et al*. (2008) noted that in Palestine, *Pyrus syriaca* Boiss. is only found as scattered trees, never as continuous populations, so is primarily conserved outside of the existing protected area network. The importance of these isolated trees was drawn to the attention of the local community by use of a leaflet designed to help raise awareness of this resource and individual trees were mapped using a GIS system so that their long-term presence was easier to monitor.

Another project with a focus on wild plant species conservation outside of protected areas that is likely to include significant CWR diversity is the '100 fields for biodiversity' in Germany (see www.schutzaecker.de). The fact that CWR are often found in disturbed habitats means they are commonly weeds of cultivated land and are associated with traditional agriculture or more intense agriculture that is linked to conservation action. The 100 fields for biodiversity project aims at establishing a nationwide conservation field network for wild arable plant species, where typical arable plant communities such as Caucalido-Adonidetum flammeae, Teesdalio-Arnoseridetum and Papaveretum argemones are seen as preferable to crop monocultures. In project fields, crop husbandry does not include the use of herbicides or growth regulators, facilitating the re-colonization of arable species. Even in the most intense agricultural systems the protection of headlands or field margins from intensive agricultural practices can provide a haven for arable weeds, including many CWR species.

By definition, unprotected areas are primarily managed for reasons other than conservation; therefore, the management interventions at the site are likely to be minimal. The management necessary to maintain CWR populations at such sites may simply involve maintaining current regimes and an agreement with the site manager not to make adverse management changes without discussion with the overseeing conservation officer. 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.

Therefore, conservation of CWR is just as feasible outside of conventional reserves as it is within fully designated genetic reserves; a site does not need a fence around it and a sign saying it is a protected area to conserve CWR species. However, both within and outside of a protected area it is important to have a management plan to ensure the target taxa are sustainably conserved. Sustainability is central to CWR conservation and lack of a management plan and management agreement is likely to impede the sustainability of conservation outside of protected areas. It should also be recognized that there are advantages and disadvantages to CWR conservation outside of specifically nominated protected areas. Due to the high levels of resource investment required to establish a more formal genetic reserve, they are likely to be more sustainable in the long-term because to abandon them would waste the resources already committed to the site. Conversely, with less resources committed to conservation outside of protected areas, CWR populations at these sites are more likely to suffer from changes in land ownership and national or local policy. 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 that an early warning system is in place to deal with 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*., in prep.):

- **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. In the case of *in situ* conservation, the protected area they manage may not be regarded as containing sufficient priority CWR diversity for it to be designated as an element within the national or global network, but due to the widespread occurrence of CWR species, it is likely to include some CWR; therefore, the manager can raise the profile of the site by highlighting the CWR diversity present. The aim of the individual CWR protected area is to ensure the conservation of the maximum CWR taxonomic and genetic diversity found at the site. 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 also be further enhanced by advertising the presence of the CWR diversity to the 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 of this approach is to maximize the protection of the nation's CWR diversity and to link the conserved diversity to its actual or potential utilization. A national CWR strategy has policy implications for the plant conservation and exploitation (primarily breeding) agencies that are responsible for its implementation. It leads, via a series of steps, to the identification of CWR hotspots and the establishment of a national network of protected areas for CWR. As already stated, genetic reserves are likely to be established within existing protected areas; therefore, there is a need for the national PGRFA and nature conservation communities 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. Priorities for the global approach can be established and applied worldwide on the basis of objective, scientific criteria. The sites selected for inclusion in the 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, which itself is a function of the uneven distribution of crop diversity around the world.

Each of these three complementary approaches aims to incorporate CWR conservation within existing protected areas, which is likely to involve some amendment of existing management plans to facilitate active conservation of CWR diversity. The national and global approaches may be seen as strategic in that they are likely to be implemented by conservation agencies or institutions and will involve the selection of the most appropriate sites in which to establish CWR genetic reserves. Each approach, to be truly effective, needs to include *ex situ* duplication of the *in situ* conserved diversity. Also, 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. Finally, 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.

The following two parts of this report propose a methodology for the development of national CWR complementary conservation strategies and a global approach to the *in situ* conservation of CWR diversity—initially focusing on a subset of critical crop gene pools.

1.9 References

Aghaee-Sarbarzeh. M., Ferrahi, M., Singh, S., Singh, H., Friebe, B., Gill, B.S. and Dhaliwal, H.S. (2002). Phi-induced transfer of leaf and stripe rust-resistance genes from *Aegilops triuncialis* and *Ae. geniculata* to bread wheat. Euphytica, 127: 377–382.

Akano, A.O., Dixon, A.G.O., Mba, C., Barrera, E. and Fregene, M. (2002). Genetic mapping of a dominant gene conferring resistance to cassava mosaic disease. Theoretical and Applied Genetics, 105: 521–525.

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.

Alston, F.H. (1977). Practical aspects of breeding for mildew (*Podosphaera leucotricha*) resistance in apples. Proceedings of Eucarpia Fruit Section. Symposium VII. 7–10 September 1976. Wageningen: 4–17.

Altieri, M.A. (2001). Agriculture, traditional. In: Encyclopaedia of Biodiversity, Vol: 1. Pp. 109–118. Academic Press, New York.

Amante-Bordeos, A., Sitch, L.A., Nelson, R., Dalmacio, R.D., Oliva, N.F., Aswidinnoor, H. and Leung. H. (1992). Transfer of bacterial blight and blast resistance from the tetraploid wild rice *O. minuta* to cultivated rice, *O. sativa*. Theoretical and Applied Genetics, 84: 345–354.

Anonymous (2000). The Gran Canaria Declaration. Botanic Gardens Conservation International, Richmond, Surrey.

Arias, G., Reiner, L., Penger, A. and Mangstl, A. (1983). Directory of barley cultivars and lines. Verlag Eugen Ulmer. Stuttgart, Germany.

Ariyanayagam, R.P., Rao, A.N. and Zavery, P.P. (1995). Cytoplasmic-genic male-sterility in interspecific matings of Cajanus. Crop Science, 35: 981–985.

Asiedu, R., Hahn, S.K., Bai, K.V., and Dixon, A.G.O. (1992). Introgression of genes from wild relatives into cassava. In: Proceedings of the Fourth Triennial Symposium of the International Society of Tropical Root Crops – Africa Branch held in Kinshasa, Zaire, 1989 (eds. Akoroda, M.O. and Arene, O.B.). Pp. 89–91. ISTRC-AB/IDRC/CTA/IITA

Avivi, L. (1978). High grain protein content in wild tetraploid wheat Triticum dicoccoides Körn. Proceedings of 5th international Wheat Genetic Symposium, New Delhi. 372–380.

Ayala, L., van Ginkel, M., Khairallah, M., Keller, B. and Henry, M. (2001). Expression of *Thinopyrum intermedium*-derived barley yellow dwarf virus resistance in elite wheat backgrounds. Phytopathology, 91: 55–62.

Bailey, K.L., Harding, H. and Knott. D.R. (1993). Transfer of bread wheat of resistance to common root rot (*Cochliobolus sativus*) identified in *Triticum timopheevii* and *Aegilops ovata*. Canadian Journal Plant Pathology, 15: 211–219.

Barclay, A. (2004). Feral play: Crop scientists use wide crosses to breed into cultivated rice varieties the hardiness of their wild kin. Rice Today, 3(1): 13–19.

Barloy, D., Lemoine, J., Dredryver, F. and Jahier, J. (2000. Molecular markers linked to the Aegilops variabilis-derived root-knot nematode resistance gene Rkn-mn1 in wheat. Plant Breed. 118:169–172.

Bartos, P., Sip, V., Chrpova, J., Vacke, J., Stuchlikova, E., Blazkova, V., Sarova, J. and Hanzalova. A. (2002). Achievements and prospects of wheat breeding for disease resistance. Czech Journal of Genetics and Plant Breeding, 38: 16–28.

Baum, M., Grando, S., Backes, G., Jahoor, A., Sabbagh, A. and Ceccarelli, S. (2003). QTLs for agronomic traits in the Mediterranean environment identified in recombinant inbred lines of the cross Arta x *H. spontaneum* 41–1. Theoretical and Applied Genetics, 107: 1215–1225.

Beentje, H.J., Adams, B. and Davis, S.D. (1994). Regional overview: Africa. In: Centres of plant diversity: a guide and strategy for their conservation. Volume 1 (Eds. Davis, S., Heywood, V.H. and Hamilton, A.C.). Pp. 101–118. WWF and International Union for Conservation of Nature and Natural Resources, Gland, Switzerland.

Bernacchi, D., Beck-Bunn, T., Emmatty, D. and Inai, S. (1998). Advanced backcross QTL analysis of tomato. II. Evaluation of near-isogenic lines carrying single-donor introgressions for desirable wild QTL alleles derived from Lycopersicon hirsutum and L. pimpinellifolium. Theoretical and Applied Genetics, 97: 170–180.

Berzonsky, W.A., Hartel, K.D., Kianian, S.F. and Leach, G.D. (2004). Registration of four synthetic hexaploid wheat germplasm lines with resistance to fusarium head blight. Crop Science, 44: 1500–1503.

Blair, M.W., Iriarte, G. and Beebe, S.E. (2003). QTL analysis of an Andean advanced backcross population for yield traits derived from wild P. vulgaris. Annual Report of Bean Improvement Cooperative, 46: 7–9.

Blair, M.W., Iriarte, G. and Beebe, S.E. (2006). QTL analysis of yield traits in an advanced backcross population derived from a cultivated Andean x wild common bean (*Phaseolus vulgaris* L.) cross. Theoretical and Applied Genetics, 112: 1149–1163.

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.

Bramel-Cox, P.J., Andrews, D.J. and Frey, K.J. (1986). Exotic germplasm for improving grain yield and growth rate in pearl millet. Crop Science, 26: 687–690.

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.

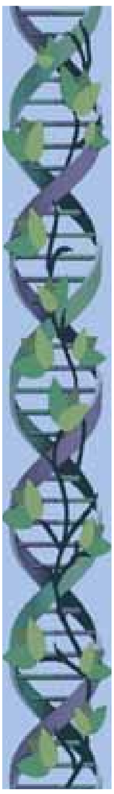
Brar, D.S. and Khush, G.S. (1997). Alien introgression in rice. Plant Molecular Biology, 35: 35–47.

Brar, D.S., Dalmacio, R., Elloran, R., Aggarwal, R., Angeles, R. and Khush. G.S. (1996). Gene transfer and molecular characterization of introgression from wild *Oryza* species into rice. In: Rice genetics III. pp. 477–486. International Rice Research Institute, Manila, Philippines.

Brondani, L.R. and Ferreira, M.E. (2002). QTL mapping and introgression of yield-related traits from *Oryza glumaepatula* to cultivated rice (*Oryza sativa*) using microsatellite markers. Theoretical and Applied Genetics, 104: 1102–1203.

Brown, A.G. (1975). Apples. In: Advances in fruit breeding (eds. Janick, J. and Moore, I.N.). Pp. 3–37. Purdue Univ. Press, West Lafayette, USA.

Brummitt, R.K. (1992). (Compiler) Vascular plant families and genera. Database. RBG Kew, UK.



Budin, K. (1973). The use of wild species and primitive forms in agricultural crop breeding in the USSR. In: Proceedings of a conference on European and regional gene banks (eds. Hawkes J.G. and W Lange, W.). Pp. 87–97. Wageningen (Netherlands).

Cai, X. (1994). Chromosome translocations in the common wheat variety Amigo. *Hereditas*, 121: 199–202.

Cai, X., Chen, P.D., Xu, S.S., Oliver, R.E. and Chen X. (2005). Utilization of alien genes to enhance fusarium head blight resistance in wheat: A review. *Euphytica*, 142: 309–318,

Carter, T.E., Jr., Huie, E.B., Burton, J.W., Farmer, F.S. and Gizlice Z. (1995). Registration of Pearl soybean. Crop Science, 35: 1713.

Chen, G., Li, C., Shi, Y. and Nevo, E. (2008). Wild Barley, *Hordeum spontaneum*, a Genetic Resource for Crop Improvement in Cold and Arid Regions. Sciences in Cold and Arid Regions, 1: 0115–0124.

CIAT (2006). CIAT Annual Report 2006. CIAT, Cali, Colombia.

CIMMYT (2004). Wild wheat relatives help boost genetic diversity. International Maize and Wheat Improvement Centre. Available online: http://www.cimmyt.org/english/wps/news/wild_wht.htm [Accessed 03 March 2009].

Clement, S.L., Hardie, D.C. and Elberson, L.R. (2002). Variation among accessions of *Pisum fulvum* for resistance to pea weevil. Crop Science, 42(6): 2167–2173.

Cohen, J.I. and Galinat, W.C. (1984). Potential use of alien germplasm for maize improvement. Crop Science, 24: 1011–1015.

Colmer, T.D., Flowers, T.J. and Munns, R. (2006). Use of wild relatives to improve salt tolerance in wheat. Journal of Experimental Botany, 57(5): 1059–1078.

Concibido, V.C., Vallee, B.L., Mclaird, P., Pineda, N., Meyer, J., Hummel, L., Yang, J., Wu, K. and Delannay, X. (2003). Introgression of a quantitative trait locus for yield from *Glycine soja* into commercial soybean cultivars. Theoretical and Applied Genetics, 106: 575–582.

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.

Cox, T.S., House, L.R. and Frey, K.J. (1984). Potential of wild germplasm for increasing yield of grain sorghum. *Euphytica*, 33: 673–684.

Cox, T.S., Hatchett, J.H., Gill, B.S., Raupp, W.J. and Sears. R.G. (1990). Agronomic performance of hexaploid wheat lines derived from direct crosses between wheat and *Aegilops squarrosa*. Plant Breeding, 105: 271–277.

Cox, T.S., Raup, W.J. and Gill, B.S. (1994). Leaf rust-resistance genes Lr41, Lr42, and Lr43 transferred from Triticum tauschii to common wheat. Crop Science, 34: 339–343.

Cox, T.S., Sears, R.G., Bequwtte, R.K. and Martin, T.J. (1995). Germplasm enhancement in winter wheat x *Triticum tauschii* backcross populations. Crop Science, 35: 913–919.

Cummins, I.N. and Aldwinckle, H.S. (1979). Breeding tree crops. In: Biology and breeding for resistance to arthropods and pathogens in agricultural plants (ed. Harris M.K.). Pp. 528–545. Texas Agricultural Experiment Station, Texas A and M University.

Cunningham, A.B. (1993). African medicinal plants: setting priorities at the interface between conservation and primary healthcare. UNESCO, Paris.

Dalmacio, R., Brar, D.S., Ishii, T., Sitch, L.A., Virmani, S.S. and Khush, G.S. (1995). Identification and transfer of a new cytoplsmic male sterility source from *Oryza perennis* into indica rice (*O. sativa*). *Euphytica*, 82: 221–225.

Dalmacio, R.D., Brar, D.S., Virmani, S.S. and Khush, G.S. (1996). Male sterile line in rice (Oryza sativa) developed with *O. glumaepatula* cytoplasm. International Rice Research Newsletter, 21: 22–23.

Darwin, C. (1868). The variation of animals and plants under domestication. John Murray Publishers, London.

De Candolle, A.L.P.P. (1855). Géographie botanique raisonnée. Victor Masson, Paris.

Delibes, A., Romero, D, Aguaded, S., Duce, A., Mena, M., López-Braña, I., Andrés, M.F., Martín-Sanchez, 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.

Diers, B.W., Kiem, P., Fehr, W.R. and Shoemaker, R.C. (1992). RFLP analysis of soybean seed protein and oil content. Theoretical and Applied Genetics, 83: 608–612.

Dujardin, M. and Hanna, W.W. (1989). Crossability of Pearl Millet with Wild *Pennisetum* Species. Crop Science, 29: 77–80.

Dvorak, J. (1977). Transfer of leaf rust resistance from *Aegilops speltoides* to *Triticum aestivum*. Canadian Journal of Genetics and Cytology, 19: 133–341.

Dwivedi S.L., Upadhyaya, H.D., Thomas Stalker, H., Blair, M.W., Bertioli, D.J., Nielen, S. and Ortiz, R. (2008). Enhancing Crop Gene Pools with Beneficial Traits Using Wild Relatives Plant Breeding Reviews, 30: 180–230.

Eenink, A.H., Groenwold, R. and Dieleman, F.L. (1982). Resistance of lettuce (Lactuca) to the leaf aphid *Nasonovia ribisnigri* 1 Transfer of resistance from *L. virosa* to *L. sativa* by interspecific crosses and selection of resistant breeding lines. *Euphytica*, 31: 291–300.

Eglinton, J.K., Evans, D.E., Brown, A.H.D., Langridge, P., McDonald, G., Jefferies, S.P. and Barr. A.R. (2001). The use of wild barley (*Hordeum vulgare* spp. *spontaneum*) in breeding for quality and adaptation. Proceedings of the 10th Barley Technical Symposium. Canberra, ACT, Australia, 16–20 September 2001. Available online: http://www.regional.org.au/au/abts/1999/eglinton.htm [Accessed 04 August 2008].

El Khlifi, O.K., Sharma, H. and Benlhabib O. (2004). Transfer of Hessian fly resistance through interspecific crosses between cultivated wheat and four *Aegilops* species. Plant Genetic Resources Newsletter, 138: 43–49.

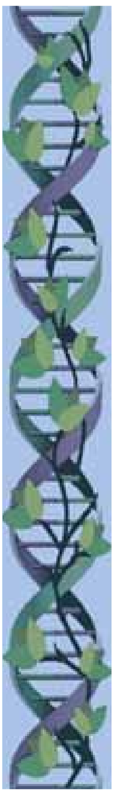
Elvira-Recuenco, M. (2000). Sustainable control of pea bacterial blight: approaches for durable genetic resistance and biocontrol by endophytic bacteria. PhD thesis, Wageningen University, The Netherlands.

Elvira-Recuenco, M., Bevan, J.R. and Taylor, J.D. (2003). Differential responses to pea bacterial blight in stems, leaves and pods under glasshouse and field conditions. European Journal of Plant Pathology, 109(6): 555–564.

Estrada-Ramos, N. (1991). Utilization of *Solanum* brevidens to transfer PLRV resistance into the cultivated potato, *Solanum tuberosum*. In: Solanaceae III: Taxonomy, Chemistry and Evolution (eds. Hawkes, J.G., Lester, R.N., Nee, M. and Estrada-R., N.). pp 413–419. Royal Botanic Gardens, Kew, London.

FAO (1996). *Global Plan of Action* for the Conservation and Sustainable Utilization of Plant Genetic Resources for Food and Agriculture. Food and Agriculture Organization of the United Nations, http://www.fao.org/ag/AGP/AGPS/GpaEN/gpatoc.htm [Accessed 21 October 2008].

