THEMATIC BACKGROUND STUDY

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

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

by

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SUMMARY

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

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

In 1989, the Commission on Genetic Resources for Food and Agriculture (CGRFA) called for the establishment of networks of *in situ* conservation areas for PGRFA, for both crops and CWR[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.

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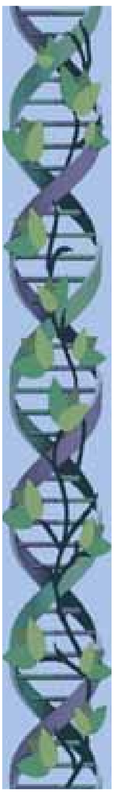
[2] CPGR/89/REP, paragraphs 32-37.

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

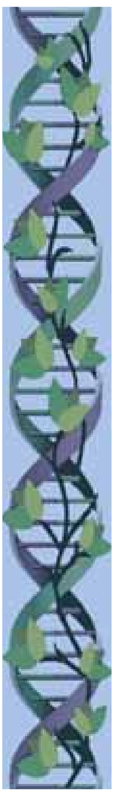
CWR are commonly defined in terms of wild species that are relatively closely related to agricultural and horticultural crops; therefore, a broad definition of a CWR would be any taxon belonging to the same genus as a crop. This definition is intuitively accurate and can be simply applied. However, application 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

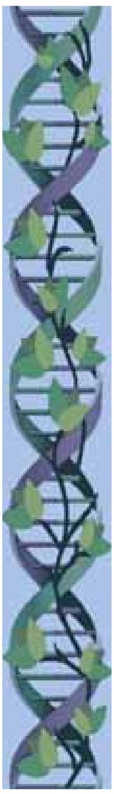
Naturally, some countries harbour greater numbers of CWR than others. In general, the greater the number of species in the country's flora, the greater the number of CWR there will be. In those countries with higher numbers of CWR, a greater injection of resources will be needed in order to secure populations *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.

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[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.

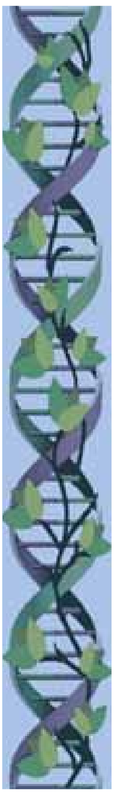
However, in many areas of the world this group of weedy CWR species is particularly threatened because of the widespread abandonment of these traditional cultivation systems. Several national governments in developed countries are responding by providing incentives or even financial subsidies to maintain 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

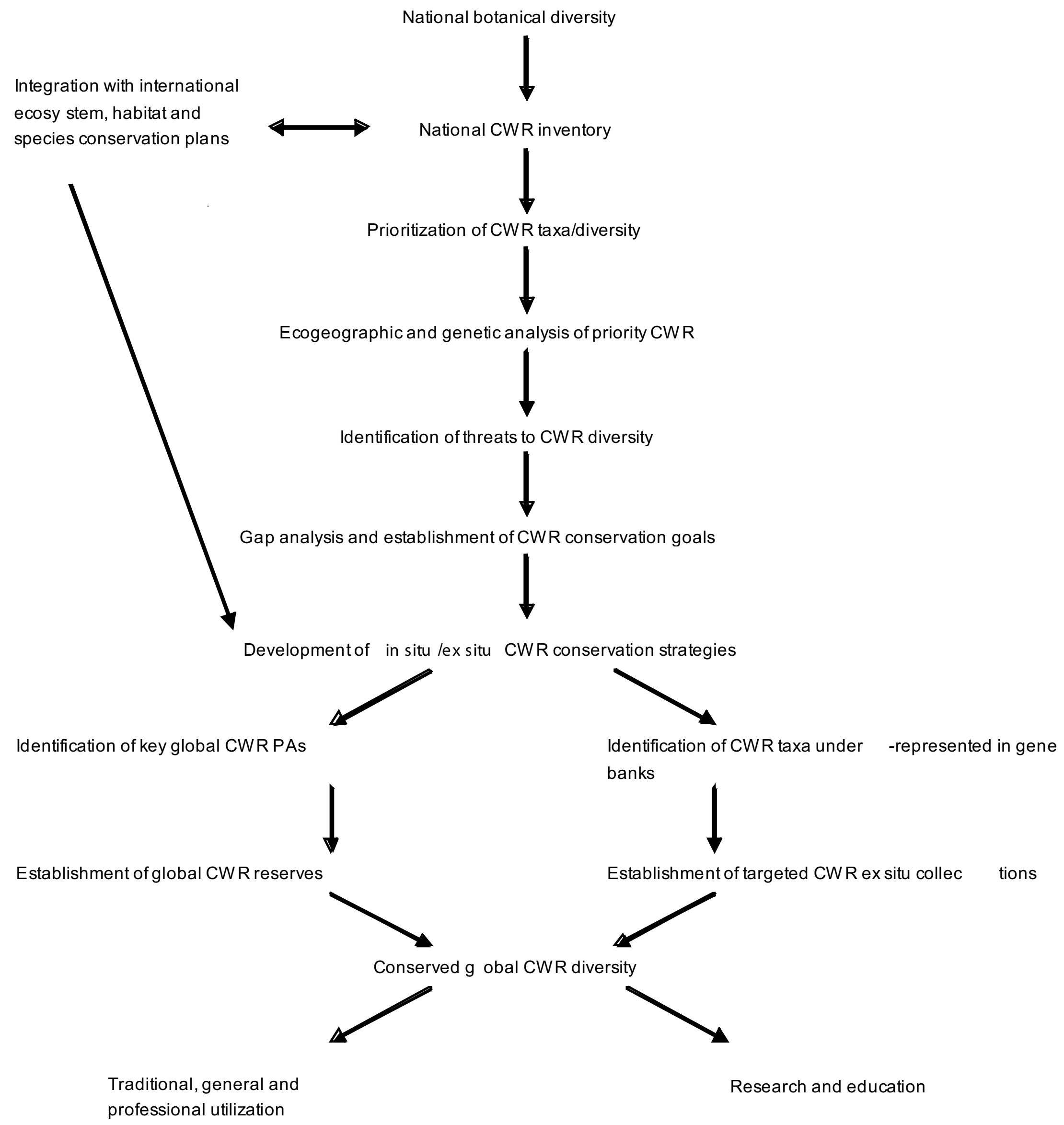
There are many potential approaches to systematic CWR conservation. But as every country contains CWR diversity, they are obliged as signatories to the CBD and ITPGRFA, or other policy instruments, to adopt a national approach to systematically conserve this diversity. This section outlines how a national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

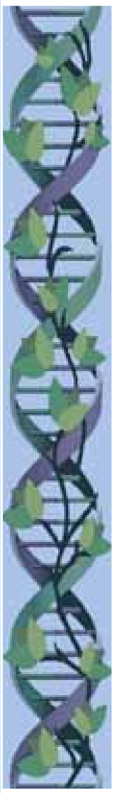
FIGURE 1

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.

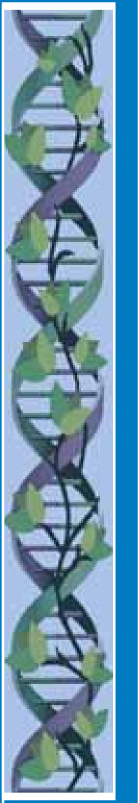
Determination of the actual number of specific CWR genetic reserves will ultimately be pragmatic—dictated by the resources available for *in situ* CWR conservation as well as the size of the country and richness of its CWR flora. For example, in UK 17 sites in existing protected areas (nine in Special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

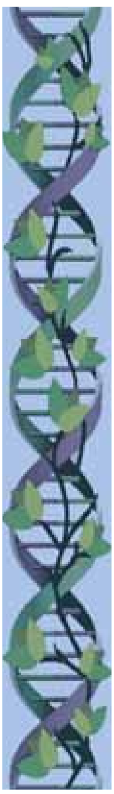
Within each crop gene pool, the wild relatives that are most closely related to the cultivated taxon are generally given priority over the more distantly related species because these are the taxa that can more easily be used in crop improvement using conventional breeding methods. However, we have also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

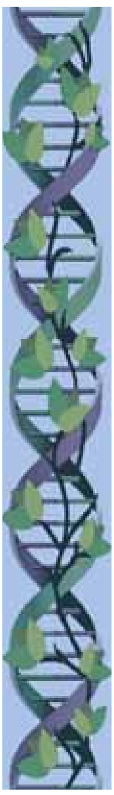
Oryza sativa L.