FAO (1998). The *State of the World's Plant Genetic Resources for Food and Agriculture*. FAO, Rome.



FAO (2005). Harvesting Nature's Diversity. Available at: http://www.fao.org/DOCREP/004/V1430E/ V1430E00.htm#TOC [Accessed 03 March 2009].

FAO (2007). State of the World's Forests 2007. Food and Agriculture Organization of the United Nations, Rome, Italy. http://www.fao.org/docrep/009/a0773e/a0773e00.htm [Accessed 21 October 2008]

FAO (2008). Climate Change and Biodiversity for Food and Agriculture. FAO, Rome.

Farooq, S., Iqbal, N., Asghar, M. and Shah T.M. (1992). Intergeneric hybridization for wheat improvement. VI. Production of salt tolerant germplasm through crossing wheat (*Triticum aestivum* L.) with *Aegilops cylindrica* and its significance in practical agriculture. Journal of Genetics and Breeding, 46: 125–132.

Farooq, S., Asghar, M., Iqbal. N., Asian, E., Arif, M. and Shah T.M. (1995). Production of salt tolerant wheat germplasm through crossing cultivated wheat with *Aegilops cylindrica*, IL Field evaluation of salt tolerant germplasm. Cereal Research Community, 23: 275–282.

Fedak, G., Chen, Q., Conner, R.L, Laroche, A., Comeau, A. and St.-Pierre G.A. (2001). Characterization of wheat-*Thinopyrum* partial amphiploids for resistance to barley yellow dwarf virus, *Euphytica*, 120: 373–378,

Fehr, W.R., Cianzio, S.R. and Welke. G.A. (1990a). Registration of SS202 soybean. Crop Science, 30: 1361.

Fehr, W.R., Cianzio, S.R., Welke, G.A. and LeRoy III A.R. (1990b). Registration of SS201 soybean. Crop Science, 30: 1361.

Feuillet, C., Langridge, P. and Waugh, R. (2008). Cereal breeding takes a walk on the wild side. Trends in Genetics, 24: 24–32.

Fischbeck, G., Schwarzbach, E., Sobel, F. and Wahl, I. (1976). Mehltauresistenz aus Israelischen Populationen der zweizeilgen Wildgerste (*Hordeum spontaneum*). Z. Pflanzenzüchtg. 76, 163–166.

Flint, M. (1991). Biological Diversity and Developing Countries. Issues and Options. Overseas Development Administration, London.

Fondevilla, S., Torres, A.M., Moreno, M.T. and Rubiales, D. (2007). Identification of a new gene for resistance to powdery mildew in *Pisum fulvum*, a wild relative of pea. Breeding Science, 57(2): 181–184.

Forster, C., North, H., Afzal, N., Domoney, C., Hornostaj, A., Robinson, D.S. and Casey, R. (1999). Molecular analysis of a null mutant for pea (*Pisum sativum* L.) seed lipoxygenase-2. Plant Molecular Biology, 39(6): 1209–1220.

Frankel, O. (1970). Genetic conservation of plants useful to man. Botanical Conservation, 2: 162–169.

Frey, K. J. (1976). Plant breeding in the seventies: Useful genes from wild plant species. Egyptian Journal of Genetics and Cytology, 5: 460–482.

Gill, B.S. and Raupp, W.J. (1987). Direct gene transfers from *Aegilops squarrosa* L. to hexaploid wheat. Crop Science, 27: 445–450.

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.

Golodriga, P.Y. and Souyatinou, I.A. (1981). *Vitis amurensis*. Habitat. Aptitudes culturales et technologiques. Variabilite de l'espece. Bulletin de l'OIV. 54: 971–982.

Goodman, R.M., Hauptli, H., Crossway, A. and Knauf. V.C. (1987). Gene transfer in crop improvement. Science, 236: 48–54, Gororo, N.N., Eagles, H.A., Eastwood, R.F., Nicolas, M.E. and Flood, R.G. (2002). Use of Triticum tauschii to improve yield of wheat in low-yielding environments. *Euphytica*, 123: 241–254.

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.

Gur, A. and Zamir, D. (2004). Unused natural variation can lift yield barriers in plant breeding. PLoS Biology, 2:e245.

Gustafsson, M. and Claësson, L. (1988). Resistance to powdery mildew in wild species of barley. *Hereditas*, 108: 231–237.

Hadjichristodoulou, A. (1993). The use of wild barley in crosses for grain production under dryland conditions. *Euphytica*, 69: 211–218.

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.

Hammons, R.O. (1970). Registration of Spancross peanuts. Crop Science, 10: 459–460.

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

Hanh, S.H., Howland, A.K. and Terry, E.R. (1980). Correlated resistance of cassava to mosaic and bacterial blight disease. *Euphytica*, 29: 305–311.

Hanna, W.W. (1989). Characteristics and stability of a new cytoplasmic nuclear male-sterile source in pearl millet. Crop Science, 29: 1457–1459.

Hanna, W.W. (1992). Utilization of germplasm from wild species. In: Desertified Grasslands: Their Biology and Management. Pp. 251–257. Academic Press, London, UK.

Hanna, W.W. (1997). Influence of cytoplasms from a wild grassy subspecies on dry matter yields in pearl millet. Crop Science, 37: 614–616.

Hanna, W.W. (2007). Total and Seasonal Distribution of Dry Matter Yields for Pearl Millet x Wild Grassy Subspecies Hybrids. Crop Science, 40: 1555–1558.

Harlan, J.R. (1992). Crops and Man. American Society of Agronomy, Madison.

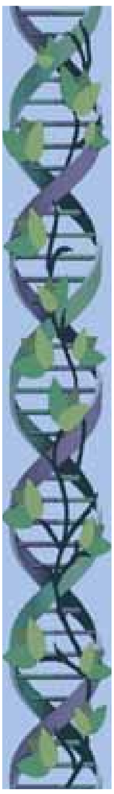
Harlan, J.R. and de Wet, J.M.J. (1971). Towards a rational classification of cultivated plants. Taxon, 20, 509–517.

Hawkes, J.G. (1947). Some observations on South American potatoes. Annals of Applied Biology, 34: 622–631.

Hawkes, J.G. (1979). Genetic poverty of the potato in Europe. In: Proceedings of the conference broadening the genetic base of crops (eds. Zeven, A.C. and van Harten A.M.). pp. 19–27. Centre for Agricultural Publishing and Documentation, Wageningen.

Hawkes, J.G., Maxted, N. and Ford-Lloyd, B.V. (2000). The *ex situ* conservation of plant genetic resources. Pp. 1–250. Kluwer, Dordrecht.

Hawtin, G.C. (1979). Strategies for the genetic improvement of lentils, broad beans, and chick peas, with special emphasis on research at ICARDA. In: Food legume improvement and development (eds. Hawtin, G.C. and Chancellor G.J.). Pp. 147–154. ICARDA, Syria.



Herrmann, J.Y.-M. (2006). Inheritance and mapping of a powdery mildew resistance gene introgressed from Avena macrostachya in cultivated oat. Theoretical and Applied Genetics, 113: 429–437,

Heywood, V.H. (1994). The measurement of biodiversity and the politics of implementation. In: Systematics and conservation evaluation (eds. Forey, P.L., C.J. Humphries and R.I. Vane-Wright) Systematic Association Special Volume 50, Pp.15–22. Oxford University Press, Oxford.

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.

Hoan, N.T., Sarma, N.P. and Siddiq, E.A. (1997). Identification and characterization of new sources of cytoplasmic male sterility in rice. Plant Breeding, 116: 547–551

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.

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.

Holbrook, C.C., Timper, P. and Culbreath A.K. (2003). Resistance to tomato spotted wilt virus and root-knot nematode in peanut interspecific breeding lines. Crop Science, 43: 1109–1113.

Hollaway, G.J., Bretag, T.W. and Price, T.V. (2007). The epidemiology and management of bacterial blight (*Pseudomonas syringae* pv. pisi) of field pea (*Pisum sativum*) in Australia: a review. Australian Journal of Agricultural Research, 58(11): 1086–1099.

Hooftman, D.A.P., De Jong, M.J., Oostermeijer, G.B. and den Nijs, H.J.C.M. (2007). TI: Modelling the long-term consequences of crop x wild relative hybridization: a case study using four generations of hybrids. Journal of Applied Ecology, 44(5): 1035–1045.

Hoyt, E. (1988). Conserving the Wild Relatives of Crops. IBPGR, IUCN, WWF, Rome and Gland.

ICRISAT (1995). ICRISAT Annual Report 1994. ICRISAT, India.

INIBAP/IPGRI (2006). Global Conservation Strategy for Musa (Banana and Plantain). INIBAP/IPGRI, Montpellier/Rome, Italy.

IPCC (2007). Fourth Assessment Report Climate Change 2007: Synthesis Report. Intergovernmental Panel on Climate Change, Geneva, Switzerland.

Iriondo, J.M., Dulloo, E., Maxted, N. (Eds.) (2008). Conserving Plant Genetic Diversity in Protected Areas: Population Management of Crop Wild Relatives. CAB International Publishing, Wallingford.

IRRI (2003). Sulfate tolerance is transferred through wide hybridization. Media Hotline, April–June 2003. International Rice Research Institute. Available at: http://beta.irri.org/news/index.php/200306295125/bulletin/hotline/Media-Hotline-April-June-2003.html [Accessed 03 March 2009].

IRRI (2004). 2003 Annual Report. Plant Breeding, Genetics, and Biochemistry Division. International Rice Research Institute, 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. http://www.irri.org/science/progsum/pdfs/DGReport2007/Project-1.pdf [Accessed 21 October 2008]

Ishii, T., Brar, D.S., Multani, D.S. and Khush. G.S. (1993). Molecular tagging of genes for brown plant hopper resistance and earliness introgressed from *Oryza australiensis* into cultivated rice, *O. sativa*. Genome, 37: 217–221.

ITTO (2006). International Tropical Timber Agreement. International Tropical Timber Organization, Geneva.

IUCN (2001). IUCN Red List Categories and Criteriia: Version 3.1. IUCN Species Survival Commission. IUCN, Gland, Switzerland and Cambridge, UK. http://www.iucnredlist.org/static/categories_criteria_3_1 [Accessed 21 October 2008].

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,

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.

Jena, K.K., and Khush. G.S. (1990). Introgression of genes from *Oryza officinalis* Well ex Watt to cultivated rice, O. sativa L. Theoretical and Applied Genetics, 80: 737–745.

Jennings, D.L. (1995). Cassava, Manihot esculenta (Euphorbiaceae). In: Smartt, J. and Simmonds, N.W., Evolution of Crop Plants, Pp. 128–132. Longman Group, Harlow, Essex.

Jiang, S.-M., Hu, J., Yin, W.-B., Chen, Y.-H., Wang, R.R.-C. and Hu Z.-M. (2005). Cloning of resistance gene analogs located on the alien chromosome in an addition line of wheat – *Thinopyrum intermedium*. Theoretical and Applied Genetics, 111: 923–931.

Johnson, N. (1995). Biodiversity in the balance: approaches to setting geographic conservation priorities. Biodiversity Support Program, Washington, D.C.

Jones, I.T. and Pickering, R.A. (1978). The mildew resistance in *Hordeum bulbosum* and its transference into *H. vulgare genotypes*. Annals of Applied Biology, 88: 295–298.

Jordan, J., Butler, D., Henzell, B., Drenth, J. and McIntyre, L. (2004). Diversification of Australian sorghum using wild relatives. New Directions for a Diverse Planet: Proceedings of the 4th International Crop Science Congress, Brisbane, Australia, 26 Sep—1 Oct 2004.

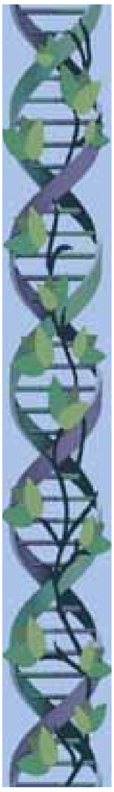
Kameswara Rao, N., Reddy, L.J. and Bramel, P.J. (2003). Potential of wild species for genetic enhancement of some semi-arid food crops. Genetic Resources and Crop Evolution, 50: 707–721.

Kansas State University (2006). Germplasm releases from the Wheat Genetic and Genomic Resources Centre. Available at: http://www.k-state.edu/wgrc/Germplasm/grmplsm.html [Accessed 03 March 2009].

Kell, S.P., Maxted, N. and Ford-Lloyd, B.V. (2003). Introducing PGR Forum. Crop Wild Relative, 1: 4–7.

Kell, S.P., Knüpffer, 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., Knüpffer, H., Jury, S.L., Ford-Lloyd, B.V. and Maxted, N. (2008). 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.



Kerber, E.R. (1987). Resistance to leaf rust in hexaploid wheat: Lr32, a third gene derived from *Triticum tauschii*. Crop Science, 27: 204–206.

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.

Kerber, E.R. and Dyck, P.L. (1973). Inheritance of stem rust resistance transferred from diploid wheat (*Triticum monococcum*) to tetraploid and hexaploid wheat and chromosome location of the gene involved. Canadian Journal of Genetics and Cytology, 15: 397–409.

Khan, I.A., Procunier, J.D., Humphreys, D.G., Tranquilli, G., Schlatter, A.R., Marcucci-Poltri, S., Frohberg, R., and Dubcovsky D. (2000). Development of PCR-based markers for a high grain protein content gene from *Triticum turgidum* ssp. *dicoccoides* transferred to bread wheat. Crop Science, 40: 518–524.

Khush, G.S., Ling, K.C., Aquino, R.C. and Acquiero. V.M. (1977). Breeding for resistance to grassy stunt in rice. Plant Breeding Papers, 1(4): 3–9.

Khush, G.S., Bacalango, E. and Ogawa. T. (1990). A new gene for resistance to bacterial blight from *O. longistaminata*. Rice Genetics Newsletter, 7: 121–122.

Kindler, S.D. and Springer, T.L. (1991). Resistance to Russian wheat aphid in wild *Hordeum* species. Crop Science, 31(1): 94–97.

King, I.F., Forster, B.P., Law, C.C., Cant, K.A., Orford, S., Gorham, J., Reader, S. and T,E. Miller, T.E. (1997a). Introgression of salt tolerance genes from *Thinopyrum bessarabicum* into wheat. New Phytologist, 137: 75–81.

King, I.P., Law, C.C., Cant, K.A., Orford, S., Gorham, J., Reader, S. and T,E. Miller, T.E. (1997b). *Tritipyrum*, a potential new salt-tolerant cereal. Plant Breeding, 116: 127–132.

Kushnir, U. and Halloran, G.M. (1984). Transfer of high kernel weight and high protein from the wild tetraploid wheat (*Triticum turgidum* var. *dicoccoides*) to bread wheat (*T. aestivum*) using homologous and homoeologous recombination. *Euphytica*, 33: 249–255.

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.

Lee, S.-J., Oh, C-S., Choi, Y.H., Suh, J.-P., Ju, H.-G., Yoon, D.B. and Ahn. S.-N. (2004). Mapping of quantitative trait loci controlling cold tolerance in an *Oryza sativa* x *O. rufipogon* BC1F7 population, Korean Journal of Breeding, 36: 1–8.

Lee, S.-J., Oh, C.-S., Suh, J.-P., McCouch, S.R. and Ahn, S.-N. (2005). Identification of QTL for domestication-related and agronomic traits in an *Oryza sativa* x *O. rufipogon* BC1F7 population. Plant Breeding, 124: 209–219.

Lehmann, L. and von Bothmer, R. (1988). Hordeum spontaneum and land races as a gene resource for barley breeding. In: Cereal Breeding Related to Integrated Cereal Production (eds. Jorna, M.L. and Slootmaker, L.A.J.). Pp. 190–194. Wageningen.

Lexer, C., Lai, Z. and Rieseberg, L.H. (2004). Candidate gene polymorphisms associated with salt tolerance in wild sunflower hybrids: implications for the origin of *Helianthus paradoxus*, a diploid hybrid species. New Phytologist, 161: 225–233.

Lin, S.C., and Yuan, L.P. (1980). Hybrid rice breeding in China. In: Innovative Approaches to Rice Breeding. pp. 35–51. International Rice Research Institute, Manila, Philippines.

Liang, F., Deng, Q., Wang, Y., Xiong, Y., Jin, D., Li, J. and Wang. B. (2004). Molecular marker assisted selection for yield-enhancing genes in the progeny of "9311" x O. rufipogon" using SSR. *Euphytica*, 139:159–165.

Liu, B., Piao, H.M., Zhao, F.S., Zhao, J.H. and Zhao R. (1999). Production and molecular characterisation of rice lines with introgressed traits from a wild species *Zizania latifolia* (Griseb.). Journal of Genetics and Breeding, 53: 279–284.

Liu, S., Park, S.J., Yu, K., Conner, R.L., Balasubramanian, P., Mündel, H.H. and Kiehn, F.A. (2004/2005). Application of molecular markers to breed resistant cultivars in dry bean. The Pulse Beat, 44: 26–27. Available at: http://www.manitobapulse.ca/pdf/mag-2004-2005_w.pdf [Accessed 03 March 2009].

Lopez, L. and Herrera, H. (1970). Manihot carthaginensis una yuca silvestre con alto contenido proteico. Contribucion del ICA a la VIII Reunion de Fitotecnica. Bogota, Colombia.

Löve, S. (1999). Founding clones, major contributing ancestors, and exotic progenitors of prominent North American potato cultivars. American Journal of Potato Research, 76: 263–272.

Ma, H., Singh, R.P. and Mujeeb-Kazi, A. (1995). Resistance to stripe rust in *Triticum turgidum*, *T. tauschii* and their synthetic hexaploids, *Euphytica*, 82: 117–124.

Mabberley, D.J. (1997). The Plant-Book. A Portable Dictionary of the Vascular Plants. Cambridge University Press, Cambridge.

Malhotra, R.S., Khalaf, G., Hajjar, S. and Arslan, S. (2003). Interspecific hybridization in chickpea. In: Chickpea research for the millennium. Proceedings of International Chickpea Conference, pp. 41–50, Indira Gandhi Agricultural University, Raipur, Chattisgarh, India.

Mallikarjuna, N. (1999). Ovule and embryo culture to obtain hybrids from interspecific incompatible pollinations in chickpea. *Euphytica*, 110: 1–6.

Mallikarjuna, N., and Saxena, K.B. (2005). A new cytoplasmic nuclear male-sterility system derived from cultivated pigeonpea cytoplasm. *Euphytica*, 142: 143–148.

Mallikarjuna, N., Pande, S., Jadhav, D.R., Sastri, D.C. and Rao. J.N. (2004). Introgression of disease resistance genes from *Arachis kempff-mercadoi* into cultivated groundnut. Plant Breeding, 123: 573–576.

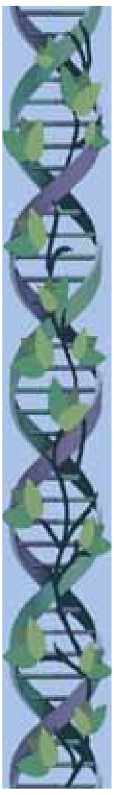
Marais, G.F., McCallum, B. and Marais, A.S. (2008). Wheat leaf rust resistance gene Lr59 derived from Aegilops peregrina. Plant breeding, 127(4): 340–345.

Marri, P.M., Sarala, N., Reddy, L.V. and Siddiq, E.A. (2005). Identification and mapping of yield and yield related QTL from art Indian accession of *Oryza rufipogon*. BMC Genetics, 6: 33.

Martín, A. and Cabrera, A. (2005). *Cytogenetics* of *Hordeum chilense*: current status and considerations with reference to breeding. Cytogenetic and Genome Research, 109(1/3): 378–384.

Martinez C.P., Borrero J., Almeida A., Duque M.C., Correa-Victoria F., Silva, J. and Tohme, J. (2002). Utilization of New Alleles from Wild Rice Species to Improve Cultivated Rice in Latin America. http://www.ciat.cgiar.org/riceweb/pdfs/poster_alleles.pdf [Accessed 01 February 2009].

Matus, I., Corey, A., Filichkin, T., Hayes, P.M., Vales, M.I., Kling, J., Riera-Lizarazu, O., Sato, K., Powell, W. and Waugh R. (2003). Development and characterization of recombinant chromosome substitution lines (RCSLs) using *Hordeum vulgare* subsp. *spontaneum* as a source of donor alleles in a *Hordeum vulgare* subsp. *vulgare* background. Genome, 46: 1010–1023.



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. and Hawkes, J.G. (1997d). Complementary Conservation Strategies. In: Plant genetic conservation: the *in situ* approach (eds. Maxted, N., Ford-Lloyd, B.V. and Hawkes, J.G.), Pp. 20–55. Chapman & Hall, London.

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., 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.

McFadden, E.S. (1930). A successful transfer of emmer characters to vulgare wheat. Journal of the American Society of Agronomy, 22: 1020–1034.

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 10th International Wheat Genetics Symposium. S.I.M.I., Rome, Vol. 4 and MacGene2003 database on CD.

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

Mesfin, A., Frohberg, R.C. and Anderson, J.A. (1999). RFLP markers associated with high grain protein from *Triticum turgidum* L. var. dicoccoides introgressed into hard red spring wheat. Crop Science, 39: 508–513.

Mesfin, A., Frohberg, R.C., Khan, K. and Olson T.C. (2000). Increased grain protein content and its association with agronomic and end-use quality in two hard red spring wheat populations derived from the *Triticum turgidum* L. var. *dicoccoides*. *Euphytica*, 116: 237–242.

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.

Moncada, P., Martínez, C., Borrero, J., Chatel, M., Gauch, Jr. H., Guimaraes, E., Tohme, J. and McCouch, S. (2001). Quantitative trait loci for yield and yield components in an *Oryza sativa* × *Oryza rufipogon* BC2F2 population evaluated in an upland environment. Theoretical and Applied Genetics, 102: 41–52.

Moseman, J.G., Nevo, E. and Zohary, D. (1983). Resistance of *Hordeum spontaneum* collected in Israel to infection with *Erysiphe graminis hordei*. Crop Science, 23: 1115–1119.

Moss, J.P., Singh, A.K., Reddy, L.J., Nigam, S.N., Subrahmanyam, P., McDonald, D. and Reddy, A.G.S. (1997). Registration of ICGV 87165 peanut germplasm with multiple resistance. Crop Science, 37: 1028.

Moss, J.P., Singh, A.K., Nigam, S.N., Hildebrand, G.L., Govinden, N., Ismael, F.M., Subrahmanyam, P. and Reddy L.J. (1998). Registration of ICGV SM 86715. Crop Science, 38: 572.

Mujeeb-Kazi, A. and Hettel, G.P. (1995). Utilizing Wild Grass Biodiversity in Wheat Improvement: 15 Years of Wide Cross Research at CIMMYT. CIMMYT Research Report No. 2. pp 1–140. CIMMYT, Mexico, D.F.

Mujeeb-Kazi, A., Villareal, R.L. Gilchrist, L.I. and Rajaram, S. (1996). Registration of five wheat germplasm lines resistant to Helminthosporium leaf blight. Crop Science, 36: 216–217.

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.

Multani, D.S., Jena, K.K., Brar, D.S., de los Reyes, B.C., Angeles, E.R. and Khush, G.S. (1994). Development of monosomic alien addition lines and introgression of genes from *O. australiensis*, Domin. to cultivated rice *O. sativa*. Theoretical and Applied Genetics, 88: 102–109.

Munoz, L.C., Blair, M.W., Duque, M.C., Tohme, J. and Roca, W. (2004). Introgression in common bean x Tepary bean interspecific congruity-backcross lines as measured by AFLP marker. Crop Science, 44: 637–645.

Nair, S.G. and Unnikrishnan, M. (2007). Recent trends in cassava breeding in India. In Ortiz, R. and N.M.A. Nassar (eds.) Cassava Improvement to Enhance Livelihoods in Sub-Saharan Africa and North-eastern Brazil. First International Meeting on Cassava Breeding, Biotechnology and Ecology, Brazil, 11–15 November 2006: Proceedings. Pp. 37–53. University of Brazil.

Nassar, N.M.A. (2000). Wild cassava, Manihot spp.: biology and potentialities for genetic improvement. Genetics and Molecular Biology, 23: 201–212.

Nassar, N.M.A. (2003). Gene flow between cassava, Manihot esculenta Crantz, and wild relatives. Genetics and Molecular Research, 2(4): 334–347.

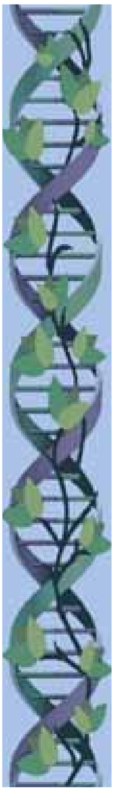
Nassar, N.M.A. (2007). Cassava genetic resources: wild species and indigenous cultivars and their utilization for breeding of the crop. In Ortiz, R. and N.M.A. Nassar (eds.) Cassava Improvement to Enhance Livelihoods in Sub-Saharan Africa and North-eastern Brazil. First International Meeting on Cassava Breeding, Biotechnology and Ecology, Brazil, 11–15 November 2006: Proceedings. University of Brazil. Pp. 5–30.

Nassar, N.M.A. and Dorea, G. (1982). Protein contents of cassava cultivars and its hybrid with *Manihot* species. *Turrialba*, 32: 429–432.

Nassar, N.M.A., Santos, E. and David, S. (2000). The transference of apomixis genes from Manihot neusana Nassar to cassava, *M. esculenta* Crantz. *Hereditas*, 132:167–170.

Nault, L.R., Gordon, D.T., Damsteegt, V.D., and Iltis, H.H. (1982). Response of annual and perennial teosintes (Zea) to six maize viruses. Plant Disease, 66: 61–62.

Nguyen, B., Brar, D., Bui, B., Nguyen, T., Pham, L. and Nguyen, H. (2003). Identification and mapping of the QTL for aluminium tolerance introgressed from the new source, *Oryza rufipogon* Griff, into indica rice (*Oryza sativa* L.). Theoretical and Applied Genetics, 106: 583–593.



Noori, S.A.S. (2005). Assessment for salinity tolerance through intergeneric hybridization: *Triticum durum* x *Ae. Speltoides*. *Euphytica*, 146: 149–155.

Novak, F.J. (1992). *Musa* (Bananas and Plantains). In: Biotechnology of Perennial Fruit Crops (eds. Hammerschlag, F. A. and Lite, R. E.). Pp. 449–488. CAB International, Wallingford, Oxon, UK.

Nwanze, K.F., Prasada, Rao, K.E. and Soman, P. (1990). Understanding and manipulating resistance mechanisms in sorghum for control of the shoot-fly. In: Proceedings of International Symposium on molecular and genetic approaches to plant stress. New Delhi. 14–17th Feb 1990.

Nweke, F. (2004). New Challenges in the Cassava Transformation in Nigeria and Ghana. Environment and Production Technology Division Discussion Paper. International Food Policy Research Institute, Washington, DC.

Oliver, R.E., Cai, X., Xu, S.S., Chen, X. and Stack. R.W. (2005). Wheat-alien species derivatives: A novel source of resistance to fusarium head blight in wheat. Crop Science, 45: 1353–1360.

Patto, M.C.V., Aardse, A., Buntjer, J., Rubiales, D., Martín, A. and Niks, R.E. (2001). Morphology and AFLP markers suggest three *Hordeum chilense* ecotypes that differ in avoidance to rust fungi. Canadian Journal of Botany, 79(2): 204–213.

Paulsen, G.M. (2000). International Contributions to the improvement and marketing of Kansas wheat. Keeping Up With Research, 126, February 2000. Kansas State University Agricultural Experiment Station and Cooperative Extension Service. Available at: http://www.oznet.ksu.edu/library/crpsl2/srl126.pdf [Accessed 03 March 2009].

Peňa, 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.

Pestsova, E.G., Borner, A. and Roder, M.S. (2006). Development and QTL assessment of *Triticum aestivum-Aegilops tauschii* introgression lines. Theoretical and Applied Genetics, 112: 634–647.

PGR Forum (2005). Crop Wild Relative Information System (CWRIS). University of Birmingham, Birmingham, UK. http://www.pgrforum.org/cwris/cwris.asp [Accessed 21 October 2008].

Phillips, O.L. and Meilleur, B. (1998). Usefulness and economic potential of the rare plants of the United States: a status survey. Economic Botany, 52(1): 57–67.

Pickering, R. and Johnston, P.A. (2005). Recent progress in barley improvement using wild species of *Hordeum*. Cytogenetic and Genome Research, 109: 344–349.

Pickering, R., Steffenson, B.J., Hill, A.M. and Borovkova I. (1998). Association of leaf rust and powdery mildew resistance in a recombinant derived from a *Hordeum vulgare* x *H. bulbosum hybrid*. Plant Breeding, 117: 83–84.

Pickering, R.A., Hill, A.M., Michel, M. and Timmerman-Vaughan. G.M. (1995). The transfer of a powdery mildew resistance gene from *Hordeum bulbosum* L. to barley (*H. vulgare* L.) chromosome 2 (2I). Theoretical and Applied Genetics, 91: 1288–1292.

Pillen, K., Zacharias, A. and Leon, J. (2003). Advanced backcross QTL analysis in barley (*Hordeum vulgare* L). Theoretical and Applied Genetics, 107: 340–352.

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.

Porte, W.A. and Walker, H.B. (1945). A cross between *Lycopersicon esculentum* and disease resistant *L. peruvianum*. Phytopathology, 35: 931–933.

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. (1986). The first resource: wild species in the North American economy. Yale University, New Haven.

Prescott-Allen, R. and Prescott-Allen, C. (1988). Genes From the Wild: Using Wild Genetic Resources for Food and Raw Materials. 2nd edn. International Institute for Environment and Development/Earthscan Publications, London.

Putt, E.D. (1978). History and present world status. In: Sunflower and science and technology (ed. Carter, J.P.). Pp. 1–29. American Society of Agronomy, Madison, WI (USA).

Qiu, Y.C., Zhou, R.H., Kong, X.Y., Zhang, S.S. and Jia, J.Z. (2005). Microsatellite mapping of a Triticum urartu Tum. derived powdery mildew resistance gene transferred to common wheat (*Triticum aestivum* L.). Theoretical and Applied Genetics, 111: 1524–1531.

Rao, G.U., Ben Chaim, A., Borovsky, Y. and Paran, I. (2003). Mapping of yield-related QTLs in pepper in an interspecific cross of *Capsicum annum* and *C. frutescens*. Theoretical and Applied Genetics, 106: 1457–1466.

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.

Reddy, L.J. (1990). Morphology. In: The *pigeonpea* (eds. Nene, Y.L., Hall, S.D., Sheila, V.K.). Pp. 47–87. ICRISAT, CAB International, Wallingford, UK.

Reddy, L.J., Green, J.M., Bisen, S.S., Singh, U. and Jambunathan R. (1979). Seed protein studies on Cajanus cajan, Atylosia spp. and some hybrid derivatives. In: Proceedings of Symposium on Seed Protein Improvement in Cereals and Grain Legumes. Vol. II. pp. 105–117. IAEA, FAO and GSF, Neuherberg, Federal Republic of Germany.

Reddy, L.J., Nigam, S.N., Moss, J.P., Singh, A.K., Subrahmanyam, P., McDonald, D. and Reddy. A.G.S. (1996). Registration of ICGV 86699 peanut germplasm line with multiple disease and insect resistance. Crop Science, 36: 821

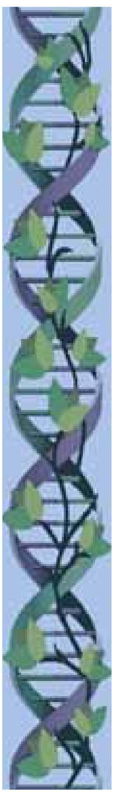
Richardson, D.M., van Wilgen, B.W., Higgins, S.I., Trinder-Smith, T.H., Cowling, R.M. and McKell, D.H. (1996). Current and future threats to plant biodiversity on the Cape Peninsula, South Africa. Biodiversity and Conservation, 5: 607–647.

Rick, C.M. and Chetelat, R. (1995). Utilization of related wild species for tomato improvement, First International Symposium on Solanaceae for Fresh Market. *Acta Horticulturae*, 412: 21–38.

Riggs, R.D., Wang, S., Singh, R.J. and Hymowitz, T. (1998). Possible transfer of resistance to *Heterodora glycine* from *Glycine tomentella* to *Glycine max*. Journal of Nematology, 30: 547–552.

Rong, J.K., Millet, E., Manisterski, J. and Feldman, M. (2000). A new powdery mildew resistance gene: Introgression from wild emmer into common wheat and RFLP-based mapping. *Euphytica*, 115: 121–126.

Ross, H. (1979). Wild species and primitive cultivars as ancestors of potato varieties. In: Proceedings of the conference broadening the genetic base of crops (eds. Zeven, A.C. and van Harten A.M.). Pp. 237–245. Centre for Agricultural Publishing and Documentation, Wageningen.



Ross, H. (1986). Potato Breeding – Problems and Perspectives. Fortschritte der Pflanzenzüchtung 13. Paul Parey, Berlin and Hamburg.

Ruge, B., Linz, A., Pickering, R., Proeseler, G., Greif, P. and Wehling. P. (2003). Mapping of Rym14HB, a gene introgressed from *Hordeum bulbosum* and conferring resistance to BaMMV and BaYMV in barley. Theoretical and Applied Genetics, 107: 965–971.

Ruge-Wehling, B., Linz, A., Habeku, A. and Wehling. P. (2006). Mapping of RYMl6Hb, the second soilborne virus resistance gene introgressed from *Hordeum bulbosum*. Theoretical and Applied Genetics, 113: 867–673.

Russell, G.E. (1978). Plant breeding for pest and disease resistance. Butter¬worths. London, Boston, 485 pp.

Sakamoto, S. (1976). Breeding of a new sweet potato variety, Minamiyutaka, by the use of wild relatives. Japanese Agricultural Research Questions, 10(4): 183–186.

Saxena, K.B. and Kumar. R.V. (2003). Development of a cytoplasmic nuclear male-sterility system in pigeonpea using *C. scarabeoides* (L.) Thouars. Indian Journal of Genetics, 63: 225–229.

Saxena, K.B., Srivastava, D.P. and Tikka, S.B.S. (1998). Breaking yield barrier in pigeonpea through hybrid breeding. In: Proceedings of National Symposium on Biotic and Abiotic Stress of Pulse Crops. 26–28 June 1998. Pp. 55–64. Indian Institute of Pulses Research, Kanpur

Saxena, K.B., Kumar, R.V., Srivastava, N. and Shiying, B. (2005). A cytoplasmic-nuclear male-sterility system derived from a cross between Cajanus cajanifolius and Cajanus cajan. *Euphytica*, 145: 289–294

Schooler, A.B. and Franckowiak J.D. (1981). Registration of North Dakota 497 and North Dakota 586 barley germplasm Crop Science, 21: 352.

Sebolt, A.M., Shoemaker, R.C. and Diers, B.W. (2000). Analysis of a quantitative trait locus allele from wild soybean that increases seed protein concentration in soybean. Crop Science, 40: 1438–1444.

Septiningsih, E.M., Prasetiyono, J., Lubis. E., Tai, T.H., Tjubaiyat, T., Moelijopawiro, S. and McCouch, S.R. (2003). Identification of quantitative trait loci for yield and yield components in an advanced backcross population derived from the *Oryza sativa* variety IR64 and the wild relative *O. rufipogon, Theoretical* and Applied Genetics, 107: 1419–1432.

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.

Sharma, H.C. and Gill, B.S. (1983). Current status of wide hybridization in wheat. *Euphytica*, 32: 17–31.

Sharma, H.C., and Franzmann. B.A. (2001). Host-plant preference and oviposition responses of the sorghum midge, *Stenodiplosis sorghicola* (Coquillett) (Dipt., Cecidomyiidae) towards wild relatives of sorghum. Journal of Applied *Entomology*, 125: 109–114.

Sharma, H., Ohm, H., Goulart. L., Lister, R., Appels, R. and Benlhabib, Q. (1995). Introgression and characterization of barley yellow dwarf virus resistance from *Thinopyrum intermedium* into wheat. Genome, 38: 406–413.

Shen, X. and Ohm, H. (2007). Molecular mapping of a QTL for resistance to Fusarium head blight introgressed from *Thinopyrum ponticum* into wheat. Plant and Animal Genome, XV: 307.

Simpson, C. and Starr, J. (2001). Registration of "COAN" peanut. Crop Science, 41: 918.

Simpson, C.E. and Smith, O.D. (1975). Registration of Tamnut 74 peanut. Crop Science, 15: 603–604.

Simpson, C.E., Starr, J.L., Church, G.T., Burow, M.D. and Paterson A.H. (2003). Registrations of cultivars: registration of 'nematam' peanut. Crop Science, 43: 1561.

Singh, S. (2001). Broadening the genetic base of common bean cultivars. Crop Science, 41: 1659–1675.