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]

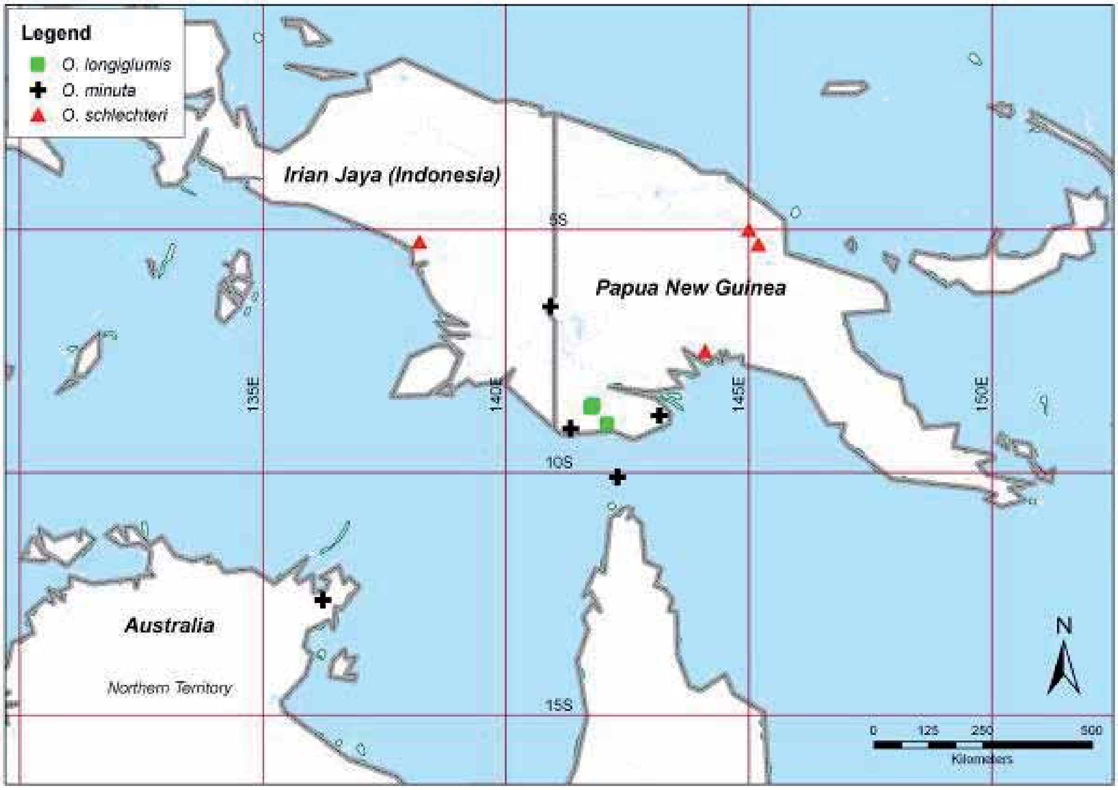
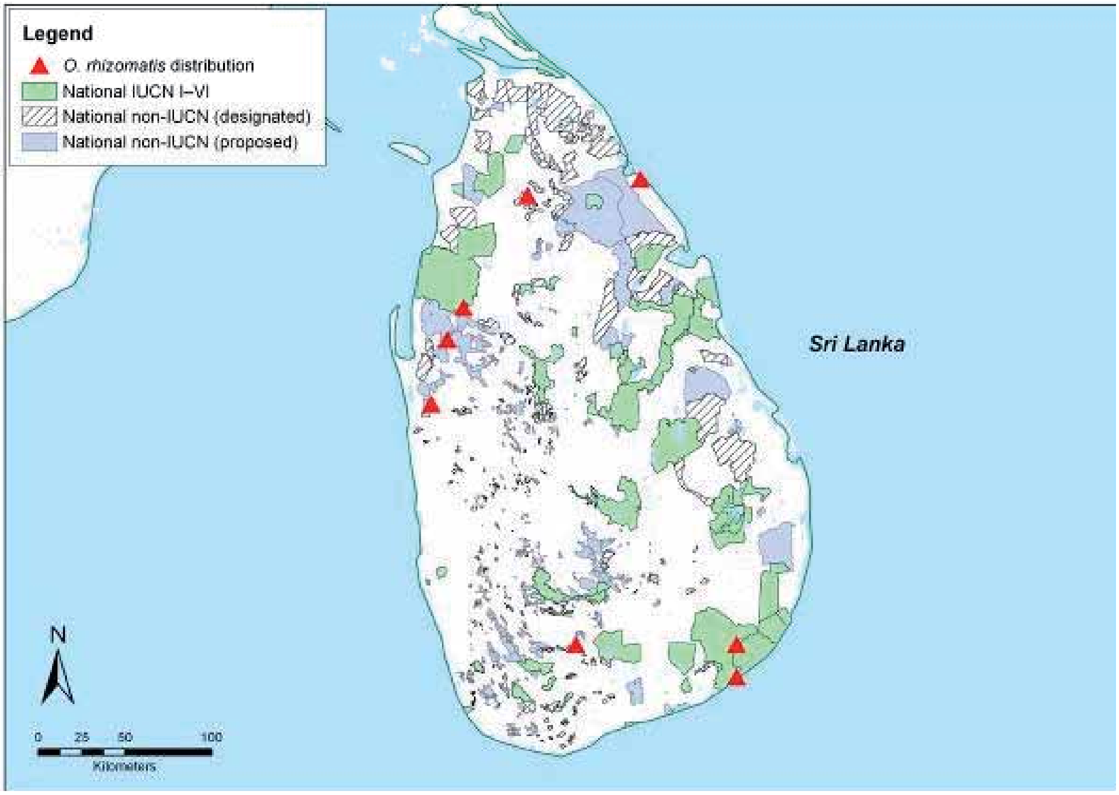


FIGURE 3

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.

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

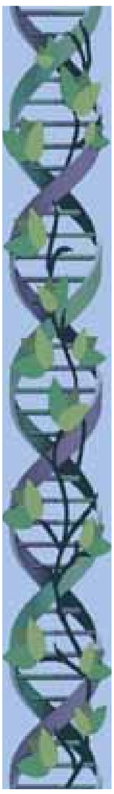
[5] Data sources – *O. longiglumis* and *O. minuta*: Plants of Papua New Guinea (accessed through GBIF data portal, http://data.gbif.org/datasets/resource/969 04/08/2008), Australian National Herbarium (CANB) (http://data.gbif.org/datasets/resource/47 04/08/2008), NSW herbarium collection (http://data.gbif.org/datasets/resource/968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

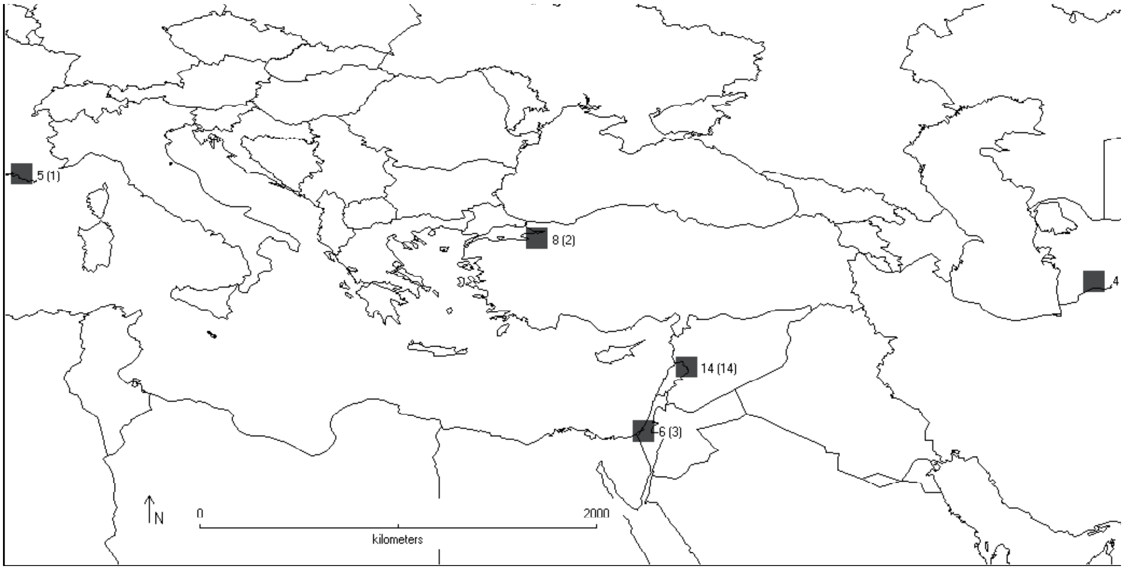
Priority sites

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):

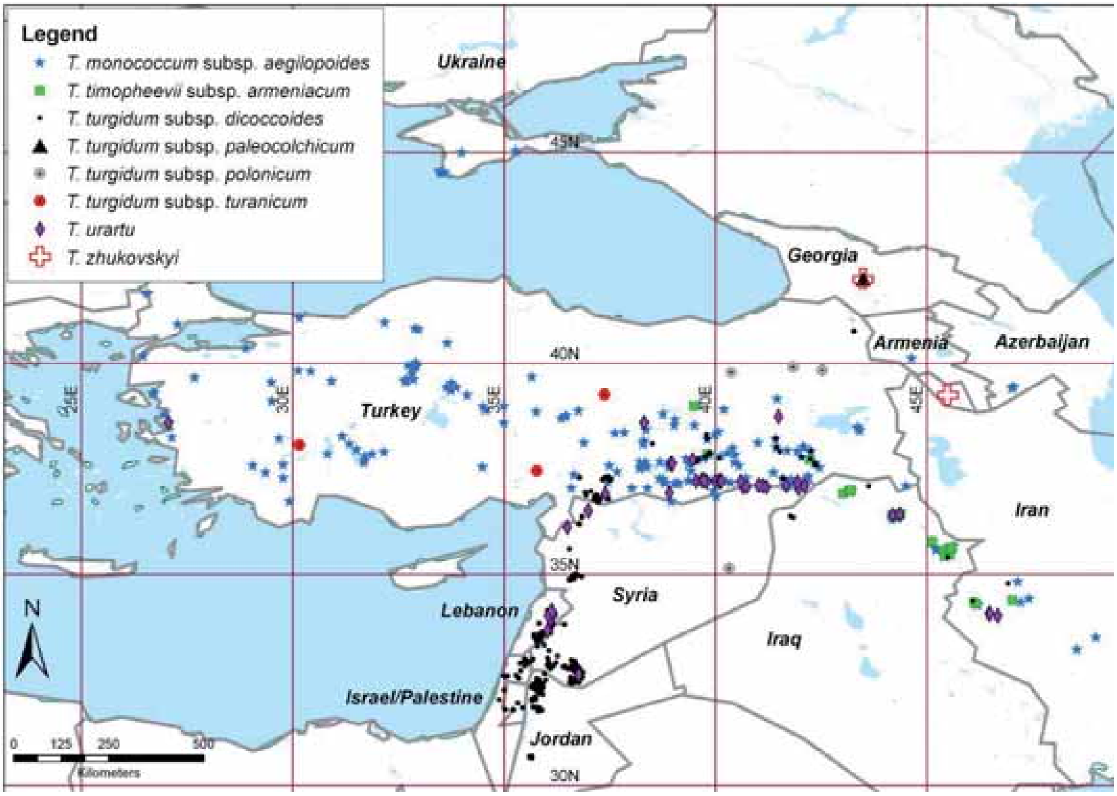
- Qal'at Al Hasn, Homs province, Syria. Maxted *et al*. (2008c) identified this location as the best option for a single reserve for *Aegilops* as it has the highest concentration of taxa (14). However, there are currently no protected areas in the vicinity and a recent study (Keisa *et al*., 2008) found 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

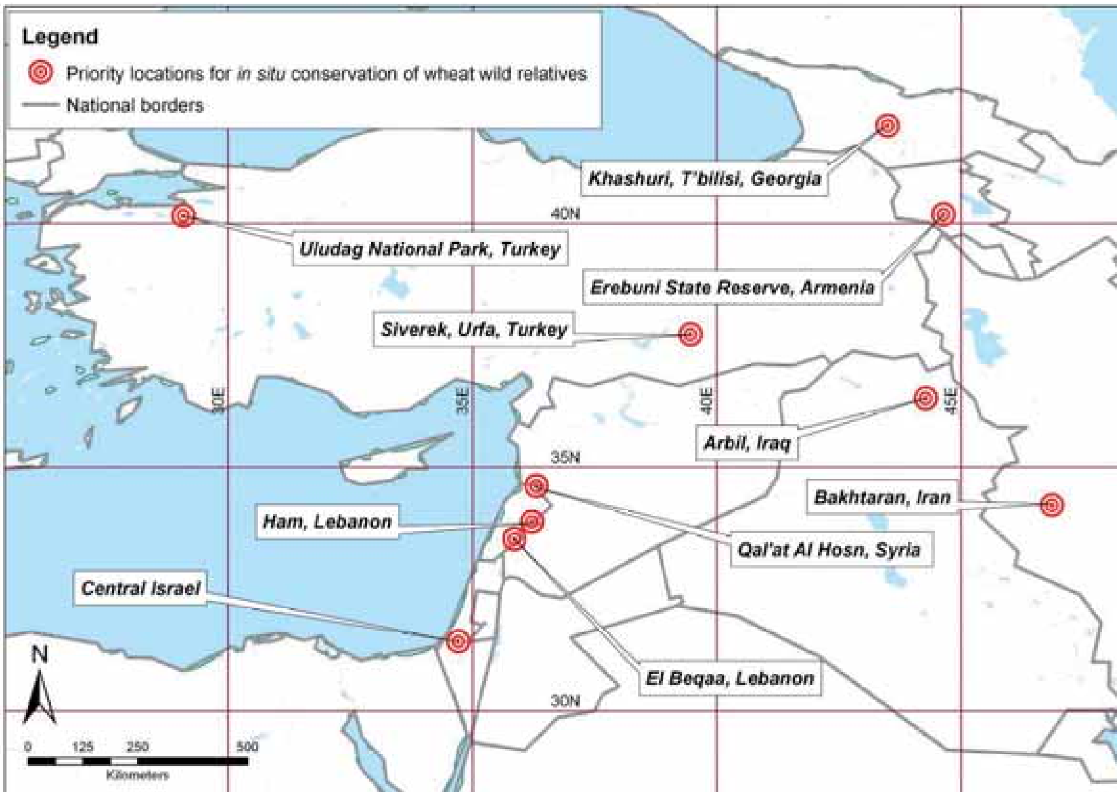
Distribution of high priority wheat wild relatives (*Triticum* spp.). Data sources: *T. monococcum* subsp. *aegilopoides, T. timopheevii* subsp. *armeniacum, T. turgidum* subsp. *dicoccoides*, subsp. *paleocolchicum, T. urartu* and *T. zhukovskyi* – USDA, ARS, National Genetic Resources Program. pcGRIN. 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