Singh, K.B. and Ocampo, B. (1997). Exploitation of wild Cicer species for yield improvement in chickpea. Theoretical and Applied Genetics, 95: 191–222.

Singh, A.K., Dwivedi, S.L., Pande, S., Moss, J.P., Nigam, S.N. and Sastri D.C. (2003). Registration of rust and late leaf spot resistant peanut germplasm lines. Crop Science, 43: 440–441.

Singh, S., Gumber, R.K., Joshi, N. and Singh, K. (2005). Introgression from wild *Cicer reticuiatum* to cultivated chickpea for productivity and disease resistance. Plant Breeding, 124: 477–480.

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.

Sondahl, M.R. Evans, D.A. Prioli, L.M. and Silva, W.J. (1984). Tissue Culture Regeneration of Plants in *Zea diploperennis*, a Close Relative of Corn. Nature Biotechnology, 2: 455–458.

Song, Z., Li, B., Chen, J. and Lu, B.-R. (2005). Genetic diversity and conservation of common wild rice (Oryza rufipogon) in China. Plant Species Biology, 20: 83–92.

Spetsov, P., Mingeot, D., Jacquemin, J.M., Samardjieva, K. and Marinova, E. (1997). Transfer of powdery mildew resistance from *Aegilops variabilis* into bread wheat. *Euphytica*, 93: 49–54.

Stalker, H.T. and Lynch, R.E. (2002). Registration of Four Insect-Resistant Peanut Germplasm Lines. Crop Science, 42: 313–314.

Stalker, H.T., Beute, M.K., Shew, B.B. and Isleib, T.G. (2002a). Registration of five leafspot resistant peanut germplasm lines. Crop Science, 42: 314–316.

Stalker, H.T., Beute, M.K., Shew, B.B. and Barker, K.R. (2002b). Registration of two root-knot nematode-resistant peanut germplasm lines. Crop Science, 42: 312–313.

Stebbins, G.L. (1958). The inviability, weakness, and sterility of interspecific hybrids. Advances in Genetics, 9: 147–215.

Stevens, M.A., and Rick, C.M. (1986). The tomato crop. A scientific basis for improvement. Chapman and Hall, New York.

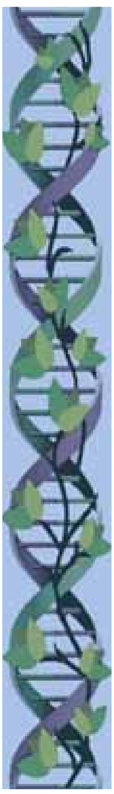
Stolton, S., Maxted, N., Ford-Lloyd, B., Kell, S.P. and Dudley, N. (2006). Food Stores: Using Protected Areas to Secure Crop Genetic Diversity. WWF Arguments for protection series. WWF, Gland, Switzerland.

Stuart, S.N. and Adams, R.J. (1990). Biodiversity in Sub-Saharan Africa and its Islands: Conservation, Management and Sustainable Use. International Union for Conservation of Nature and Natural resources, Gland.

Sun, H., Zhao, L. and Huang, M. (1997). Cytoplasmic-nuclear male sterile soybean line from interspecific crosses between *G. max* and *G. soja*. In: B. Napompeth (ed.), Proceedings of 5th World Soybean Research Conference , pp. 99–102. Kasetsart University Press, Bangkok, Thailand.

Suneson, C.A. (1967a). Registration of Rapida oats. Crop Science, 7: 168.

Suneson, C.A. (1967b). Registration of Sierra oats. Crop Science, 7: 168.



Suszkiw, J. (2005). Hessian Fly-Resistant Wheat Germplasm Available Agricultural Research Service. News and Events, United States Department of Agriculture.

Szigat, G. and Pohler, W. (1982). *Hordeum bulbosum* x *H. vulgare* hybrids and their back-crosses with cultivated barley. Cereal Research Communications, 10: 73–78.

Takeda, K. and Frey. K.J. (1976). Contributions of vegetative growth rate and harvest index to grain yield of progenies from *Avena sativa* x *A. sterilis* crosses. Crop Science, 16: 817–821.

Talame, V., Sanguineti, M.C., Chiapparino, E., Bahri, H., Salem, B.M., Forster, B,P., Ellis, R.P., Rhouma, S., Zoumarou, W., Waugh, R. and Tuberosa R. (2004). Identification of *Hordeum spontaneum* QTL alleles improving field performance of barley grown under rainfed conditions. Annals of Applied Biology, 144: 309–319.

Tanksley, S.D. and McCouch, S.R. (1997). Seed banks and molecular maps: Unlocking genetic potential from the wild. Science, 277: 1063–1066.

Tanksley, S., Grandillo, S., Fulton, T.M., Zamir, D., Eshed, Y., Petiard, V., Lopez, J. and Beck-Bunn, T. (1996). Advanced backcross QTL analysis in a cross between an elite processing line of tomato and its wild relative *L. pimpinellifolium*. Theoretical and Applied Genetics, 92: 213–224.

Thieme, R., Rakosy-Tican, E., Gavrilenko, T., Antonova, O., Schubert, J., Nachtigall, M., Heimbach, U. and Thieme, T. (2008). Novel somatic hybrids *Solanum tuberosum* L. + *Solanum tarnii*) and their fertile BC1 progenies express extreme resistance to potato virus Y and late blight. Theoretical and Applied Genetics 116, 691–700.

Thomson, M.J., Tai, T.H., McClung, A.M., Lai, X.H. and Hinga, M.E., *et al*. (2003). Mapping quantitative trait loci for yield, yield components and morphological traits in an advanced backcross population between *Oryza rufipogon* and the *Oryza sativa* cultivar Jefferson. Theoretical and Applied Genetics, 107: 479–493.

Thuiller, T., Lavorel, S., Araújo, M.B., Sykes M.T. and Prentice, I.C. (2005). Climate change threats to plant diversity in Europe. PNAS, 102(23): 8245–8250.

Tian, F., Zhu, Z., Zhang, B., Tan, L., Fu, Y., Wang, X. and Sun, C.Q. (2006). Fine mapping of a quantitative trait locus for grain number per panicle from wild rice (*Oryza rufipogon* Griff.). Theoretical and Applied Genetics, 113: 619–629.

Toubia-Rahme, H., Johnston, P.A., Pickering, R.A. and Steffenson. B.J. (2003). Inheritance and chromosomal location of *Septoria passerinii* resistance introgressed from *Hordeum bulbosum* into *Hordeum vulgare*. Plant Breeding, 122: 405–409.

UNCCD (2005). United Nations Convention to Combat Desertification in those Countries Experiencing Serious Drought and/or Desertification, Particularly in Africa. Secretariat of the United Nations Convention to Combat Desertification. http://www.unccd.int/convention/text/pdf/leaflet_eng.pdf [Accessed 12 March 2009].

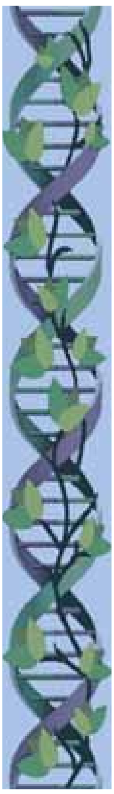
Unnikrishnan, M., Easwari Amma, C.S., Sreekumari, M.T., Sheela, M.N. and Mohan, C. (2007). Cassava germplasm conservation and improvement in India. In: Howeler, R.H. (ed.), Cassava Research and Development in Asia: Exploring New Opportunities for an Ancient Crop: Proceedings of the Seventh Regional Workshop held in Bangkok, Thailand. Oct. 28–Nov. 1, 2002. Pp. 87–100.

Valkoun, J.J. (2001). Wheat pre-breeding using wild progenitors. *Euphytica*, 119: 17–23.

Van der Maesen, L.J.G. (1979). Cicer L. In: *Flora Iranica* (ed. Rechinger, K.H.) 140: 1–15. Graz, Akademische Druck- und Verlagsanstalt.

Vavilov, N.I. (1949). The origin, variation, immunity and breeding of cultivated plants. *Chronika Botanica*, 13: 1–54.

Vega, U. and Frey, K.B. (1980). Transgressive segregation in inter- and intra-specific crosses of barley. *Euphytica*, 29: 585–594.



Villareal, R.L., Mujeeb-Kazi, A., Fuentes-Davila, G. and Rajaram, S. (1996) Registration of four synthetic hexaploid wheat germplasm lines derived from *Triticum turgidum* x *T. tauschii* crosses and resistance to kernal bunt. Crop Science, 36: 218.

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.

Virmani, S. and Shinjyo, C. (1988). Current status of analysis and symbols for male sterile cytoplasms and fertility restoring genes. Rice Genetics Newsletters, 5: 9–15.

Vollbrecht, E. and Sigmon, B. (2005). Amazing grass: developmental genetics of maize domestication. Biochemical Society Transactions, 33: 1502–1506.

von Korff, M., Wang, H., Leon, J, and Pillen. K. (2005). AB-QTL analysis in spring barley. I, Detection of resistance genes against powdery mildew, leaf rust and scald introgressed from wild barley. Theoretical and Applied Genetics, 111: 583–590.

von Korff, M., Wang, H., Leon, J. and Pillen K. (2006). AB-QTL analysis in spring barley; II. Detection of favourable exotic alleles for agronomic traits introgressed from wild barley (*Hordeum vulgare* ssp. *spontaneum*), Theoretical and Applied Genetics, 112: 1221–1231.

Vuylsteke, D.R., Swennen, R.L. and Ortiz, R. (1993). Development and performance of black sigatoka-resistant tetraploid hybrids of plantain (Musa spp., AAB group). Euphytica, 65: 33–42.

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.

Walther, U., Rapke, H., Proeseler, G. and Szigat. G. (2000). *Hordeum bulbosum*: A new source of disease resistance-transfer of resistance to leaf rust and mosaic viruses from *H. bulbosum* into winter barley. Plant Breeding, 119: 215–218.

Wang, W., Vinocur, B. and Altaian, A. (2003). Plant responses to drought, salinity and extreme temperatures: Towards genetic engineering for stress tolerance. Planta, 218: 1–14.

Wanjari, K.B., Patil, A.N., Manapure, P., Manjayya, J.G. and Manish, P. (2001). Cytoplasmic male sterility in pigeonpea with cytoplasm from *Cajanus volubilis*. Annals of Plant Physiology, 13: 170–174,

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., Peňa, R.J. and Mujeeb-Kazi, A. (1993). Seed protein and isozyme variations in *Triticum tauschii* (*Aegilops squarrosa*). Theoretical and Applied Genetics, 87: 257–263.

Williams, J.T, Lamoureux, C.H. and Wulijarni-Soetjipto, N. (eds). (1975). South East Asian plant genetic resources. IBPGR, BIOTROP and LIPI. Bogor. 272 pp.

Wilson, J.P. and Gates, R.N. (1993). Forage yield losses in hybrid pearl millet due to leaf blight caused primarily by *Pyricularia grisea*. Phytopathology, 83: 739–743.

Wilson, J.P., Gates, R.N. and Hanna, W.W. (1991). Effect of rust on yield and digestibility of pearl millet forage. Phytopathology, 81: 233–236.

Wilson, J.P., Hess, D.E. and Hanna, W.W. (2000). Resistance to Striga hermonthica in wild accessions of the primary gene pool of *Pennisetum glaucum*. Phytopathology, 90: 1169–1172.

Wroth, J.M. (1998). Possible role for wild genotypes of *Pisum* spp. to enhance ascochyta blight resistance in pea. Australian Journal of Experimental Agriculture, 38(5): 469 – 479.

Xiao, J., Grandillo, S., Sang, N., McCouch, S. and Tanksley, S. (1996). Genes from wild rice improve yield. Nature, 384: 223–224.

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.

Xing, Q., Zhao, B., Xu, K., Yang, H., Liu, X., Wang, S., Jin, D., Yuan, L. and Wang, B. (2004). Test of agronomic characteristics and amplified fragment length polymorphism analysis of new rice germplasm developed from transformation of genomic DNA of distant relatives. Plant Molecular Biology Reporter, 22(2): 155–164.

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.

Xu, J. and Kasha. K.J. (1992). Transfer of a dominant gene for powdery mildew resistance and DNA from Hordeum bulbosum into cultivated barley (*H. vulgare*). Theoretical and Applied Genetics, 84: 771–777.

Xu, J. and Snape, J.W. (1988). The cytology of hybrids between *Hordeum vulgare* and *H. bulbosum* revisited. Genome, 30: 486–494.

Yadav, S.S., Kumar, J., Turner, N.C., Berger, J., Redden, R., McNeil, D., Materne, M., Knights, E.J. and Bahl P.N. (2004). Breading for improved productivity, multiple resistance and wide adaptation in chickpea (*Cicer arietinum* L.). Plant Genetic Resources: Characterization and Utilization, 2: 181–187.

Yoon, D.B., Kang. K.-H., Kim, H.-J., Hong, S.-M., Ju, H.-G. and Ahu S.-N. (2005). Confirmation and identification of additional QTL for grain traits using an advanced backcross line from a cross between *Oryza sativa* and *O. grandiglumis,* Korean Journal of Breeding, 37: 101–108.

Yoon, D.B., Kang, K.-H., Kim, H.-J., Ju, H.-G., Kwon, S.-J., Suh, J.-P., Jeong. O.-Y. and Ahu S.-N. (2006). Mapping quantitative trait loci for yield components and morphological traits in an advanced backcross population between *Oryza grandiglumis* and the *O. japonica* cultivar Hwaseongbyeo. Theoretical and Applied Genetics, 112: 1052–1062.

Yu, M.Q., Person-Dedryver, F. and Jahier, J. (1990). Resistance to root-knot nematode, Meloidogyne naasi (Franklin), transferred from *Aegilops variabilis* Eig to bread wheat. Agronomie, 6: 451–456.

Zamir, D., Ekstein-Michelson, I., Zakay, Y., Navot, N., Zeidan, M., Sarfatti, M., Eshed, Y., Harel, E., Pleban, T., v. Oss, H., Kedar, N., Rabinowitch, H.D. and Czosnek, H. (1994). Mapping and introgression of a tomato yellow leaf curl virus tolerance gene, TY-1. Theoretical and Applied Genetics, 88: 141–146.

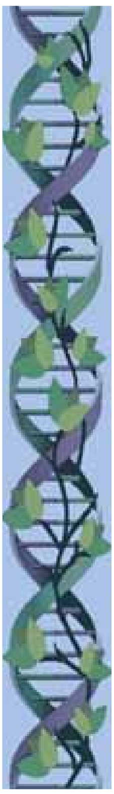
Zeven, A.C., Knott, D.R. and Johnson. R. (1983). Investigation of linkage drag in near isogenic lines of wheat by testing for seedling reaction to races of stem rust, leaf rust, and yellow rust. *Euphytica*, 32: 319–327.

Zhang, L., Pickering, R.A. and Murray. B.G. (2001). Hordeum vulgare x H. bulbosum tetraploid hybrid provides useful agronomic introgression lines for breeders. New Zealand Journal of Crop Horticultural Science, 29: 239–246.

Zhang, X., Zhou, S., Fu, Y., Su, Z., Wang, X. and Sun, C. (2006). Identification of a drought tolerant introgression line derived from Dongxiang common wild rice (*Oryza rufipogon* Griff.). Plant Molecular Biology, 62: 247–259.

Zhao, T.J., and Gai, J.Y. (2006). Discovery of new male-sterile cytoplasm sources and development of a new cytoplasmic-nuclear male-sterile line NJCMS3A in soybean. *Euphytica*, 152: 387–396.

ANNEXE 2: NATIONAL CWR CONSERVATION STRATEGIES



There are many potential approaches to systematic CWR conservation, but as every country contains CWR diversity, their obligations as signatories to the CBD and ITPGRFA, or other policy instruments, require that they systematically conserve this diversity. We review here how a national approach to developing a CWR conservation strategy can be implemented, including both complementary *in situ* and *ex situ* measures.

2.1 Introduction to CWR strategy planning

Although the planning and implementation of a national CWR conservation strategy will differ slightly from one country to another, there are some basic steps in the process that can be followed by all nations in order to formulate an effective strategy for the conservation of their wealth of CWR diversity. The three primary steps in the production of a national strategy are:

1. **Preparation of a national CWR inventory** – The foundation of a national CWR strategy is a taxonomic checklist of CWR diversity; therefore, the first step is to prepare a national CWR inventory.
1. **Prioritization of national CWR taxa** – Once the included taxa are known, there is usually a need for a second step in which the CWR taxa are prioritized, particularly if the number of taxa exceeds the number that can be conserved using the available resources.
1. **Ecogeographic diversity analysis** – The third step is to collate the available baseline ecogeographic data for the priority taxa and undertake threat assessment and gap analysis, which culminates in a clear national CWR strategy.

These three steps are expanded on in the model for development of national CWR strategies (Figure 1), which is explained in detail below. To illustrate the application of this model, a recent study outlining how the UK National Inventory of CWR was prepared, the content of the inventory, the conservation and threat status of the species included and how the inventory may be used to generate CWR conservation action plans and identify sites where CWR genetic reserves should be established, is also summarized in Annexe 3.

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), where PA managers, in collaboration with gene bank managers, are responsible for conserving actual populations *in situ* or *ex situ*; these responsibilities are reflected in the model shown in Figure 1.

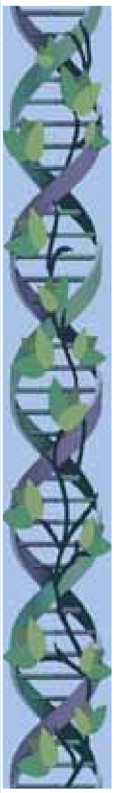
Although the two levels of responsibility (national and individual) are interconnected, they can also be seen as distinct and with quite separate goals. The national CWR strategy developed for an individual country aims to ensure the conservation of the maximum taxonomic and genetic diversity of the country's CWR. It leads to the conservation of priority CWR taxa in key protected areas, with back-up in *ex situ* collections, and has policy implications for national conservation and exploitation agencies, such as support for maintenance of key CWR hotspots or systematic collection and *ex situ* holding of representative CWR diversity. 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. Their contribution to the implementation of the strategy is more focused and practical in terms of conserving CWR; for example, it may involve the identification of CWR found in a single, existing protected area, possibly re-focusing the management plan or filling gaps identified in the gene bank's CWR coverage.

FIGURE 1

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

Thus, the national approach to developing a CWR strategy is composed of various steps that lead to the selection of key protected area sites and identification of diversity under-represented in *ex situ* collections, but should also be linked to multiple applications in individual protected areas or targeted collecting to ensure the maximum taxonomic and genetic diversity of the country's CWR are conserved. As such, the two levels of conservation activity, national and individual, must work together to ensure a successful national CWR strategy.