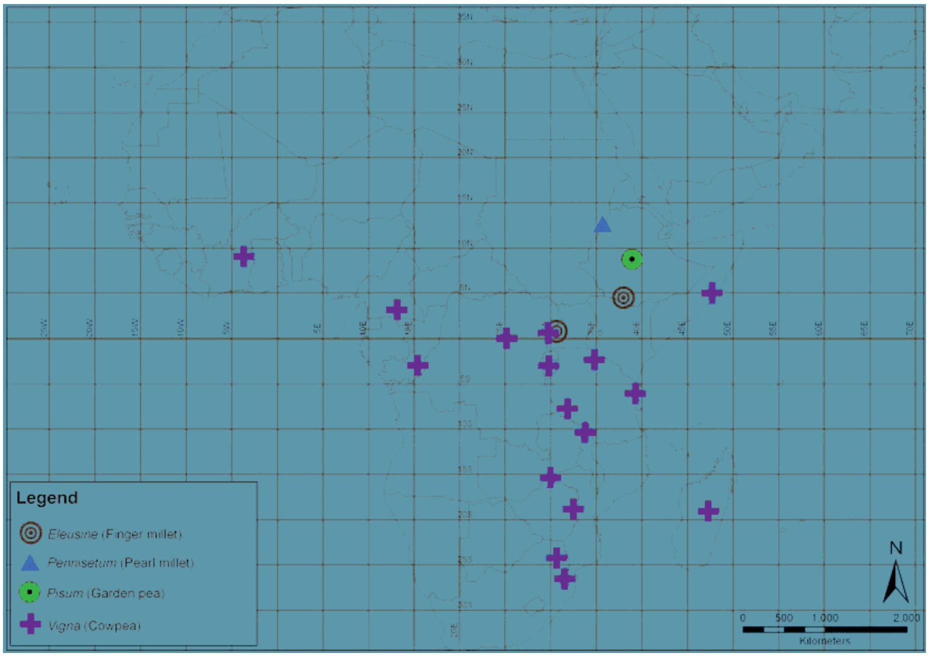


FIGURE 8

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

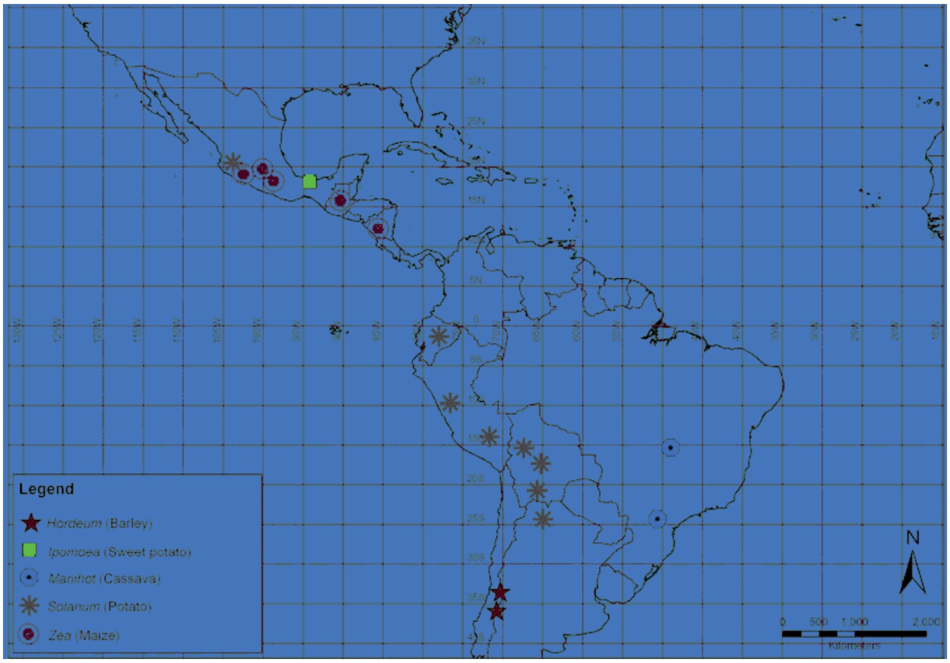


FIGURE 9

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

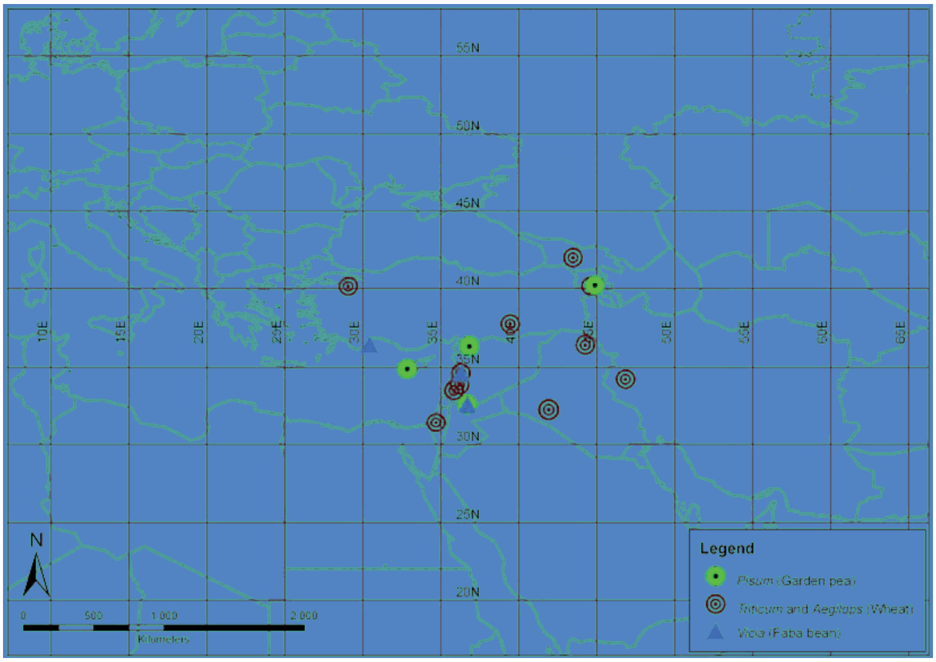
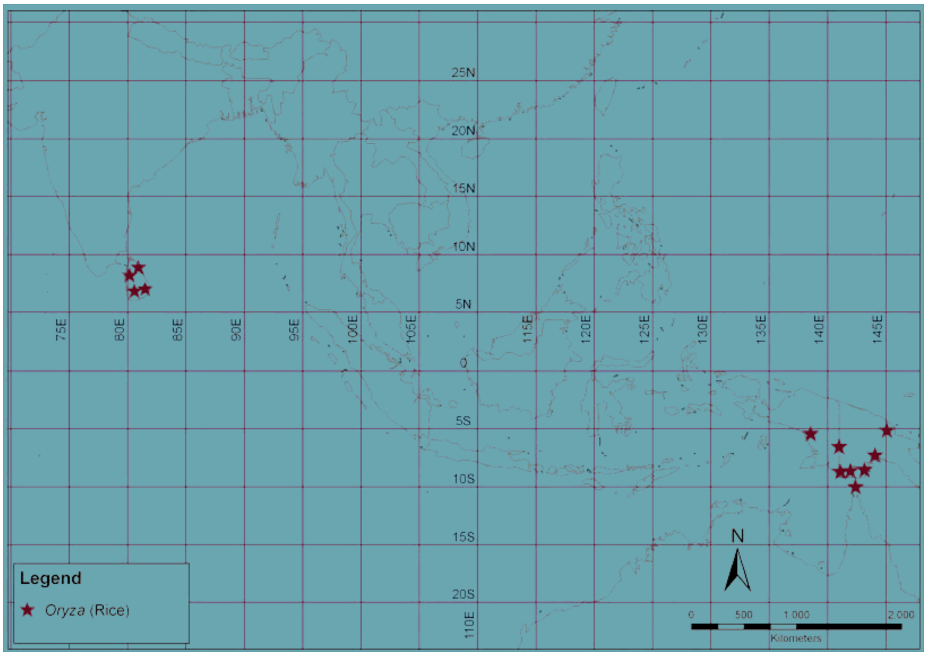


FIGURE 10

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.

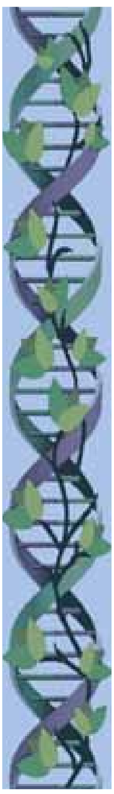
There are several high priority CWR taxa in the *Vigna* gene pool and they are widespread throughout sub-Saharan Africa. The taxa have restricted distributions and there is little overlap between them; therefore, opportunities for multi-taxon reserves for high priority *Vigna* wild relatives are limited.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

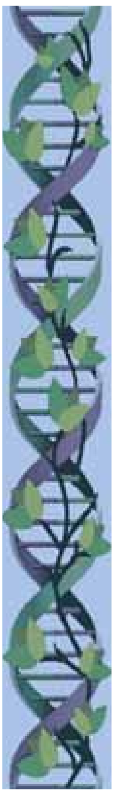
Asia and the Far East is also the centre of distribution of banana/plantain wild relatives in the genus *Musa*. Priority locations for *in situ* conservation of this genus are not shown in Figure 10 because distribution data were not readily available for analysis. However, ten priority banana/plantain 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.

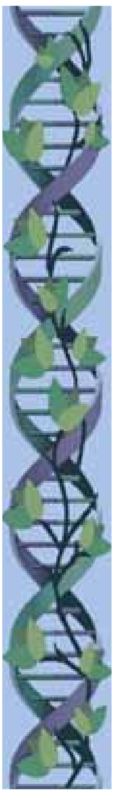
4.6 Improve information dissemination

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.

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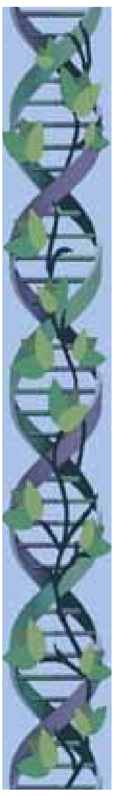

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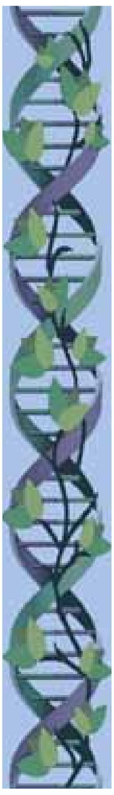

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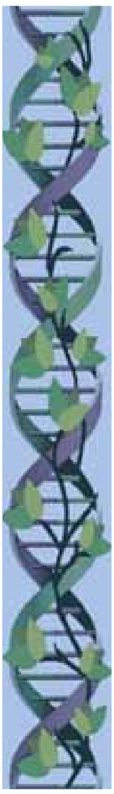

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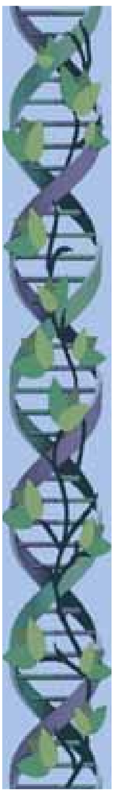

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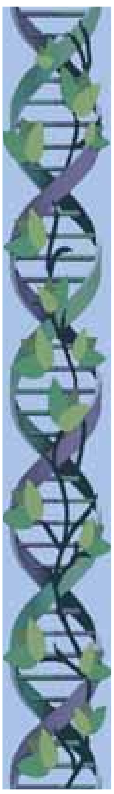
ANNEXE 1: INTRODUCTION TO CROP WILD RELATIVES



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:

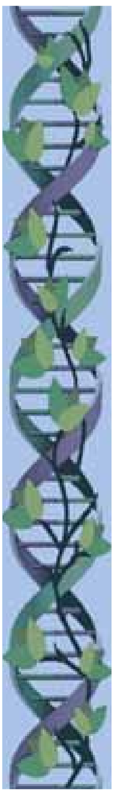
- Identify which important areas for CWR are already part of existing protected areas, in particular in the centres of origin or diversification;
- Pinpoint existing conservation gaps, in order to assess which important areas for CWR are yet to be protected within and outside existing protected areas;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

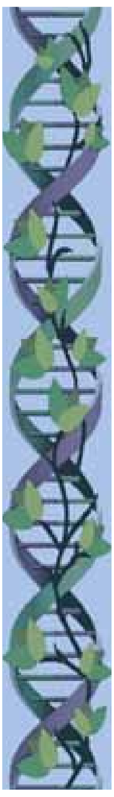
Development in the biotechnology industries has also allowed the transfer of genes from more distantly related species, further enhancing the value of CWR—both those closely and more distantly related (see Hajjar and Hodgkin, 2007; Hodgkin and Hajjar, 2008). CWR have contributed significantly to improving 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)

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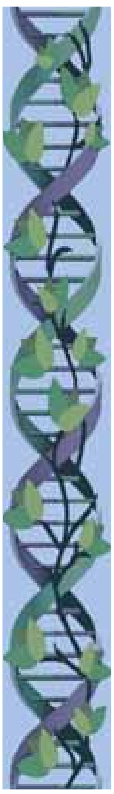
[8] Further discussion of CWR use is included in the individual CWR crop case studies presented in Part 3.