Although many protected areas are likely to contain CWR, some will be regarded as more important—for example, those where CWR diversity of national importance is concentrated—while other protected areas may not be considered of such critical national importance they are likely to contain CWR diversity and it would still be useful to highlight the CWR that are present to raise the public profile of the reserve itself. In this context the selection of key protected area sites where CWR should be conserved *in situ* is comparable with Important Plant Areas (Anderson *et al*., 2005; Plantlife, 2008). IPAs are not legal site designations but are a virtual network of the very best sites for plants and fungi identified to support conservation actions and initiatives. IPAs sites are selected on the basis of three criteria: threatened species, species richness/diversity and threatened habitats and were derived from the concept of Important Bird Areas (IBAs) used so effectively by Birdlife International to identify bird conservation priorities (Birdlife International, 2008). Thus protected area sites selected for their richness of CWR diversity might be referred to as Important CWR Areas (ICWRA) and once identified these could be form a virtual national, regional or global network that aids the actual conservation of CWR diversity as well as raising consciousness of the importance of CWR conservation (see below for further discussion of ICWRA).



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. Useful information for a floristic checklist for any target area can be identified using two country-based lists of the world's Floras; namely, Davis *et al*. (1986) and Frodin (2001), while Prendergast (1995) also lists other published sources of information on wild species. 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. However, this approach must be taken with caution as there will be taxa present in neighbouring countries that are absent in the target country, and vice versa.

With reference to the UK case study (Annexe 3), the CWR inventory was derived from the Crop Wild Relative Catalogue for Europe and the Mediterranean[14] (Kell *et al*., 2005), which in turn was derived from Euro+Med PlantBase (Euro+Med PlantBase, 2005)—a digitized database of the European and Mediterranean flora. The basic UK CWR inventory was extracted from this Catalogue using a country filter. However, some editing of the inventory was necessary in order to standardize the nomenclature used by Euro+Med PlantBase to that applied within the UK using the standard national Flora (Stace, 1997). In the case of the UK and other European countries, access to a digitized regional flora is obviously a great aid to the creation of a national CWR inventory. However, for other regions of the world, the availability of such data is less likely. Nonetheless, many countries are now in the process of digitizing their Floras (if they have not done so already) and, given access to these data, national PGR programmes can fairly easily create their CWR inventories, as described below.

Having identified the national botanical checklist, the CWR can be extracted by applying a definition of a CWR to the taxa in the list. Maxted *et al*. (2006) have proposed a precise definition of what constitutes a CWR, but to apply this definition requires detailed knowledge of the taxonomy and/or genetic diversity of each CWR taxon. It would therefore be difficult to apply this precise definition to an entire country's flora, so pragmatically, it may be necessary to apply the general definition of a CWR, as discussed by Maxted *et al*. (2006) and as applied in the creation of the CWR Catalogue for Europe and the Mediterranean (Kell *et al*., 2005, 2008). 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.

For countries included in the Euro-Mediterranean region, the national CWR inventory can be extracted from the CWR Catalogue for Europe and the Mediterranean (see PGR Forum, 2005). For countries in other regions, a global list of agricultural and horticultural crop genera can be extracted from Mansfeld's World Database of Agricultural and Horticultural Crops (http://mansfeld.ipk-gatersleben.de; Hanelt & IPK 2001), these genera can then be matched against the national botanical checklist, and all taxa within the matching genera extracted to produce the national CWR inventory (as described by Kell *et al*., 2008). Genus lists for forestry and ornamental taxa can also be added to create a more complete inventory. This approach is simplest if a digitized flora exists because the national flora can be more easily matched with the list of crop genera. However, for countries where no adequate flora or checklist exists, this approach cannot be applied so easily. Where this is the case, an alternative manual approach is to: a) agree a priority list of crops for a country, b) match these crops with known taxonomic treatments for the crop genera, and c) extract the wild species

---

[14] The Crop Wild Relative Catalogue for Europe and the Mediterranean contains in excess of 25 000 species and more than 280 000 records of taxon occurrences in 130 geographical units across the Euro-Mediterranean region (Kell et al., 2008a).

within the priority genera present in the country to generate the national CWR inventory. The digitized approach is comprehensive because all possible CWR taxa are encompassed, and the advantage of this approach is that it can be semi-automated. The manual approach is more 'hands-on' and is ideally facilitated by organizing a national workshop, including both taxonomists and crop experts. The crop experts define a list of important national crops (the definition of crops here can be broadened to include all socio-economically important species, if appropriate). Once the list of crop genera has been generated, the taxon experts produce a list of taxa present in the same genus as the priority crops to generate the national CWR inventory. This approach could be limited to include only native CWR taxa; however, as any CWR taxon present in the country may be of potential use in breeding, it is beneficial to include introduced taxa as well. This approach was recently successfully implemented for Bhutan (Tamang, 2004) and the Seychelles (Antoine, 2004). The digitized and manual approaches are summarized in Figure 2.

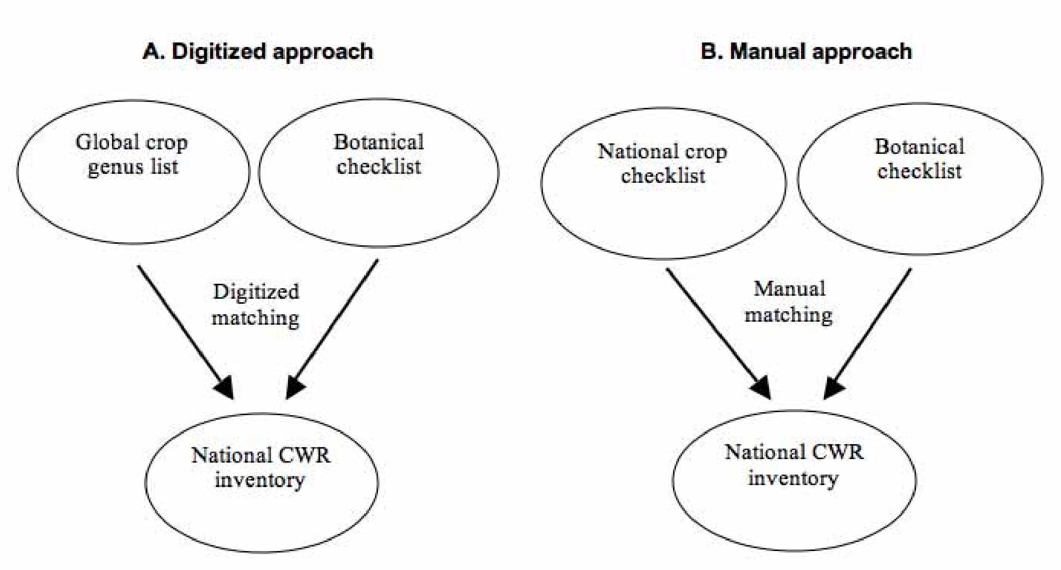
Having established the national CWR inventory, there are two routes for potential interactions with individual conservationists:

1. Sites or taxa of national importance can be identified and appropriate conservation action taken;
2. 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.

For example, as already noted, most protected areas are likely to have been established to conserve specific habitats or individual rare or threatened species; not explicitly to conserve CWR taxa. However, the manager can consult the national CWR inventory and match this against the species list for the protected area to generate a list CWR species present. If necessary, the manager can then adapt the management of the site to facilitate CWR conservation, where such changes do not conflict with the established management goals for the site. The manager may also wish to publicize the presence of CWR species in the protected area to the general public as a means of emphasizing its role; for instance, in helping to ensure national and global food security, as well as economic and environmental stability, through conservation of essential genetic resources.

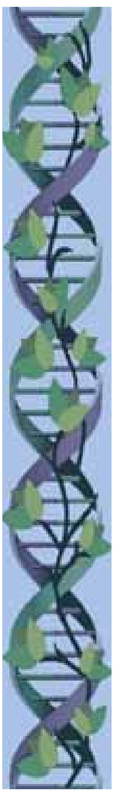
FIGURE 2

Two approaches to generating a national CWR inventory (Maxted *et al*., in prep.)



For example, as already noted, most protected areas are likely to have been established to conserve specific habitats or individual rare or threatened species; not explicitly to conserve CWR taxa. However, the manager can consult the national CWR inventory and match this against the species list for the protected area to generate a list CWR species present. If necessary, the manager can then adapt the management of the site to facilitate CWR conservation, where such changes do not conflict with the established management goals for the site. The manager may also wish to publicize the presence of CWR species in the protected area to the general public as a means of emphasizing its role; for instance, in helping to ensure national and global food security, as well as economic and environmental stability, through conservation of essential genetic resources.

As well as the need to raise the conservation priority of CWR within existing protected areas and to showcase the CWR species included, there is also a need as part of the national CWR conservation strategy to identify a number of key protected areas where CWR conservation is the predominant aim and to focus *ex situ* collection activities on the highest priority CWR taxa. The following actions are a possible approach to determining how specific CWR protected areas might be identified and CWR taxa targeted for *ex situ* collection.



2.3 Prioritizing CWR taxa/diversity

Applying a broad definition of a CWR will result in the national CWR inventory containing a relatively large number of taxa, even for a country like the UK that is regarded internationally as relatively floristically depauperate. If all the taxa in the same genus as the crop are included, the number is therefore likely to be too large a conservation target for the available resources. There will inevitably be a need to apply a strategy to prioritize the CWR that require most immediate conservation action to determine how best to utilize the available conservation resources. Opinions vary as to how this prioritization should be undertaken and it is inevitable that prioritization will vary according to needs within a region as a whole, or an individual country or specific organization within a country. Biodiversity conservationists may have opposing views to plant breeders, and the views of a forester will differ from those of a horticulturist.

Maxted *et al*. (1997) reviewed the various factors that can be used to ascribe 'value' and prioritize taxa for conservation. These included current conservation status, socio-economic use, threat of genetic erosion, genetic distinctiveness, ecogeographic distribution, biological importance, cultural importance, cost, feasibility and sustainability, legislation, ethical and aesthetic considerations, and the priorities of the conservation agency. However, there is some consensus for an initial, simple prioritization on the basis of economic value and relative threat alone (Barazani *et al*., 2008; Ford-Lloyd *et al*., 2008; Magos Brehm *et al*., 2007). To undertake this analysis the data must be available for the taxa in the National CWR Inventory, which will often at least be the case for broad economic value as these kinds of data are recorded within national agricultural statistics. However, 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. 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.

For the UK, a combination of relative economic value and threat was used to prioritize the CWR taxa. For economic value, UK national statistics on the economic value of UK crops were used to prioritize CWR at genus level based on UK production (in £ '000) for 2002 (Anonymous, 2004), Basic Horticultural Statistics (Defra, 2004a) averaged over 1993 – 2003 and the estimated value of production of forages was calculated using seed supply data (Defra, 2004b) (see Annexe 3 for more details). The most economically important UK crop is wheat; however, it has no naturalized CWR in the UK. Therefore, the genus containing CWR taxa of highest economic importance in the UK is *Brassica*, which has three CWR species in the UK, two of which are native. Threat was assessed for all UK taxa using the IUCN (2001) criteria by Cheffings *et al*. (2005), and all those CWR they assessed as being Critically Endangered (CR), Endangered (EN) or Vulnerable (VU) taxa were given priority. Combining relative economic value and threat generated a priority list of 250 UK CWR taxa (see Annexe 3).

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. This involves the collation and analysis of all available ecological, geographic, genetic and taxonomic data, which are obtained from the literature, passport data associated with herbarium specimens and germplasm accessions, and possibly from novel studies as well. These data are ecologically and geographically predictive because they aid the location of the CWR taxonomic (inter-taxa) and genetic (intra-taxon) diversity that can then be targeted for either *in situ* or *ex situ* conservation. 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, possibly identified using GIS analysis of ecological, geographic, genetic and taxonomic data. These areas might be considered analogous to the broader taxonomic Important Plant Areas for all plant species (Target 5 of the CBD Global Strategy for Plant Conservation – CBD, 2002a) and could be referred to as Important

CWR Areas. 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. In this context 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 and so the assessment should involve a comparison of the full range of the taxon with the range of that proportion of the taxon's genetic diversity sampled and held *ex situ* — a single accession in a genebank does not mean the taxon's genetic diversity is effectively conserved *ex situ*.

The UK flora is one of the most well studied floras of the world with records stretching back hundreds of years and being constantly updated, the New Atlas of the British and Irish Flora (Preston *et al*., 2002a) uses this resource to provide distribution records for all wild plant taxa as occurrence in 10 × 10 km squares of the UK Ordnance Survey National Grid. These occurrence records can be analysed using regression analysis to indicate change and significance of change over time (Preston *et al*., 2002b; Telfer *et al*., 2002). As an example of the kind of analysis that is possible of the UK CWR taxa with known distributions, more than 40% are common to very common, as they occur in >50–25% of UK hectads, while an additional 26% can be considered near-scarce as they occur in <25% but more than 100 grid squares and more than a third of the taxa with known distributions are scarce to very rare.

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

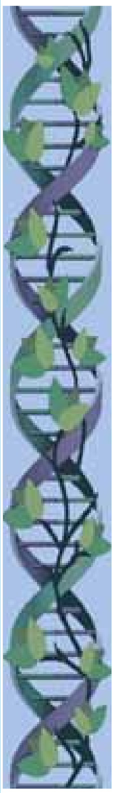
As well as assessing threat in relation to individual CWR taxa (in order to assist prioritization for conservation), there is also a need to assess threat in relation to conservation planning (i.e. to identify those important CWR areas most likely to be threatened). In terms of threat assessment for taxa, IUCN categories has recently been applied by Cheffings (2004) for all the taxa included in the New Atlas of the British and Irish Flora (Preston *et al*., 2002a), using the most recent IUCN Red List criteria (IUCN, 2001). Thirteen of the UK's CWR taxa have been assessed as threatened: *Apium repens* (Jacq.) Lag. and *Valerianella rimosa* Bastard are critical; *Lactuca saligna* L., *Allium sphaerocephalon* L. and *Pyrus cordata* Desv. are endangered; and *Scorzonera humilis* L., *Trifolium bocconei* Savi, *Trifolium incarnatum* subsp. *molinerii* (Balb. ex Hornem.) Ces, *Trifolium strictum* L., *Asparagus officinalis* subsp. *prostratus* (Dumort.) Corb., *Cynodon dactylon* (L.) Pers., *Festuca longifolia* Thuill. and *Poa flexuosa* Sm. are vulnerable; and one is extinct in the wild (*Bromus interruptus* (Hackel) Druce). Only one UK CWR species is currently covered by international obligations for the protection that is *Apium repens* L. which is listed in the EU Habitats Directive, Annexes IIb and IVb, under the Bern Convention Annex II and under CITES Appendix II. However, all wild plants are protected by law in the United Kingdom. Under the Wildlife and Countryside Act 1981, it is illegal to uproot any plant without permission from the landowner or occupier. Active conservation measures, such as Biodiversity Action Plans, exist for three taxa: *Apium repens* L., *Asparagus officinalis* subsp. *prostratus* (Dumort.) Corb and *Valerianella rimosa* Bastard.

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, over-grazing, 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. This involves some form of comparative assessment of the various putative causative factors of genetic erosion in Important CWR Areas, possibly by application of some form scoring technique like that proposed by Guarino (1995) for genetic erosion assessment of taxa.

2.6 CWR gap analysis

The identification of 'gaps' in conserved diversity is widely referred to as 'gap analysis', a concept that was initially proposed as a conservation evaluation technique to identify areas in which selected elements of biodiversity are under-represented (Margules, 1989) and which was largely applied to indigenous forests, particularly on small islands rich in endemic species. However, the concept of gap analysis can equally be used to evaluate CWR taxonomic and genetic diversity and help develop future strategies for CWR genetic conservation.

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*., 2008). Ideally, conservationists would assess the inherent genetic diversity within the taxa being reviewed; however, this is rarely possible because existing knowledge of patterns of genetic diversity are not generally available (except for a limited number of rare or threatened taxa of high conservation value), and resources are not usually available to collate the genetic diversity information *de novo*. Therefore, 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 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

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 protected area chosen is not necessarily the site with the second highest CWR richness because the species and diversity present in the second site may simply duplicate those in the first; therefore, 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). There is, however, likely to be some duplication of species between protected areas because of the widespread distribution of common species; therefore, 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. For the UK, detailed distribution data at a 10x10 km grid square scale were made available by the Botanical Society of the British Isles via the NBN Gateway for 226 of the 250 CWR priority taxa, and these were overlaid to identify the UK CWR hotspots (see Annexe 3) (Maxted *et al*., 2007).

The CWR gap analysis and subsequent development of national CWR conservation priorities leads to the identification of Important CWR Areas, i.e. those sites to establish national CWR reserves and priority CWR populations under-represented in *ex situ* collections. Thus far, the process has been focused at the national level; however, specific decisions will require implementation at the local level. Although ideal locations for CWR reserve sites may have been identified at a national level, there is an obvious need to confirm that the desired CWR diversity is actually present at the site. Although the location and establishment of specific CWR genetic reserves within existing protected areas is an ideal way forward, given possible financial constraints, the creation of new protected areas for CWR conservation should not be excluded from consideration, especially as many CWR species are located in disturbed habitats that may not previously have been considered appropriate for the establishment of protected areas. 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. However, if the case of the UK is cited as an example, 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 already stressed, it is undoubtedly the case that numerous, existing protected areas contain a wealth of CWR taxa; however, these 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 unless they are coincidentally keystone or indicator species as well as being CWR. Therefore, in general, CWR conservation within existing protected areas is likely to be passive, and individual populations may possibly decline or even be lost entirely. It is therefore important that if an existing protected area is provided with the designation of a 'national CWR genetic reserve', the management plan is amended to give priority to active CWR conservation and positive action is triggered before any deleterious effect can impact on the CWR populations present.

The original protected area designation is also likely to have been based on charismatic fauna, rare or threatened taxa, or a beautiful landscape; few protected areas have yet been established because they contain priority CWR taxa. Therefore, when designating key national CWR protected areas, the sites are likely to have been selected because they contain abundant and genetically diverse CWR populations; but the management of these populations may conflict with the management required for the species that the protected area was originally designated to conserve. Therefore, amendment to the protected area management plan to accommodate the new CWR priority needs to avoid any detrimental effects on other sympatric species. The first step in formulating the revised management plan is to observe the biotic and abiotic dynamics of the site for both CWR and non-CWR species. There is a need to survey the species present in the ecosystem to help understand the ecological interactions within the reserve. A clear conservation goal should be decided and a means of implementation agreed that may involve some compromise between the priorities for CWR and non-CWR species conservation.

When undertaking *ex situ* gap analysis, the conservation of the target taxon should take account of all *ex situ* techniques; however, for the majority of species, *ex situ* conservation is likely to be restricted to germplasm accessions held in gene banks. Therefore, the process of establishing *ex situ* CWR conservation priorities involves comparing the CWR taxon's actual distribution to the pattern of distribution recorded by gene bank holdings for the same taxon. Non-congruent sampling will highlight areas that are future *ex situ* CWR conservation priorities.

Associated with implementation of the *in situ* and *ex situ* strategies identified by the gap analysis it is useful conservation statements for individual taxa that outline the actual and proposed actions to be implemented. As such the production of CWR Action Plans is a useful way of summarizing the conservation strategy developed for individual CWR taxa. The CWR Action Plan would ideally contain information on nomenclature, classification, description, image, distribution, ecogeography, current conservation status and action, threat assessment, uses, additional conservation action required, research and monitoring requirements, and incorporation in existing national or local conservation initiatives. Examples of CWR Action Plans for the UK are available at http://www.grfa.org.uk/.

In obligation to the CBD Strategic Plan (decision VI/26) (CBD, 2002b), it is necessary to achieve a significant reduction of the current rate of biodiversity loss at global, regional and national levels by 2010, as a contribution to poverty alleviation and to the benefit of all life on earth. Also, more specifically, decision VII/30 of the Conference of the Parties (COP) to the CBD was adopted to facilitate the assessment of progress towards the 2010 Biodiversity Target (CBD, 2002b) by identifying indicators of biodiversity 'trends in genetic diversity of domesticated animals, cultivated plants, and fish species of major socioeconomic importance'. Once established, the key national CWR protected areas provide an opportunity to monitor and assess short and longer term changes in CWR diversity as a contribution towards the CBD 2010 Biodiversity Target.

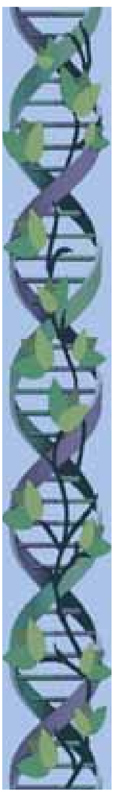
2.8 CWR utilization

The establishment and management of the national CWR reserves is not an end in itself. There is an explicit link, especially for socio-economically important species like CWR, between genetic conservation and utilization—genetic conservation must facilitate utilization, either now or in the future. This point is highlighted in the CBD and in this context any utilization should be 'sustainable' and 'meet the needs and aspirations of present and future generations' (CBD, 1992).

The national utilization of the material conserved in the protected area may be divided among general and professional users. 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). Some members of the public may wish to visit protected areas and this clearly should be encouraged as an educational exercise. Therefore, the protected area design should ideally take into account the needs of visitors by including visitor centres, nature trails, lectures, etc. They are also likely to bring additional income to the protected area itself through guided tours and the sale of protected area information packs.

The long-term sustainability of protected areas can only be ensured through their use; therefore, interest among stakeholders in the biodiversity located in the protected area needs to be stimulated. Just as botanic gardens often stimulate interest in the general public by including specimens of crops, to show for example what the banana, coffee or rice plant looks like, the protected area manager can raise the profile of the site they manage by paying particular attention to the CWR species native to the site and advertising their presence to potential user communities.

Professional utilization of CWR species conserved in a protected area is similar to professional utilization of *ex situ* conserved germplasm. One of the main disadvantages of *in situ* as opposed to *ex situ* conservation of CWR is that it is more difficult for the plant breeder to gain access to the CWR material and seed is only available for a proportion of the year (Hawkes, 1991). To avoid or lessen this problem, 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

The protected area can act as a general research platform for field experimentation. 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 establishing the protected area.

Specifically in terms of research priorities, the establishment of the national CWR reserves, possibly within a network of regional and international CWR reserves, will clearly facilitate national monitoring of CWR species as required by the CBD Strategic Plan (decision VI/26) (CBD, 2002b). This will necessarily involve routine monitoring of taxonomic, demographic and genetic diversity changes. Linked to the identification of drivers of change, it would mean that action could be taken to reduce current rates of CWR loss, and enable modelling and prediction of future changes associated with future habitat management scenarios.

In many cases, the work of professional users, the general public and local people can be linked through partnership within non governmental organizations (NGOs), especially those that are conservation volunteers, or are involved in sustainable rural development or use of resources in accordance with traditional cultural practices. Raising public and professional awareness of the need to conserve CWR can only engender sustainability, both for specific protected areas and conservation actions in general. All partners will therefore share the goals of sustainable use of biological resources taking into account social, economic, environmental and scientific factors which form a cornerstone of the nations' proposals to implement Agenda 21.

2.10 Linkage to *ex situ* conservation and duplication

It would be foolish to implement a national CWR strategy and establish key national CWR protected areas without a safety back-up to ensure the conservation of the germplasm; therefore, population samples should be collected and deposited in appropriate *ex situ* collections. In this context, if the germplasm user does not have a specific requirement for material from a reserve, the gene bank may be seen to act as a staging post for those wishing to utilize the germplasm originally conserved *in situ*. 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. By definition, it is not possible to duplicate material from one reserve to another without the material being taken *ex situ*. But it is worth emphasizing here that it would again be foolish to entirely focus *in situ* conservation effort on a single reserve—multiple reserves should be established where possible to ensure that sufficient populations are actively conserved so that a catastrophic event affecting one reserve would not lead to the loss of all the germplasm conserved *in situ*.

As already highlighted, the national and global strategic approaches to CWR conservation should not be seen as alternative approaches—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 the 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 the global network. Conversely, it is logical that each protected area included in the global network is also nominated as part of a country's national CWR genetic reserve network.

2.11 References

Anderson S., Kusík T. and Radford E. (Eds.) (2005). Important Plant Areas in Central and Eastern Europe. Plantlife International.

Anonymous (2004). The Official Yearbook of the United Kingdom of Great Britain and Northern Ireland. Her Majesty's Stationery Office, London.

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

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.

BirdLife International (2008). http://www.birdlife.org/action/science/sites/ [Accessed 16 May 2008].

CBD (1992). Convention on Biological Diversity. Secretariat of the Convention on Biological Diversity, Montreal, Quebec, Canada.

CBD (2002a). Global Strategy for Plant Conservation. Secretariat of the Convention on Biological Diversity, Montreal, Quebec, Canada.

CBD (2002b). Strategic Plan for the Convention on Biological Diversity. Secretariat of the Convention on Biological Diversity, Montreal, Quebec, Canada.

Cheffings, C. (2004). New plant status lists for Great Britain. BSBI News, 95: 36–43.

Cheffings, C.M. and Farrell, L. (Eds.) (2005). The vascular plant red data list for Great Britain. Species Status, 7: 1–116. Joint Nature Conservation Committee, Peterborough.

Davis, S.D., Droop, S.J.M., Gregerson, P., Henson, L., Leon, C.J., Lamlein Villa-Lobos, J., Synge, H. and Zantovska, J. (1986). Plants in Danger: What Do We Know? International Union for Conservation of Nature and Natural Resources, Gland, Switzerland.

Defra (2004a). Plant Variety Rights Office and Seeds Division Seed Trader's Annual return for year ended 30 June 2003. Defra, London.

Defra (2004b). Seed Traders' Annual Return – Year ended 30 June 2004. Plant Variety Rights Office and Seeds Division, Defra, London.

Euro+Med PlantBase (2005). Euro+Med PlantBase: The Information Resource for Euro-Mediterranean Plant Diversity. Dipartimento di Scienze botaniche ed Orto botanico, Università degli Studi di Palermo. http://www.emplantbase.org/home.html [Accessed 21 October 2008].

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.

Frodin, D.G. (2001). Guide to the standard floras of the world [Second edition]. Cambridge University Press, Cambridge.

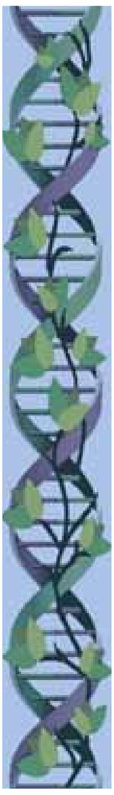
Guarino, L. (1995). Assessing the threat of genetic erosion. In: Guarino, L., Rao, V.R. and Reid, R. (Eds.), Collecting Plant Genetic Diversity: Technical Guidelines. Pp. 67–74. CAB International, Wallingford.

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

Hawkes, J.G. (1991). International workshop on dynamic *in situ* conservation of wild relatives of major cultivated plants: summary of final discussion and recommendations. Israel Journal of Botany, 40, 529–536.

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 [Accessed 21 October 2008].

Kell, S.P., Knüpffer, 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., Knüpffer, H., Jury, S.L., Ford-Lloyd, B.V. and Maxted, N. (2008). 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.

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.

Margules, C.R. (1989). Introduction to some Australian developments in conservation evaluation. Biological Conservation, 50: 1–11.

Maxted, N., Hawkes, J.G., Guarino, L. and Sawkins, M. (1997). 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. (2008). Genetic gap analysis: a tool for more effective genetic conservation assessment. Diversity and Distributions, 14: 1018–1030.

PGR Forum (2005). Crop Wild Relative Information System (CWRIS). University of Birmingham, Birmingham, UK. http://www.pgrforum.org/cwris/cwris.asp [Accessed 21 October 2008].

PlantLife (2008). Important plant areas. http://www.plantlife.org.uk/international/plantlife-ipas-about.htm [Accessed 16 May 2008].

Prendergast, H.D.V. (1995). Published sources of information on wild species. In: Guarino, L., Ramanatha Rao, V.R. and Reid, R. (Eds.), Collecting plant genetic diversity: technical guidelines. Pp. 255–280. CAB International, Wallingford.

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.

Preston, C.D., Pearman, D.A. and Dines, T.D. (2002a). New Atlas of the British and Irish Flora. Oxford University Press, Oxford.

Preston, C.D., Telfer, M.G., Arnold H.R., Carey, P.D. Cooper, J.M., Dines, T.D., Hill, M.O., Pearman, D.A., Roy, D.B. and Smart, S.M. (2002b). The changing flora of the UK. Defra, London.

Rebelo, A.G. (1994). Iterative selection procedures: centres of endemism and optimal placement of reserves. In: Huntley, B.J.(Ed.), Botanical Diversity in Southern Africa. Pp. 231–257. National Botanical Institute, Pretoria.

Stace, C. (1997). New Flora of the British Isles. Cambridge University Press, Cambridge.

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

Telfer, M.G., Preston, C.D. and Rothery, P. (2002). A general method for measuring relative change in range size from biological atlas data. Biological Conservation, 107: 99–109.

ANNEXE 3: CASE STUDY: NATIONAL CWR CONSERVATION STRATEGY FOR THE UK

The following text has been adapted from Maxted *et al*. (2008). The first step in the establishment of a National CWR Conservation Strategy is to generate the CWR checklist, followed by prioritizing the CWR taxa, particularly if the number of taxa exceeds those that can be actively conserved using the resources available. The third step will be to collate the available baseline ecogeographic data, undertake threat assessment and gap analysis, from which follow the *in situ* and *ex situ* recommendations that form the basis of the national CWR strategy. This section illustrates the process of creating a National CWR Conservation Strategy using a case study for the UK, explaining how the National Inventory of CWR was created, discusses the content of the inventory, reviews the conservation and threat status of the species included and how the inventory may be used to generate CWR conservation action plans and identify sites where CWR genetic reserves should be established.

Creation of the UK National Inventory of Crop Wild Relatives

The foundation of the UK National Inventory of CWR was within the EC-funded European Crop Wild Relative Diversity Assessment and Conservation Forum (PGR Forum) project (www.pgrforum.org). One of the main objectives was to create a European CWR database, incorporating baseline biodiversity data with current conservation and threat status. The database/on-line catalogue was created through a process of data harmonization and cross-checking between a number of existing databases, primarily Euro+Med PlantBase (http://www.euromed.org.uk/), Mansfeld's World Database of Agricultural and Horticultural Crops (Hanelt and IPK 2001; http://Mansfeld.ipk-gatersleben.de/Mansfeld/), with forestry genera from Enumeration of cultivated forest plant species, ornamental genera from the Community Plant Variety Office (www.cpvo.eu.int) and medicinal and aromatic plant genera from the MAPROW (Medicinal and Aromatic Plant Resources of the World) database (Shipmann, 2004, pers. comm.). The final catalogue, the PGR Forum Crop Wild Relative Catalogue for Europe and the Mediterranean (Kell *et al*., 2008a, b), contains in excess of 25 000 species and more than 273 000 records of taxon occurrences in 130 geographical units across the Euro-Mediterranean region (see http://www.pgrforum.org/cwris/cwris.asp).

The PGR Forum Crop Wild Relative Catalogue for Europe and the Mediterranean is managed by the Crop Wild Relatives Information System that facilitates the extraction of national CWR data sets from the main catalogue using the geographic unit filter. The resulting UK National Inventory of CWR can be queried via the UK Genetic Resources for Food and Agriculture portal (http://grfa.org.uk/search/plants/index.html?#sr). The structure of the database is shown in Appendix A. It contains basic taxonomic and usage data, along with conservation data such as occurrences and trends, legal status, IUCN threat assessment status and conservation action plans. Due to inconsistencies between European and UK plant nomenclature, once the initial UK catalogue was extracted from the European and Mediterranean catalogue, it was necessary to standardize the nomenclature to that applied within the UK using the standard national flora, New Flora of the British Isles, second edition (Stace, 1997). In addition to the data extracted from the European CWR inventory additional UK data sets were added. All CWR taxa were ascribed use categories (Cook, 1995): agriculture, horticulture, forestry, medicinal and aromatic plants, technical or environmental, and social and religious depending on the crop and associated use to which the taxon was most closely related. The crop use information was derived from Hanelt and IPK (2001), Wiersema and Leon (1999), Mabberley (1997) and Mabey (1996, 2003). Baseline conservation data such as occurrence and trends were taken from Preston *et al*. (2002a), UK legal status from (www.jncc.org.uk), IUCN red list assessment from Cheffings and Farrell (2005) and conservation action plans from (www.ukbap.org.uk).

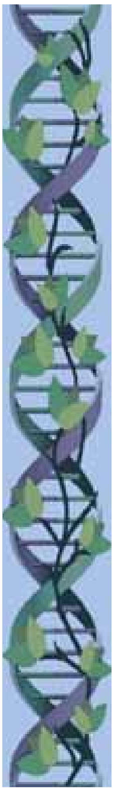
UK national CWR inventory content

The UK National Inventory of CWR contains 413 genera, and 1 955 species (2 644 if micro- and subspecies are included). Approximately 65% of the 2 300 UK native taxa are CWR, 78% of the approximately 1 400 native taxa listed by Preston *et al*. (2002a) and 98% of the 149 archaeophyte taxa listed in Preston *et al*. (2004) are wild plants having either direct use or potential use as CWR. Of these 85% are wild relatives of medicinal and aromatic plants, 82% of agricultural and horticultural crops, 15% of forestry plants and 30% of ornamentals. In all 72 plant families are included, but five show particularly high CWR taxon richness: Poaceae, Rosaceae, Fabaceae, Brassicaceae and Asteraceae (Table 1). The most taxon rich use classes are the medicinal and aromatic plants, closely followed by ornamental plants. The general food plant category ranks fifth, with most taxa associated with use as vegetables (herbs included) with 71 taxa, followed by 45 fruit related taxa, 10 starch and 7 oil producing taxa.

TABLE 1

Major UK agricultural crop wild relative families and genera (ornamentals excluded)

Family	Genera	Taxa	Genera and numbers of species
Poaceae	15	113	*Agrostis* (6), *Alopecurus* (6), *Arrhenaterum* (1), *Avena* (3), *Bromus* (8), *Cynodon* (1), *Dactylis* (1), *Festuca* (13), *Festulolium* (5), *Hordeum* (3), *Lolium* (2), *Phalaris* (1), *Phleum* (5), *Poa* (15), *Trisetum* (1)
Fabaceae	6	59	*Trifolium* (23), *Vicia* (13), *Onobrychis* (1), *Medicago* (5), *Lotus* (5), *Lupinus* (2)
Rosaceae	5	29	*Fragaria* (2), *Malus* (2), *Prunus* (7), *Pyrus* (2), *Rubus* (7)
Brassicaceae	4	28	*Brassica* (3), *Sinapis* (2), *Rorippa* (8), *Raphanus* (1)
Apiaceae	7	22	*Apium* (4), *Anthriscus* (3), *Petroselinum* (2), *Carum* (2), *Foeniculum* (1), *Daucus* (1), *Pastinaca* (1)
Liliaceae	2	12	*Allium* (9), *Asparagus* (1)
Papaveraceae	1	11	*Papaver* (6)
Solanaceae	1	7	*Solanum* (5)
Grossulariaceae	1	6	*Ribes* (6)
Asteraceae	3	5	*Cichorium* (1), *Lactuca* (3), *Scorzonera* (1)
Valerianaceae	1	4	*Valerianella* (4)
Linaceae	1	3	*Linum* (3)
Chenopodiaceae	1	3	*Beta* (1)
Polygonaceae	1	1	*Rheum* (1 hybrid)
Cannabaceae	1	1	*Humulus* (1)
Totals	**50**	**303**	



The UK national CWR inventory includes 9 genera and 44 endemic taxa, most of which are related to ornamentals, with *Limonium* (Sea Lavender) containing 24 endemic taxa and *Sorbus* with 13 endemic species; only one, *Linum perenne* subsp. *anglicum* (Mill.) Ockendon is related to a major agricultural crop, flax. Although not a UK endemic, an important European CWR endemic include in the UK flora is wild asparagus, *Asparagus officinalis* subsp. *prostratus* (Dumort.) Corb. and this is found on the coast of Southwest England (WWF and IUCN, 1994). It should also be noted that most of the endemic CWR taxa have a restricted UK 10 × 10 km grid square occurrence and 24 of the 44 taxa have IUCN threat status assigned to them, yet only one, *Sorbus leyana* Wilmott, has a current national Biodiversity Action Plan.