[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.

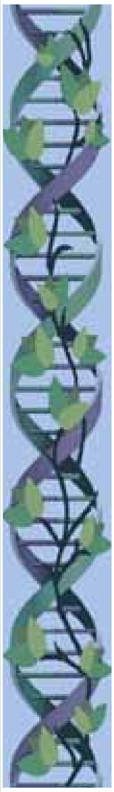
Crop	CWR	Application(s)	Reference(s)
Beets (*Beta vulgaris*)	*B. maritima*	Leaf spot resistance	Prescott-Allen and Prescott-Allen (1986)
	B. patellaris, B. procumbens, B. webbiana	Sugar beet nematode resistance	Prescott-Allen and Prescott-Allen (1986)
Oil-seed rape (*Brassica napus*)	*B. rapa, B. oleracea*	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)

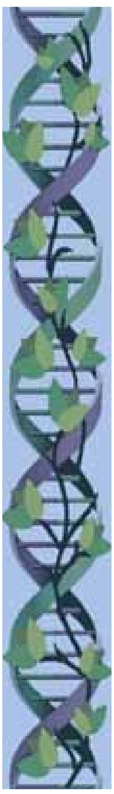


Crop	CWR	Application(s)	Reference(s)
Wheat (*Triticum aestivum*)	*Ae. squarrosa*	Hessian fly, leaf rust and soil-borne-mosaic virus resistance	Cox *et al.* (1990)
	Ae. tauschii	Drought tolerance	Gororo *et al.* (2002)
	Ae. tauschii	Hessian fly resistance	Cox and Hatchett (1994), Suszkiw (2005)
	Ae. tauschii	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.

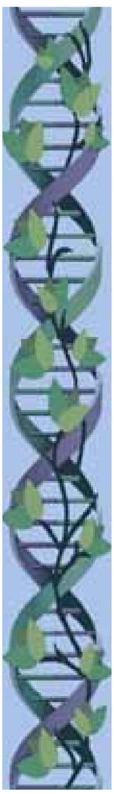
The Taxon Group concept assumes that taxonomic distance is positively correlated to genetic distance. Flint (1991), Heywood (1994), Johnson (1995) and Maxted *et al*. (2006) (among others) have drawn attention to the fact that this relationship may not always hold because of inconsistencies amongst taxonomists 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

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[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 100	47 2.06	100 4.39	6.45

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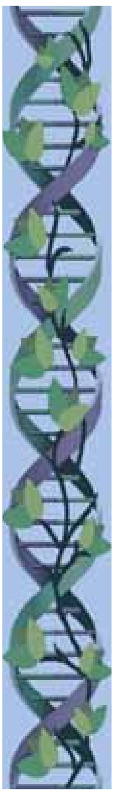
[11] Percentages based only on the degree of relationship of the species to the crop taxon. In this study, a refinement of this level of prioritization was undertaken based on the degree of threat of these species and to include cases where tertiary wild relatives are also known to be important for crop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

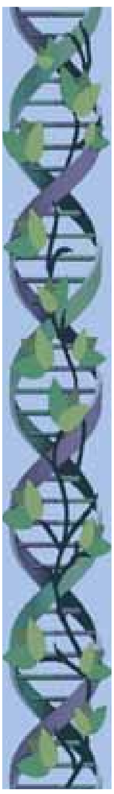
- **Deforestation** – Forest clearance and repeated burning for agriculture, as well as logging and hunting have resulted in severe degradation of natural forest communities. FAO (2007) report that during the 15 year period from 1990–2005, the world lost 3% of its total forest area. During this period, 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.

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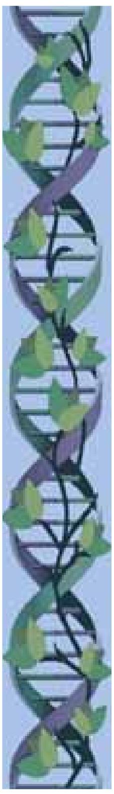
[12] Synonymous terms include 'genetic reserve management units' (GRMUs), 'gene management zones' (GMZs), 'gene sanctuaries' or 'genetic sanctuaries' and 'crop reservations'.

[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).

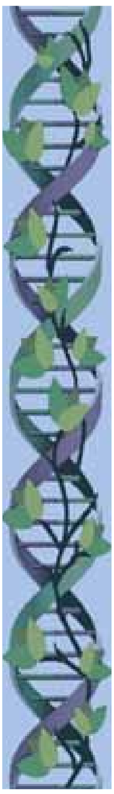
Many CWR species are also found growing as weeds in agricultural, horticultural and silvicultural systems—particularly those associated with traditional cultural practices or marginal environments. In many areas of the world this group of weedy CWR species is particularly threatened because of the widespread 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.

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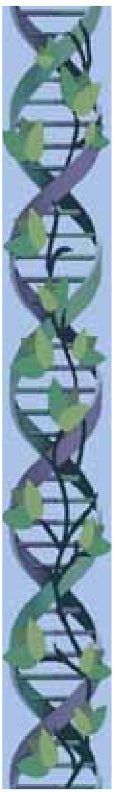

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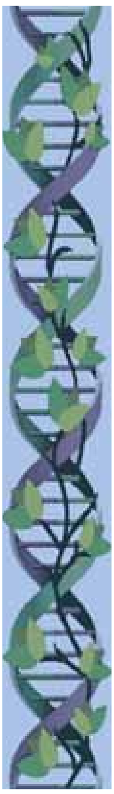

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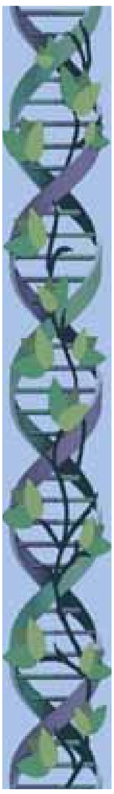

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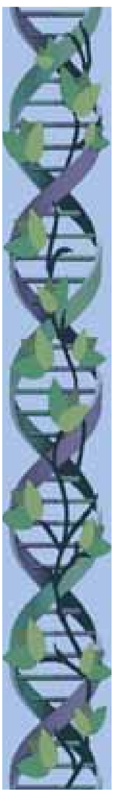

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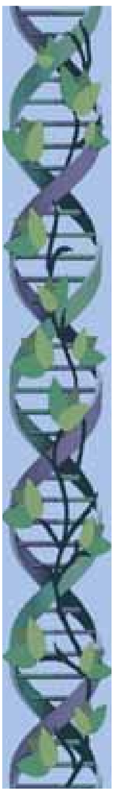

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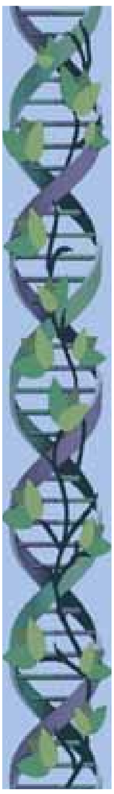

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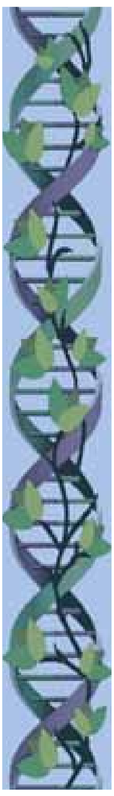

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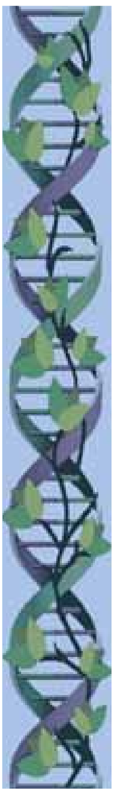

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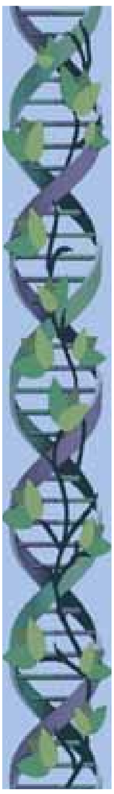

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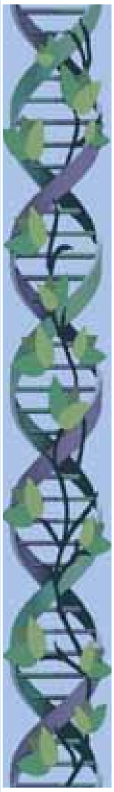
ANNEXE 2: NATIONAL CWR CONSERVATION STRATEGIES



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

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[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.