UK national statistics were used to rank CWR genera on UK production (in £ '000) for 2002 (Anonymous, 2004) and Basic Horticultural Statistics (Defra, 2004a) averaged over 1993–2003. The estimated value of production of forages was calculated using seed supply data (Defra, 2004b), which cover 15 major forages from 12 genera and includes 87 crop wild relatives. The most economically important UK crop is wheat, but it has no naturalized CWR in the UK, which highlights the desirability of a global approach to CWR conservation. Consequently the genus with UK taxa of highest economic importance is *Brassica* with 3 CWR species, 2 of which are native. However, certain families show significant numbers of introduced taxa, which reflect their history of cultivation in the UK, e.g. *Fabaceae*. The genera with highest CWR taxon diversity are those of fodder/forage crops, such as clover, fescue, meadow grass, vetches, broom grass, watercress, and bent grass (micro-species were excluded not to bias results). The four crop genera each with more than 10 UK native CWR are all forage species: *Trifolium*, *Poa*, *Festuca* and *Vicia*. The *Poaceae* outnumbers other families by far in number of genera, as well as in total CWR taxa, followed by *Fabaceae*, then *Rosaceae* and *Brassicaceae*. The highest number of sub-specific taxa is found within Festuca with more than 10% of the total taxa being inter-specific hybrids. The genus with the highest number of hybrids is watercress, *Rorippa*. Of the fruits, the highest CWR diversity is found within *Prunus*.

Distribution of major CWR taxa

The UK flora is perhaps the most well studied globally and the New Atlas of the British and Irish Flora (Preston *et al.*, 2002a) provides distributional records for all taxa, both CWR and non-CWR, as presence in 10 × 10 km squares of the UK Ordnance Survey National Grid. The data provided can be analysed using regression analysis to indicate change and significance of change over time (Preston *et al.*, 2002b; Telfer *et al.*, 2002). The data can also be used to assign rarity categories (Preston *et al.*, 2002a) so that a taxon is Nationally Scarce (NS) if it occurs in 16 to 100 hectads, Nationally Rare (NR) if it occurs in 3 to 16 hectads and "very rare" if in < 3 hectads. Therefore the New Atlas data (Preston *et al.*, 2002a) can be analysed for CWR taxa and an occurrence is summarized in Table 2.

TABLE 2

Taxon occurrence categories for 303 CWR taxa using New Atlas data (Preston *et al.*, 2002a)

Hectad occurrence	Description	Number of taxa	Percentage of total
> 1426	Very common (50% hectads)	54	17.82
713–1426	Common (25–50% hectads)	31	10.23
100–712	Uncommon (< 25% hectads)	57	18.82
16–100	Nationally scarce	52	17.16
3–15	Nationally rare	14	4.62
< 3 Grids	Nationally (very) rare	8	2.64
	Taxa without data	87	28.71

For UK CWR taxa with known distributions, more than 40% are common to very common as they occur in > 50–25% of UK hectads. An additional 26% can be considered near-scarce as they occur in < 25% but more than 100 grid squares. More than a third of the taxa with known distributions are scarce to very rare. For a few taxa more detailed distribution data are available, e.g. the UK BAP taxon *Asparagus officinalis* subsp. *prostratus* has been well documented (Rich *et al*., 2002), and the New Atlas data show a loss of 7 hectads, which is a 40% loss since 1970. However, Rich *et al*. (2002) in a focused investigation of the taxon found that of the 34 historic sites, 28 still existed in 1999–2001, implying a lower level of loss of 18%. As the taxon occurs on inaccessible sea cliffs it is quite possible that this taxon is under-surveyed and the taxon may be less threatened than indicated. The 28 sites located by Rich *et al*. (2002) had approximately 1 200 plants in total and ranged from 1 to 398 plants per site. Trends for populations were difficult to assess because of lack of comparability in recording methods, but 5 sites had fewer than 10 plants and 4 only had a single plant. However Rich *et al*. (2002) noted that of these nine sites, a third are thought to be seriously at risk of extinction and only 3 were considered secure, having more than 100 plants.

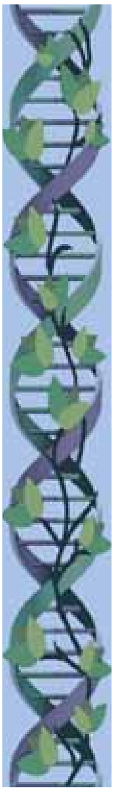
IUCN threat assessment for priority UK CWR taxa

The IUCN threat assessment for the taxa covered by Preston *et al*. (2002a) has recently been updated (Cheffings, 2004) using the most recent IUCN Red List Categories and Criteria (IUCN, 2001). Using these criteria five factors are considered: (a) declining population (past, present and/or projected), (b) geographic range size, and fragmentation, decline or fluctuations, (c) small population size and fragmentation, decline, or fluctuations, (d) very small population or very restricted distribution, and (e) quantitative analysis of extinction risk assessed by using population viability analysis. The threat categories in decreasing order of threat are: Extinct (EX), Extinct in the Wild (EW), Critically Endangered (CR), Endangered (EN), and Vulnerable (VU), as well as Data Deficient (DD). The criteria are applied only to taxa that are 'native' or 'archaeophytes' and only taxa in the categories CR, EN and VU are considered to be threatened. An overview of IUCN assessments for UK CWR related to agricultural and horticultural crops taken from Cheffings and Farrell (2005) is given in Table 3. Thirteen of these CWR taxa have been assessed as threatened and one as extinct in the wild.

UK CWR conservation action: legal status and biodiversity action plans

Only one UK CWR species is currently covered by International Obligations for the Protection of UK Plant Species. *Apium repens* L. is listed in the EC Habitat and Species Directive IIb and IVb, under the Bern Convention II and under Cites II. However, all wild plants are protected by law in the United Kingdom. Under the Wildlife and Countryside Act 1981, it is illegal to uproot any plant without permission from the landowner or occupier. Furthermore, many nature reserves, including National Trust land, have bylaws in force making it illegal to pick, uproot or remove plants. Several of the UK's rarest plants are specifically protected under Schedule 8 of the Wildlife and Countryside Act and this list includes five of the 303 UK CWR related to agricultural and horticultural crops. Active conservation measures such as the application of Biodiversity Action Plans exist for three taxa: *Apium repens* L., *Asparagus officinalis* subsp. *prostratus* (Dumort.) Corb. and *Valerianella rimosa* Bastard. As can be seen from Table 3, 10 out of the 13 taxa that have been assessed as threatened according to IUCN criteria have no Biodiversity Action Plans nor are they listed by the Wildlife & Country Act Schedule 8.

Identification of priority sites to establish CWR genetic reserves



Conservation *in situ* is particularly important for CWR because of the need to conserve the full range of infra-specific genetic diversity, the need to maintain the evolution of that diversity within each population and the sheer numbers of CWR involved, which makes *ex situ* conservation for all species impractical. However, a single reserve is unlikely to adequately conserve the genetic diversity of a species, due primarily to local ecotypic adaptation, unless that species has a very restricted distribution. Therefore networks of reserves are required for the long-term maintenance of biodiversity (Hopkinson, *et al*., 2000; Margules and Pressey, 2000; Ortega-Huerta and Peterson, 2004). The creation of a network of national CWR genetic reserves is therefore likely to be a priority within any national CWR conservation strategy.

TABLE 3

IUCN threat status, legislative protection and Biodiversity Action Plans for UK CWR taxa

Taxon name	IUCN threat status	WCA Schedule 8[15]	Biodiversity Action Plan
Apium repens (Jacq.) Lag.	CR	WCA-8	BAP
Lactuca saligna L.	EN	WCA-8	
Scorzonera humilis L.	VU	WCA-8	
Trifolium bocconei Savi	VU		
Trifolium incarnatum subsp. *molinerii* (Balb. ex Hornem.) Ces.	VU		
Trifolium strictum L.	VU		
Allium sphaerocephalon L.	EN	WCA-8	
Asparagus officinalis subsp. *prostratus* (Dumort.) Corb.	VU		BAP
Bromus interruptus (Hackel) Druce	EW		
Cynodon dactylon (L.) Pers.	VU		
Festuca lemanii Bastard	DD		
Festuca longifolia Thuill.	VU		
Festuca rubra subsp. *litoralis* (G. Mey.) Auquier	DD		
Festuca rubra subsp. *arctica* (Hack.) Gover.	DD		
Festuca rubra subsp. *scotica* S. Cunn. ex Al-Bermani	DD		
Poa flexuosa Sm.	VU		
Pyrus cordata Desv.	EN	WCA-8	
Valerianella rimosa Bastard	CR		BAP

Often the selection of reserves has been 'ad-hoc', depending largely on land use or human habitation, recreation and tourism or historical protection, leading to a biased representation of natural features and an increased cost of achieving representative reserve systems (Pressey, 1994; Ortega-Huerta and Peterson, 2004). Although site selection methods vary they have centred around two main concepts, hotspots and complementary areas, which are used to produce 'ideal' reserve networks using distribution data for a taxonomic group (Hopkinson, *et al*., 2000). The hotspot approach identifies the most taxon-rich grids in a region (Prendergast *et al*., 1993). The complementary approach attempts to include maximum biodiversity in the minimum number of sites (Hopkinson, *et al*., 2000), whereby once a reserve is selected, all other sites are selected to complement the previous ones, and thus replication is minimal.

In the CWR context an essential component of the development of a national CWR conservation strategy is to identify the most appropriate sites to establish genetic reserves (Maxted *et al*., in prep.), which would be widely recognized as gap analysis. There is now an extensive literature associated with the latter conservation evaluation technique which essentially identifies areas in which selected elements of biodiversity are under-represented (Margules, 1989; Margules and Pressey, 2000; Balmford, 2003; Brooks *et al*., 2004; Dietz and Czech 2005; Riemann and Ezcurra, 2005) and has largely been applied to indigenous forests, particularly on small islands rich in endemic species. Burley (1988) identified four steps in gap analysis: (a) identifying and classifying biodiversity, (b) locating areas managed primarily for biodiversity, (c)

---

[15] UK legislative protection specified under the Wildlife and Countryside Act Schedule 8 (WCA-8).

identifying biodiversity that is under-represented in the managed areas, and (d) setting priorities for conservation action. This application has been clearly associated with ecosystem conservation, but the basic methodologies can equally be applied to taxonomic and genetic diversity and its distribution in existing wild populations, as was illustrated in the recent application for cowpea (*V. unguiculata* (L.) Walp.) and its wild relatives from Africa (Maxted *et al*., 2004). For CWR conservation the four steps involve: (a) establishment of the national CWR inventory and prioritization of taxa, if necessary, (b) use of distribution data for the priority CWR taxa to identify national complementary CWR hotspots, (c) matching CWR hotspots to the existing protected area network and (d) assessment of effectiveness of current conservation coverage and identification of unprotected CWR hotspots ("gaps") where genetic reserves for CWR conservation within existing protected areas might most profitably be established.

Establishing and prioritizing the UK CWR inventory

The establishment of the UK CWR inventory is discussed above. As the UK national CWR inventory contains a relatively large proportion of the UK flora and conservation resources are limited there was a need to prioritize taxa for inclusion in the exercise. There are many criteria that can be used to establish priority taxa for conservation (Maxted *et al*., 1997b; Ford-Lloyd *et al*., 2008) but here relative threat assessment using the IUCN Red List Criteria as well as economic value (see above) were used to prioritize the UK National Inventory of CWR taxa. All national CWR inventory taxa assessed by Cheffings and Farrell (2005) as Critically Endangered (CR), Endangered (EN) or Vulnerable (VU) were given priority and this generated a priority list of 250 UK CWR taxa.

Identifying national UK CWR hotspots

Detailed distribution data from throughout the UK at a 10 × 10 km grid square scale were made available by the Botanical Society of the British Isles via the NBN Gateway for 226 of the 250 CWR priority taxa and these were used in order to identify UK CWR hotspots. The initial task was to identify the UK hotspots with the highest numbers of CWR taxa, irrespective of whether these hotspots were or were not associated with existing protected areas. This was achieved using the iterative selection procedure that results in complementary conservation of maximum taxon diversity (Kirkpatrick and Harwood, 1983; Margules *et al*., 1988; Pressey and Nicholls, 1989; Pressey *et al*., 1993; Rebelo, 1994; Bonn *et al*., 2002). The site with the highest taxon number is allocated as the first site, then the taxa located in this first site are excluded from the analysis and the second site is selected using the remaining taxa and so on (Rebelo, 1994).

The question then arises as to how many CWR taxa need to be present to be regarded as a hotspot? Also more pragmatically because of the obvious relationship to resource availability how many hotspots can be nominated to effectively conserve national CWR diversity? In regard to the former, the data illustrate that as the number of sites increases the percentage diversity added decreases and the economic cost of adding additional sites for smaller diversity gain may therefore become less attractive (Figure 1). If the aim is to conserve two thirds of the total priority CWR taxa diversity then 17 sites would be required for the location of UK CWR genetic reserves. Table 4 shows the cumulative numbers and percentages of CWR taxa in each 10 × 10 km tetrad for the top 17 UK CWR hotspots, and Figure 2 their location. As well as the absolute number of CWR taxa present, the additional taxa present as a result of the iterative process are also indicated for each site. It should be noted that the percentage CWR diversity added per additional site included levels off to less than 2% after the tenth site.

Matching of UK CWR hotspots with existing protected areas

Once the UK CWR hotspots have been identified they can be matched against the existing protected area network to identify potential sites where genetic reserves for *in situ* conservation of CWR could be established. If the distribution of the existing UK protected areas is compared with the 17 top 10 × 10 km CWR hotspots (17 sites in this case being chosen as this is the number of sites required to cover two thirds of the 226 priority CWR taxa), nine CWR hotspots overlap with SAC sites and eight overlap with SSSIs (see Table 4).

Assessing effectiveness of current conservation and identifying CWR hotspots

Although 20.4% of UK land is protected in some form (IUCN, 1998), there are no protected areas in the UK where the conservation of CWR genetic diversity is a priority. However, the combination of the 17 SAC and SSSI sites (Table 4) has identified where CWR genetic reserves might be nominated to conserve two thirds of all UK priority CWR taxa. No CWR hotspots were identified that did not overlap with existing UK protected areas, but it should be acknowledged that the UK does have an exceptionally comprehensive network of protected areas and this may not be the case for similar exercises in other countries.

Selection of priority sites to establish CWR genetic reserves

Why establish CWR in existing protected areas as recommended by Maxted *et al*. (1997a), Heywood and Dulloo (2006) and Iriondo *et al*. (2008)? CWR like any other group of wild plant species are located both within and outside existing protected areas. The reasons for locating reserves in existing protected areas are that (a) these sites already have an associated long-term conservation ethos and are less prone to hasty management changes to situations where conservation value and sustainability are not considered, (b) it is relatively easy to amend the existing site management structure to facilitate genetic conservation of CWR species, and (c) creating novel conservation sites can be avoided avoiding possibly prohibitive costs of acquiring previously non-conservation managed land (Iriondo *et al*., 2008). Therefore often the simplest way forward in economic and political terms is for countries to locate genetic reserves in existing protected areas, e.g. national parks and heritage sites or specifically in the UK context Special Areas for Conservation (SAC), Sites of Special Scientific Interest (SSSI) or Special Protection Areas (SPA) providing they can be shown to encompass adequate CWR diversity.

FIGURE 1

Percentage CWR gain with increasing iterative grid square addition

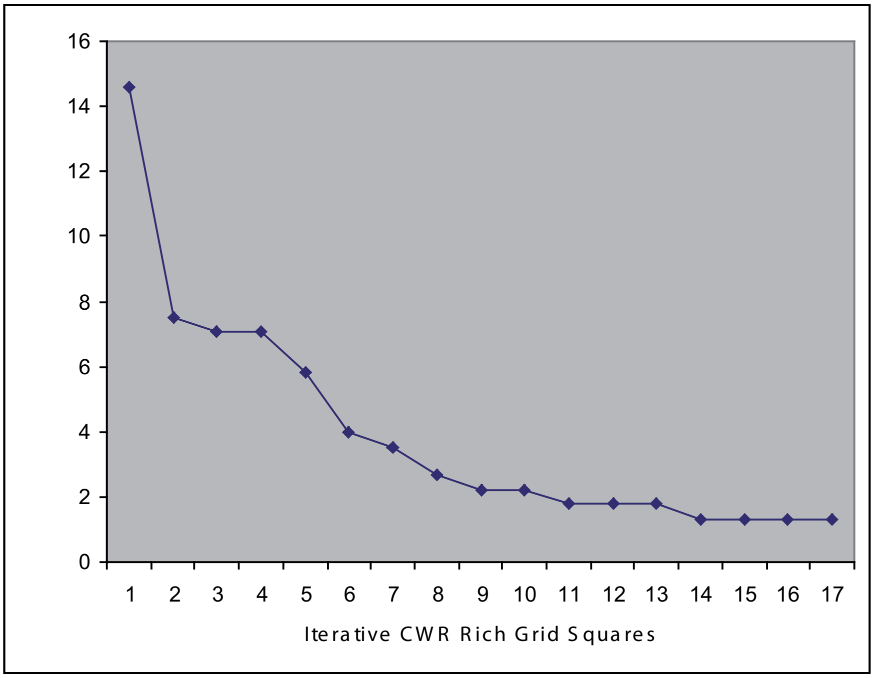


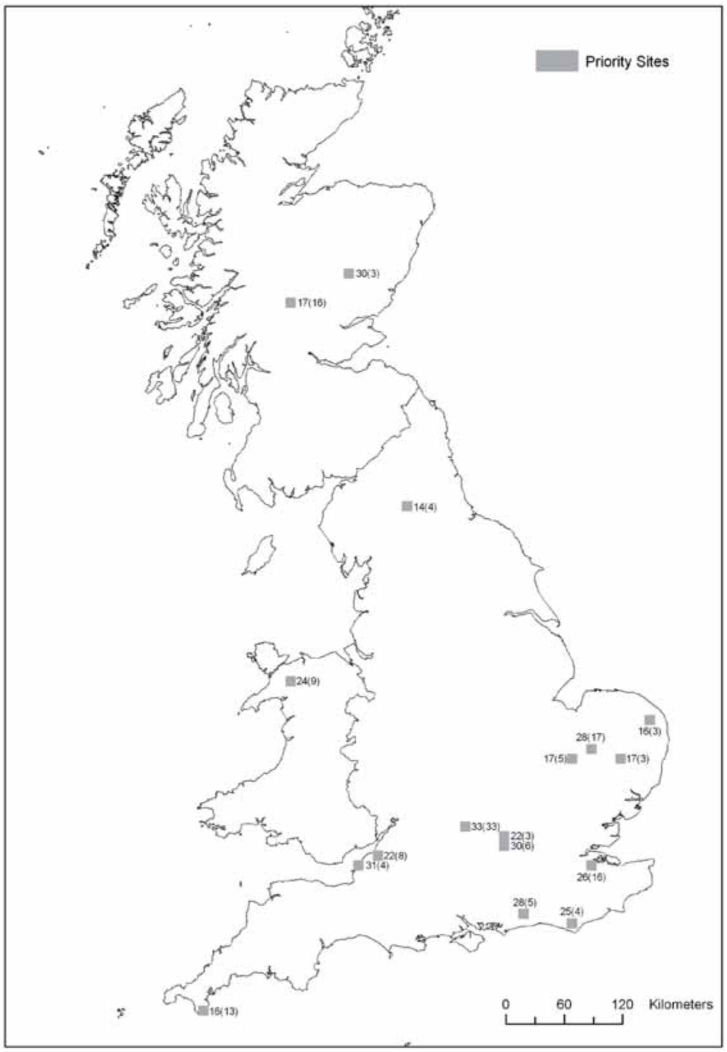
TABLE 4

Grid references with most CWR species present and the cumulative percentage of species covered by each grid