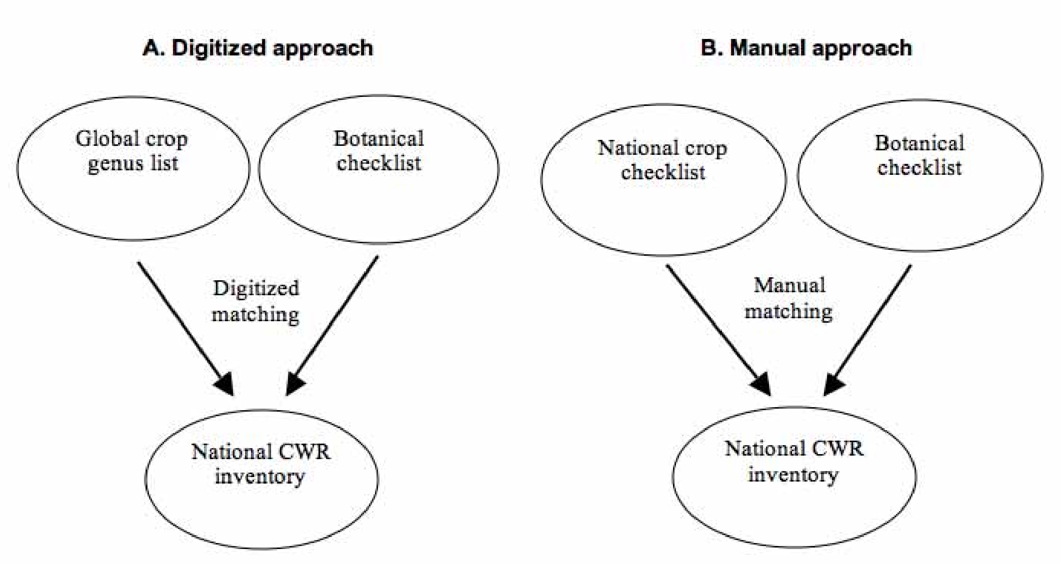
Having established the national CWR inventory, there are two routes for potential interactions with individual conservationists:

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.

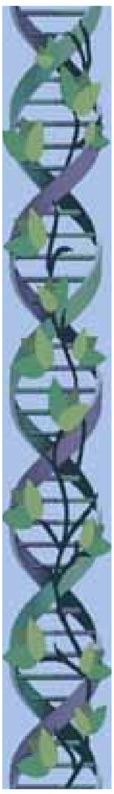
FIGURE 2

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

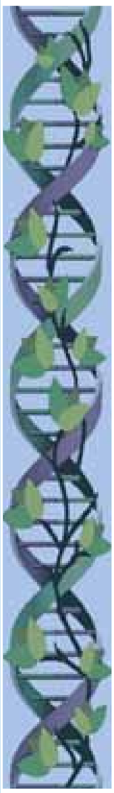
As well as assessing threat in relation to individual CWR taxa (in order to assist prioritization for conservation), there is also a need to assess threat in relation to conservation planning (i.e. to identify those important CWR areas most likely to be threatened). In terms of threat assessment for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

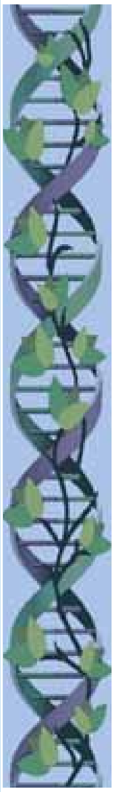
2.8 CWR utilization

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.

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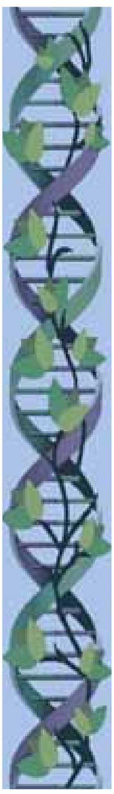

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ANNEXE 3: CASE STUDY: NATIONAL CWR CONSERVATION STRATEGY FOR THE UK

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).

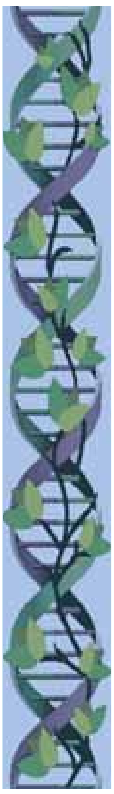
UK national CWR inventory content

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

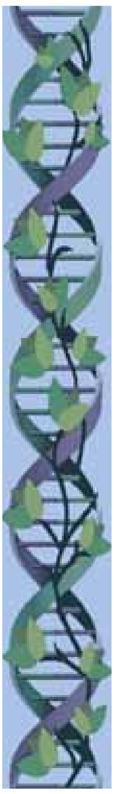
For UK CWR taxa with known distributions, more than 40% are common to very common as they occur in > 50–25% of UK hectads. An additional 26% can be considered near-scarce as they occur in < 25% but more than 100 grid squares. More than a third of the taxa with known distributions are scarce to very rare. 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)

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[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

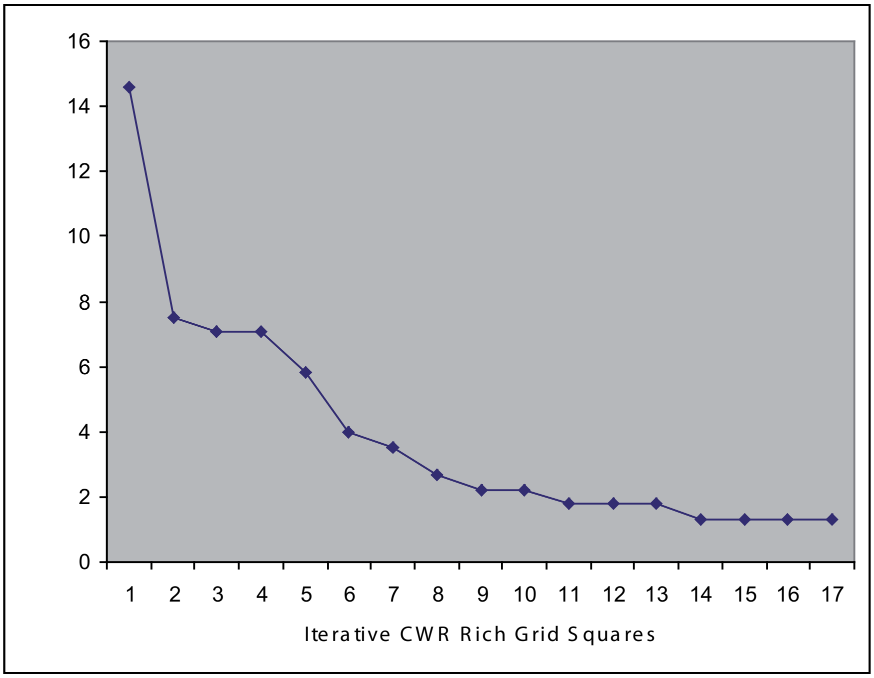


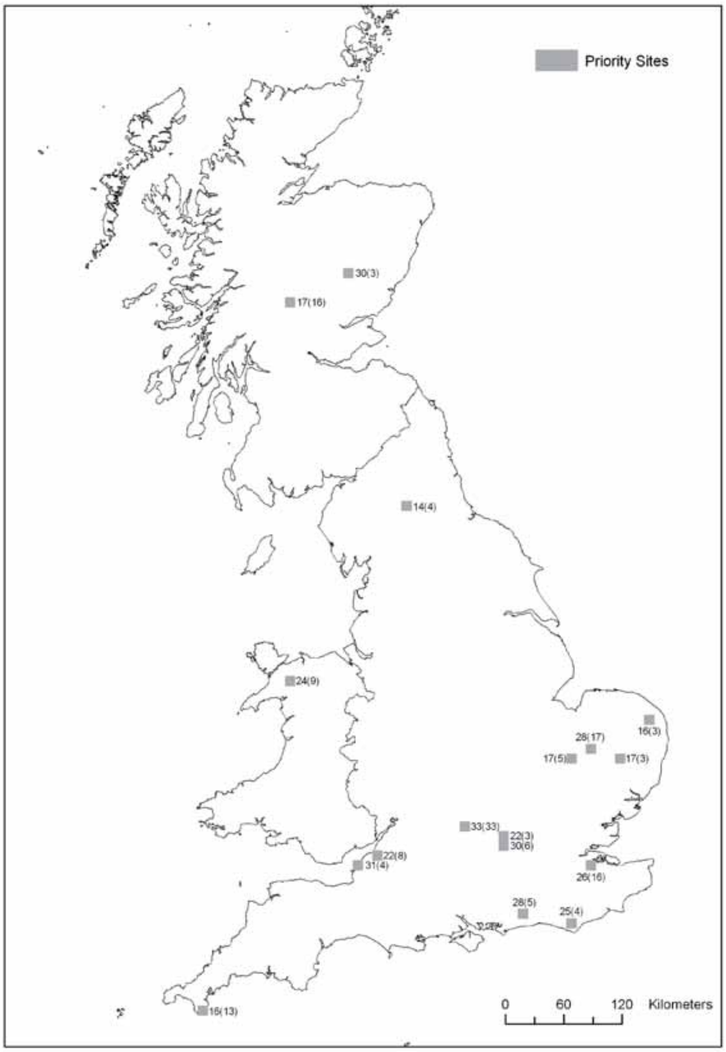
TABLE 4

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.