UK grid reference	Total no. of CWR taxa	Additional CWR taxa covered	Additional % of CWR taxa	Iterative site priority	Protected area name	Site designation	Site location
SP40	33	33	14.6	1	Oxford Meadows	SAC	51.4637N/01.1712W
TL78	28	17	7.5	2	Breckland	SAC	52.3108N/00.4442E
TQ76	26	16	7.1	3	Peter’s Pit	SAC	51.2016N/00.2756E
NN64	17	16	7.1	4	Ben Lawers	SAC	56.3315N/04.1330W
SW71	16	13	5.8	5	The Lizard	SAC	50.0041N/05.1328W
SH65	24	9	4.0	6	Meirionnydd Oakwoods	SAC	52.5541N/03.5941W
ST57	22	8	3.5	7	Avon Gorge Woodlands	SAC	51.2750N/02.3801W
SU88	30	6	2.7	8	Harpsden Wood	SSSI	51.3102N/005.409W
TQ01	28	5	2.2	9	Arundel Park	SSSI	50.5151N/003.325W
TL57	17	5	2.2	10	Fenland	SAC	52.1823N/00.1644E
TQ50	25	4	1.8	11	Seaford to Beachy Head	SSSI	51.3902N/001.337E
ST36	31	4	1.8	12	Severn Estuary	SPA/SSSI/ RAMSAR	51.1329N/03.0257W
NY83	14	4	1.8	13	Moor House-Upper Teesdale	SAC	54.4259N/02.1844W
SU89	22	3	1.3	14	Moorend Common	SSSI	51.3627N/005.028W
NO27	30	3	1.3	15	Caenlochan	SAC	56.5230N /03.1730W
TG31	16	3	1.3	16	Broadland	SPA/RAMSAR	52.4356N/01.3600E
TM07	17	3	1.3	17	Waveney and Little Ouse Valley Fens	SAC	52.2242N/01.0106E
Totals	**396**	**152**	**67.3%**				

FIGURE 2

Seventeen UK CWR hotspots using the iterative method (total numbers of CWR taxa present in each shown, as well as additional CWR taxa in brackets) (Maxted *et al.*, 2008)



Why select two thirds of taxa as the number of priority CWR to target in genetic reserves? Because of resource limitations the conservationist is unlikely to be able to give priority to all CWR. Using the iterative selection procedure 69 sites would be required to include all 226 priority CWR taxa in reserves, a number that is unrealistic in practical terms. As shown in Figure 1, as the number of sites increases the percentage diversity added decreases and the economic cost of adding additional sites for smaller diversity gain would become unacceptable. The actual percentage of CWR taxa covered or the number of genetic reserves nominated will thus involve some form of cost–benefit analysis bearing in mind the resources available. Most examples in the literature primarily relate to ecosystems services (Chan *et al*., 2006; Naidoo and Ricketts, 2006; Siikamaki and Layton, 2007) and there are no current examples of cost-benefit analysis for CWR *in situ* conservation. Therefore it has been argued that if genetic reserves can be nominated within existing protected areas only the additional costs of the genetic reserves need to be estimated, which may be low in comparison to total running costs of the whole reserve.

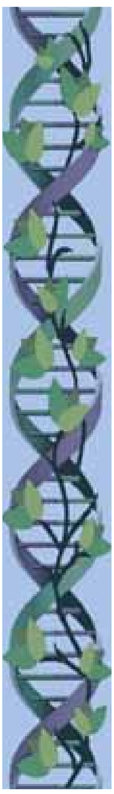
Why do we need to establish genetic reserves when the CWR taxa are present in protected areas anyway? Within the UK, as elsewhere, the majority of protected areas are established to conserve specific habitats or faunal elements, fewer are for flora and none specifically for CWR. So within the existing protected area networks none of the UK priority CWR taxa are targeted for routine demographic monitoring. Maxted *et al*. (1997a) distinguish between active and passive protected area conservation, where active management implies some form of dynamic intervention at the site, even if that intervention were simply limited to demographic monitoring of target populations. Passive conservation involves little or no intervention, and by definition there is no management or monitoring of target population. There may be general ecosystem management and all taxa will be passively conserved if the entire ecosystem or habitat is stable, but genetic diversity within individual taxa could be eroded or change. Also if the goal is CWR genetic conservation then it may be important for the patterns of genetic diversity and the natural dynamics of that diversity to be better understood. Therefore completely passive conservation of CWR in protected areas is unlikely to prove effective in CWR genetic conservation and the more active demographic and genetic monitoring and management of target CWR populations offered by genetic reserve conservation is required. Also the management of CWR may differ significantly from that required for more traditional protected areas where the objective will be to sustain climax communities. For example, the CWR of major crop plants are often located in pre-climax communities (Jain, 1975; Maxted *et al*., 1997a; Stolton *et al*., 2006) and therefore the site management may need to be intense; where some UK archaeophyte CWR are closely associated with traditional farming practices the genetic reserve management would require the maintenance of the farming system.

Finally, matching UK CWR hotspots with existing protected areas can only be used to predict CWR presence in protected areas; in each case field visits will be required to confirm the prediction before the final site is selected for a CWR genetic reserve. Also any gap analysis is constrained in its precision by the data resolution available. In the UK, floristic geographic taxon occurrence data are available primarily in the form of 10 × 10 km tetrad presence/absence, although some 2x2 km data were available for some but not all taxa. Although all UK protected areas have species lists, not all are comprehensive, so the absence of a CWR from a list cannot be taken to imply the species is not found at that location; this could be the case but it could also mean that recording that species has not be a priority at that site.

UK CWR Conservation Action Plans

Another essential component of a national CWR conservation strategy is to produce individual CWR Conservation Action Plans (CAP) for at least the highest priority CWR taxa (Maxted *et al*., in prep.). The use of coordinated conservation action plans to reverse the damaging impacts of human social, demographic and economic changes on plant diversity are well established, and are combined with integrated conservation actions, encompassing species recovery programmes and habitat management (Maunder, 2001). Within the UK's Biodiversity Action Plan the aim is to produce Biodiversity Action Plans (UK BAP) to enable targeting of conservation action and thus far BAPs cover 391 taxa and 45 habitats (www.ukbap.org.uk). For CWR the plan is likely to have a more specific focus, the maintenance of intra-specific genetic diversity and making that diversity available for utilization. The focus of a CWR conservation action plan may be amended to meet this demand. CWR conservation action plans have been prepared for 47 priority UK CWR taxa and are available via the UK Genetic Resources portal (http://grfa.org.uk/search/plants/index.html?#sr); the taxa covered are listed in Appendix C. Each CWR conservation action plan follows the same format and the information and categories for each Action Plan are:

- **Taxonomy** – the family, genus, species (sub-specific category), common name and important synonyms. The information was primarily derived from Stace (1997), and the GRIN (http://www.ars-grin.gov/npgs/tax/) and Plants for a Future (http://www.pfaf.org/) databases.
- **Plant characteristics** – general plant characteristics e.g. size, leaf shape, flower colour and number, flowering times, germination times and conditions and the behaviour of the seeds in a gene bank. The information was primarily derived from Stace (1997) and Seed Information Database (http://www.rbgkew.org.uk/data/sid/) of the Royal Botanic Gardens, Kew.
- **Current distribution** – current locations and abundance. The information was primarily derived from the National Biodiversity Network Gateway (http://www.searchnbn.net/).
- **Ecogeographic summary** – habitat, soil, pH and altitude preferences of the plant, as well as pests and diseases, pollinators and any other biotic associations. The information was primarily derived from Preston, *et al*. (2002a), and the GRIN (http://www.ars-grin.gov/npgs/) and Plants for a Future (http://www.pfaf.org/) databases.
- **Conservation status** – current IUCN category, whether the taxon is included in Schedule 8 of the UK Wildlife and Countryside Act (1981) and if a Biodiversity Action Plan is available. The information was derived from Cheffings and Farrell (2005) and the UK Defra website (http://www.defra.gov.uk/). The *in situ* and *ex situ* status was established by searching the UK protected areas species lists via the NBN Gateway (http://www.searchnbn.net/) and for *ex*



situ conservation by searching the Seed Information Database (http://www.rbgkew.org.uk/data/sid/) of the Royal Botanic Gardens, Kew.

- **Current uses** – contemporary uses of the taxon. The information was primarily derived from Smartt and Simmonds (1995) and the GRIN (http://www.ars-grin.gov/npgs/) and Plants for a Future (http://www.pfaf.org/) databases.
- **Current factors causing loss and decline** – current factors believed to threaten the CWR taxon. The information was primarily derived from internet searches but tended to be repeated for most taxa, habitat fragmentation and changes in land use, notably intensification of agriculture.
- **Current conservation action** – current conservation programmes, such as English Nature's 'Species Recovery Programme' and Plantlife's 'Back from the Brink' programme or specific inclusion in Local Biodiversity Action plans (LBAPs).
- **Proposed Action Plan objectives and targets** – proposed targets of the Action Plan and any future conservation work required. This segment of the CWR CAP was subdivided into five sections as follows:
- **Policy and legislation** – any legal action needed to improve protection, such as the addition of the taxon onto Schedule 8 of the Wildlife and Countryside Act, 1981.
- **Site safeguard and managemen**t – specific action required to safeguard specific CWR sites, e.g. inclusion in Countryside Stewardship Schemes.
- **Taxon management and protection** – specific management requirements for taxa.
- **Advisory** – specific advice for landowners and managers of the actions needed to safeguard the CWR taxa located on their land.
- **Future research and monitoring** – the research required to improve current conservation of the CWR taxa, highlighting the most appropriate form of population monitoring.
- **Local conservation** – an evaluation of current Local Authorities conservation efforts, listing Local Biodiversity Action Plans in which the taxa are included. The information was primarily derived from the National Biodiversity Network Gateway (http://www.searchnbn.net/).

Some of the taxa for which CWR conservation action plans have been developed are not endemic to Britain, and some are widespread and common elsewhere in Europe. It was important to include these taxa as they are a UK resource and they are rare or threatened within the UK often with declining populations. Currently they receive little conservation activity in the UK, which increases their vulnerability to extinction. The specific CWR conservation action plans will hopefully raise awareness of these taxa and so improve their conservation.

References

Anonymous (2004). The Official Yearbook of the United Kingdom of Great Britain and Northern Ireland. Her Majesty's Stationery Office, London.

Balmford, A. (2003). Conservation planning in the real world: South Africa shows the way. Trends in Ecology and Evolution, 18: 435–438.

Bonn, A., Rodrigues, A.S.L. and Gaston, K.J. (2002). Threatened and endemic species: are they good indicators of patterns of biodiversity on a national scale? Ecology Letters, 5: 733–741.

Brooks, T.M., Bakarr, M.I., Boucher, T., Da Fonesca G.A.B., Hilton-Taylor, C. and Hoekstra, J.M. (2004). Coverage provided by the global protected area system: is it enough? Bioscience, 54: 1081–1091.

Chan, K.M.A., Shaw, M.R., Cameron, D.R., Underwood, E.C. and Daily, G.C. (2006). Conservation planning for ecosystem services. PLoS Biology, 4(11): e379 doi:10.1371/journal.pbio.0040379.

Cheffings, C. (2004). New plant status lists for Great Britain. BSBI News, 95: 36–43.

Cheffings, C.M. and Farrell, L. (Eds.) (2005). The vascular plant red data list for Great Britain. Species Status, 7: 1–116. Joint Nature Conservation Committee, Peterborough.

Cook, F.E.M. (1995). Economic Botany Data Collection Standards. Royal Botanic Gardens, Kew.

Defra (2004a). Plant Variety Rights Office and Seeds Division Seed Trader's Annual return for year ended 30 June 2003. Defra, London.

Defra (2004b). Seed Traders' Annual Return – Year ended 30 June 2004. Plant Variety Rights Office and Seeds Division, Defra, London.

Dietz, R.W. and Czech, B. (2005). Conservation deficits for the continental United States: an ecosystem gap analysis. Conservation Biology, 19: 1478–1487.

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.

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

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.

Hopkinson, P., Evans, J. and Gregory, R.D. (2000). National-scale conservation assessments at an appropriate resolution. Diversity and Distributions, 6: 195–204.

Iriondo, J.M., Dulloo, E., Maxted, N. (Eds.) (2008). Conserving Plant Genetic Diversity in Protected Areas: Population Management of Crop Wild Relatives. CAB International Publishing, Wallingford.

IUCN (1998). 1997 United Nations list of protected areas. IUCN World Commission on Protected Areas, IUCN Gland, Switzerland and Cambridge, UK.

IUCN (2001). IUCN Red List Categories and Criteriia: Version 3.1. IUCN Species Survival Commission. IUCN, Gland, Switzerland and Cambridge, UK. http://www.iucnredlist.org/static/categories_criteria_3_1 [Accessed 21 October 2008].

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,

Kell, S.P., Knüpffer, 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.

Kirkpatrick, J.B. and Harwood, C.E. (1983). Conservation of Tasmanian macrophyte wetland vegetation. Proceedings of the Royal Society of Tasmania, 117: 5–20.

Mabberley, D.J. (1997). The Plant-Book. A Portable Dictionary of the Vascular Plants. Cambridge University Press, Cambridge.

Mabey, R. (1996). Flora Britannica. Chatto & Windus, London.

Mabey, R. (2003). Food for Free. Harper Collins Publishers, London.

Margules, C.R. (1989). Introduction to some Australian developments in conservation evaluation. Biological Conservation, 50: 1–11.

Margules, C.R. and Pressey, R.L. (2000). Systematic conservation planning. Nature, 405: 243–253.

Margules, C.R., Nicholls, A.O. and Pressey, R.L. (1988). Selecting networks of reserves to maximize biological diversity. Biological Conservation, 43, 63–76.

Maunder, M. (2001). Plant conservation. Encyclopaedia of Biodiversity: (Vol. 4). Pp. 645–657. Academic Press, London,

Maxted, N., Hawkes, J.G., Ford-Lloyd, B.V. and Williams, J.T. (1997a). 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. (1997b). The selection of taxa for plant genetic conservation. Genetic Resources and Crop Evolution, 44: 337–348.

Maxted, N., Mabuza-Dlamini, P., Moss, H., Padulosi, S., Jarvis, A. and Guarino, L. (2004). An Ecogeographic Survey: African *Vigna*. Systematic and Ecogeographic Studies of Crop Genepools 10. International Plant Genetic Resources Institute, Rome, Italy.

Maxted, N., Ford-Lloyd, B.V. and Kell, S.P. (2008). Crop wild relatives: establishing the context. 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. 3–30. CAB International, Wallingford, UK.

Naidoo, R and Ricketts, T.H. (2006). Mapping the Economic Costs and Benefits of Conservation. PLoS Biology, 4(11): e360 doi:10.1371/journal.pbio.0040360

Ortega-Huerta, M.A., and Peterson, A.T. (2004). Modelling spatial patterns of biodiversity in Northeastern Mexico. Diversity and Distributions, 10: 39–54.

Prendergast, J.R., Quinn, R.M., Lawton, J.H. Eversham, B.C., Gibbons, D.W. (1993). Rare species, the coincidence of diversity hotspots and conservation strategies. Nature, 365: 335–337.

Pressey, R.L. (1994). Ad hoc reservations: forward or backward steps in developing representative reserve systems? Conservation Biology, 8: 662–668.

Pressey, R.L. and Nicholls, A.O. (1989). Efficiency in conservation evaluation: scoring versus iterative approaches. Biological Conservation, 50: 199–218.

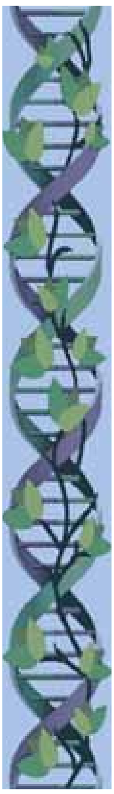
Pressey, R.L., Humphries, C.R., Vane-Wright, R.I. and Williams, P.H. (1993). Beyond opportunism: key principles for systematic reserve selection. Trends in Ecology and Evolution, 8: 124–128.

Preston, C.D., Pearman, D.A. and Dines, T.D. (2002a). New Atlas of the British and Irish Flora. Oxford University Press, Oxford.

Preston, C.D., Telfer, M.G., Arnold H.R., Carey, P.D. Cooper, J.M., Dines, T.D., Hill, M.O., Pearman, D.A., Roy, D.B. and Smart, S.M. (2002b). The changing flora of the UK. Defra, London.

Preston, C.D., Pearman, D.A. and Hall, A.R. (2004). Archaeophytes in Britain. Botanical Journal of the Linnean Society, 145: 257–294.

Rebelo, 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.



Rich, T.C.G., Bennallick, I.J., Cordrey, L. Kay, Q.O.N., Lockton, A.J. and Rich, L.K. (2002). Distribution and population sizes of Asparagus prostrates Dumort.: wild asparagus in Britain. Watsonia, 24: 183–192.

Riemann, H. and Ezcurra, E. (2005). Plant endemism and natural protected areas in the peninsula of Baja California, Mexico. Biological Conservation, 122, 141–150.

Siikamaki, J. and Layton, D.F. (2007). Discrete choice survey experiments: A comparison using flexible methods. Journal of Environmental Economics and Management, 53(1): 122–139.

Smartt, J. and Simmonds, N.W. (Eds.) (1995). Evolution of Crop Plants (Second Edition). Longman Scientific and Technical, England.

Stace, C. (1997). New Flora of the British Isles. Cambridge University Press, Cambridge.

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.

Telfer, M.G., Preston, C.D. and Rothery, P. (2002). A general method for measuring relative change in range size from biological atlas data. Biological conservation, 107: 99–109.

Wiersema, J. and Leon, B. (1999). World economic plants – a standard reference. CRC Press, Baco Raton, Florida, US.

WWF and IUCN (1994). Centres of plant diversity. A guide and strategy for their conservation. 3 volumes. IUCN Publications Unit, Cambridge, U.K.