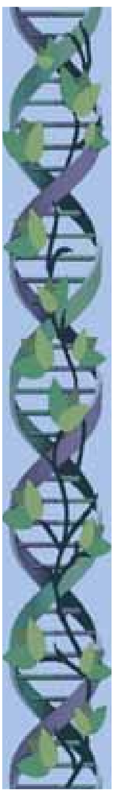
Why do we need to establish genetic reserves when the CWR taxa are present in protected areas anyway? Within the UK, as elsewhere, the majority of protected areas are established to conserve specific habitats or faunal elements, fewer are for flora and none specifically for CWR. So within the existing 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.

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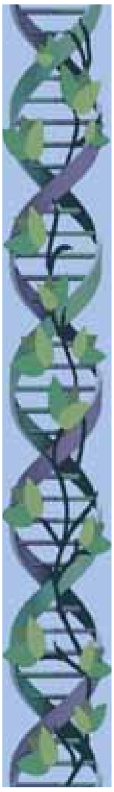

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ANNEXE 4: IMPORTANT AREAS AND CONSERVATION GAPS FOR CWR

As outlined in Part 1 of this report, there are two primary strategic approaches to systematic CWR conservation—the national and global approaches. 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*. Due to the vast number of CWR that exist globally, this approach focuses on the conservation of a selection of globally important crop gene pools; thus, the approach is monographic (i.e., focusing on the conservation of particular taxa), rather than floristic (i.e., where the entire CWR flora of a country or area is conserved). In this part of the report, we explain how the global approach can be implemented, from 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 the global network of CWR genetic reserves. This is a preliminary background study which provides the basis for further research into each of the crop gene pools selected. It should not be viewed as a final concrete proposal for the establishment of specific genetic reserves. For each of the crop gene pools included in this study, specific recommendations are provided, and where further research is needed, this has been highlighted.

1. Methodology

1.1 Selection of priority crop gene pools

The crops included in this background study are, firstly, those that have been identified as being of major importance for food security in one or more sub-regions of the world (FAO, 1997) and are listed in Annex I of the ITPGRFA (FAO, 2001), which is a list of PGRFA established according to criteria of food security and interdependence. These are: finger millet (*Eleusine coracana*), barley (*Hordeum vulgare*), sweet potato (*Ipomoea batatas*), cassava (*Manihot esculenta*), banana/ plantain (*Musa acuminata*), rice (*Oryza sativa*), pearl millet (*Pennisetum glaucum*), potato (*Solanum tuberosum*), sorghum (*Sorghum bicolor*), wheat (*Triticum aestivum*) and maize (*Zea mays*). Each of these crops supplies more than 5% of the plant-derived energy intake in one or more sub-regions of the world (FAO, 1997). Both finger millet and pearl millet are included in this study because they are listed independently in the ITPGRFA. Secondly, 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*).

Analysis of data extracted from the FAOSTAT database (major food and agricultural commodities and producers – http://www.fao.org/es/ess/top/country.html) shows that most of these crops, as well as being globally and/or regionally important for food security, are also of high economic value to many countries; in particular, bananas, rice, potatoes, wheat and maize. Millet, barley, sweet potato, cassava, cowpea and sorghum also frequently appear in country lists of the 20 most important food and agricultural commodities, ranked by monetary value. However, the main selection criterion for priority crops is based on their importance for global and/or local food security. For example, if selection was based on crops of the highest economic value, tomatoes would be ranked as one of the most important crops. Tomato is not considered to be significant in terms of food security and is therefore not included in this study.

As noted by FAO (1997), the selection of crops treated in this background study does not constitute a definitive list of staple or important food crops. However, in addition to their importance for food security, this selection also 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. Furthermore, a great deal of resources have already been invested in the conservation (mainly *ex situ*) and improvement of some of these crops—most notably rice, wheat and maize—while for others (e.g., cassava, sweet potato and plantain), there has been relatively little investment (FAO, 1997); therefore, useful comparisons can be made. Note that while sugar cane and soybean are identified as crops of major importance for food security in The *State of the World's Plant Genetic Resources for Food and Agriculture* (FAO, 1997), they are not included in Annex I of the ITPGRFA and have therefore been excluded from this study. 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.

This background study therefore provides information on the status and needs of a selection of crops of major importance for food security in one or more sub-regions of the world and/or locally important, as the baseline for the establishment of a network of *in situ* genetic reserves to conserve the wild relatives of these crops. Not all globally and locally important food crops have been included in this study—only a sample of the food crops of global importance for food security are included. The intention of this report is to provide preliminary recommendations for the *in situ* conservation of a selection of important food crops, but also to provide a platform for further research into these, and other important crop groups. Furthermore, the methodology presented in this report can be applied to other crop groups in the future.

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).

It has been argued that in the light of recent biotechnological advances, all wild species are potential gene donors to crops (Maxted *et al*., 1995). However, this kind of advanced breeding application remains relatively expensive and technically challenging and is currently mainly restricted to developed economies; therefore, the use of close CWR in inter-species gene transfer is likely to remain the global norm. However, we should point out that other distantly related taxa that have not yet been identified as potential gene donors for crop improvement may also 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 in conservation planning, 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—particularly in response to climate change. 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, ideally, all CWR, both closely and more distantly related and both rare and widespread, should eventually be actively conserved, both *in situ* and *ex situ*.

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 are actively conserved. In particular, selected populations of the primary and secondary wild relatives that are widespread and common should be actively conserved throughout their range, ensuring that populations representing the extremes of the range (both geographically and topographically) are conserved. Populations of these taxa that already occur within protected areas should also be monitored. In some cases, it may be possible to establish a reserve that conserves multiple CWR taxa, which, when possible, has obvious advantages. This possibility is explored in this study with regard to the target crops included and is also illustrated with a case study on the establishment of CWR genetic reserves in the United Kingdom (see Annex 3).

In this study, we have aimed to utilize the Gene Pool concept of Harlan and de Wet (1971), which formalizes Vavilov's earlier recognition that within each crop there is a potential pool of genetic diversity available for utilization and a gradation of that diversity dependent on the relative crossing ability between the crop itself and the primarily non-domesticated species in the primary, secondary or tertiary Gene Pool of the crop (Maxted *et al*., 2006).

The Gene Pool concept can be summarized, thus:

- GP1 – the primary Gene Pool, within which GP 1A contains the cultivated forms and GP 1B the wild or weedy forms of the crop;
- GP2 – the secondary Gene Pool, which includes the coenospecies (less closely related species) from which gene transfer to the crop is possible but difficult using conventional breeding techniques;
- GP3 – the tertiary Gene Pool, which includes the species from which gene transfer to the crop is impossible, or if possible requires sophisticated techniques such as embryo rescue, somatic fusion or genetic engineering.

Using the Gene Pool concept, those taxa that are in GP1 and GP2 should generally be afforded conservation priority over taxa in GP3, except in cases where a taxon in GP3 has shown promise as a gene donor and/or is very rare or highly threatened.

Although the Gene Pool concept provides a useful tool for conservation planning, relatively few crop gene pools are sufficiently well studied to apply the concept. For those crops for which insufficient information is available to apply the Gene Pool concept, Maxted *et al*. (2006) have proposed an alternative 'proxy' means of establishing the degree of relatedness between crops and their wild relatives by using the Taxon Group concept. This can be applied to define a crop wild relative's rank as follows:

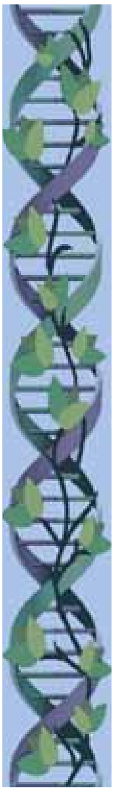
- TG 1a – crop
- TG 1b – same species as crop
- TG 2 – same series or section as crop
- TG 3 – same subgenus as crop
- TG 4 – same genus
- TG 5 – same tribe but different genus to crop

A partial constraint on the application of the Taxon Group concept is that taxonomists do not always provide a detailed infra-generic ranking for genera when they publish a classification. The solution to this is that where levels of the taxonomic hierarchy are absent, the next highest Taxon Group should be applied (Maxted *et al*., 2006). For example, if a crop is located in a genus where sections have not been defined but subgenera have, then the crop would be placed in TG1a, and other taxa within the same species (i.e., varieties or subspecies) as the crop would be placed in TG1b. It would not be possible to use TG2, but species found in the same subgenus would be members of TG3 and those in other subgenera in TG4. If no sections or subgenera are defined, all species in the same genus as the crop would be placed in TG4 and those in other related genera in TG5.

Application of the Taxon Group concept assumes that taxonomic distance is positively related to genetic distance. Although some authors have asserted that this relationship may not hold because of inconsistencies amongst taxonomists when describing species, Maxted *et al*. (2006) believe that the taxonomic hierarchy is likely to be an approximation of actual genetic distance and therefore, for practical purposes, classical taxonomy remains an extremely useful means of estimating genetic relationships.

In this study, where genetic information is available and taxa have been classified using the Gene Pool concept, 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 have restricted distributions. Therefore, for those crops where this information is not available, we have applied the Taxon Group concept, and where applicable afforded priority to those taxa within TG1b and TG2. For crop genera that have not been sub-classified 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. Readers should note that the primary, secondary and tertiary taxon groups delineated in this study do not equate to GP1, GP2 and GP3 unless a specific reference is given to a Gene Pool concept classification. Rather, the groups are indicative of the degree of relatedness of the taxon to the crop, according to the available information—the primary group being the most closely related, the secondary group is less closely related, and the tertiary group being distantly related taxa within the same genus as the crop. In cases where there are a large number of taxa in the tertiary wild relative group, we have not listed individual taxa, but noted the number of taxa in the group and provided a reference for further information. Tertiary wild relatives are also only included to species level.



Different taxonomic classifications have historically been applied to each of the crop complexes included in this study. In this study, we have used either the generally accepted classification or the most recent classification. However, it is important to note that these classifications may not be recognized by all taxonomists and conservation practitioners.

1.3 Selection of target sites

Like any other group of wild plant species, CWR are located both within and outside existing protected areas; however, the most efficient approach to establishing CWR genetic reserves is to set them up within existing protected areas when possible (Maxted *et al*., 2008). 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[16] 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. This can be achieved by contacting the protected area manager via the national organization with overall responsibility for protected area designation and management (usually a government department or government-designated organization). 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.

In some cases, the range of the target taxon will define the precise site or sites where active *in situ* conservation is needed (obviously, if a taxon is only known to occur at one location and is considered a high priority as a potential gene donor, then that single location must be targeted for genetic reserve establishment, whether the taxon occurs within an existing protected area or not). Where the geographic range of the target taxon is broader, sites should ideally be selected to represent the widest range of ecogeographic characteristics as possible. For example, if populations of the target taxon are known to occur both in lowland and mountainous areas, ideally, reserves should be established for selected populations in both habitats because the populations are likely to contain unique genetic adaptations to these different environments.

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, it is important to stress that even though a target taxon population may occur within the boundaries of a protected area, this does not automatically mean that the population is actively conserved. On the contrary, few protected areas are established to conserve specific target taxa, and those that have tend to focus on animal conservation. To conserve the range of genetic diversity inherent in CWR populations, active site management and monitoring is needed—many protected areas do not even have management plans, and those that do, are often limited by financial resources and lack of capacity to put the plan into practice.

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 (i.e., since the aim is to conserve the widest range of genetic diversity within and between CWR populations, it may be necessary to conserve populations that occur within different environmental envelopes; such as different elevations, different water regimes, or different soil types). Ideally, detailed ecogeographic surveys should be carried out for each of the target taxa in order to conserve the maximum genetic diversity. 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

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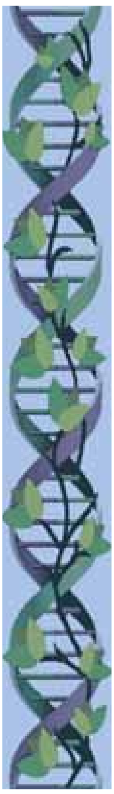
[16] For this background study, it has not been possible to obtain all available occurrence data for all the target taxa (i.e., by visiting herbaria and consulting the full range of Floras). However, we have consulted the primary references for each of the target taxa and also obtained occurrence data by using online information portals (such as the Global Biodiversity Information Facility (GBIF) and the USDA National Plant Germplasm System (NPGS)), as well as personal data based on our own research or data provided by colleagues. While the results of this analysis provide a good indication of the distribution of the target taxa, further detailed studies should be carried out to obtain the most detailed information possible before taking steps for the final recommendation and establishment of the CWR genetic reserve network.

possibility of linking protected areas to allow for this migration and 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. The end point of this background study is the identification of priority sites for CWR genetic reserve establishment, regardless of their socio-political feasibility for inclusion. Where possible, a range of alternative sites are recommended and ranked according to their suitability based on taxonomic and genetic considerations.

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.



1.4 Data collation and analysis

For this study, 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.unep-wcmc.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. An MS Access database was also created to organize the list of priority crops and taxa within each crop gene pool.

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

The crops are organized by alphabetical order according to crop genus, thus:

1. Finger millet (*Eleusine coracana*)
2. Barley (*Hordeum vulgare*)
3. Sweet potato (*Ipomoea batatas*)
4. Cassava (*Manihot esculenta*)
5. Banana/plantain (*Musa acuminata*)
6. Rice (*Oryza sativa*)
7. Pearl millet (*Pennisetum glaucum*)

8. Garden pea (*Pisum sativum*)
9. Potato (*Solanum tuberosum*)
10. Sorghum (*Sorghum bicolor*)
11. Wheat (*Triticum aestivum*)
12. Faba bean (*Vicia faba*)
13. Cowpea (*Vigna unguiculata*)
14. Maize (*Zea mays*)

2.1 Finger millet

Scientific name

Eleusine coracana (L.) Gaertn. (*Poaceae*)

Principle synonyms

E. africana K.-O'Byrne, E. indica (L.) Gaertn. subsp. africana (K.-O'Byrne) S.M. Phillips

Global, regional and local importance

Finger millet is a cereal crop cultivated for food and for making beer (Phillips, 1974), as well as fodder and medicinal uses (Bisht and Mukai, 2002; Oduori, 2005). It is a hardy crop that can be grown in very diverse environments, has an excellent food value and is easily stored for long periods. It is the most important minor millet in the tropics and, grown in more than 25 countries in Africa and Asia, accounts for 12% of the global millet area (ICRISAT, 2008). It is a potential and nutritious crop for the increasing world population, particularly in arid and semi-arid regions where it is usually ranked third in cereal production, after sorghum and pearl millet (Bisht and Mukai, 2002). Major producers are Uganda, India, Nepal, and China (ICRISAT, 2008).

Finger millet is an important staple crop in many parts of Africa (AGPC, 2008), where it competes with maize for the best agricultural land in regions with between 900 and 1200mm of annual rainfall (de Wet, 1995a). It is the most important small millet grown in eastern and southern Africa (Oduori, 2005) and is a major cereal in the Lake Victoria region, particularly in western Uganda (de Wet, 1995a). Finger millet serves as a subsistence and food security crop that is especially important for its nutritive and cultural value (Oduori, 2005). The crop is also grown in India, where it is a favoured cereal because of its high yield and resistance to pests and diseases (de Wet, 1995a).

As well as its importance as a staple crop, finger millet and its wild relatives can also serve as a gene pool for various important characters and disease resistant genes for the improvement of more widely grown cereals (Bisht and Mukai, 2002; Rasmussen, 2006). The close wild relative, *E. coracana* subsp. africana (syn. *E. africana*) is harvested as a wild cereal during times of scarcity (de Wet, 1995a), while *E. floccifolia* (Forssk.) Spreng. is locally important in Ethiopia, where it is widely used for making baskets and other household craft items (Phillips, 1995).

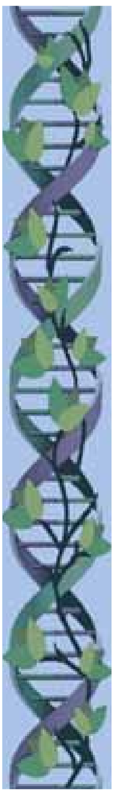
Taxonomic classification

The genus *Eleusine* Gaertn. (*Poaceae*, subfamily *Chloridoideae*) is composed of nine annual and perennial species, with eight African species recognized by Phillips (1972) and one New World species (*E. tristachya* (Lam.) Lam.) native to Argentina and Uruguay (Lovisolo and Galat, 2007). The range of the genus has been extended by widespread introduction of the crop (*E. coracana*) throughout the tropics, and the common weed often associated with cultivation, *E. indica* (L.) Gaertn. (the two species commonly introgress when grown together; Phillips, 1974). There is no formal recent classification of the genus, but in a recent study of nuclear ITS and plastid trnT–trnF sequences, Neves *et al*. (2005) confirmed the close relationship of *E. coracana* and *E. indica*, and of these taxa to *E. kigeziensis*, and further note that all three species show considerable morphological similarities.

Wild relatives

The taxonomy of the genus *Eleusine* has been the subject of considerable debate. The Gene Pool concept has not been applied to *Eleusine* and it is difficult to apply the Taxon Group concept since it is a small genus of nine species which has not been subdivided into sections or series. Assumptions regarding the primary, secondary and tertiary wild relatives have therefore been made on the basis of a review of the available literature.

In a study of genome origins and genetic diversity in *Eleusine*, Salimath (1995) found that the three species, *E. coracana, E. indica* and *E. tristachya* (Lam.) Lam. form a close genetic assemblage. More recently, Bisht and Mukai (2002) found that *E. coracana, E. africana, E. indica, E. tristachya, E. floccifolia* and *E. intermedia* (Chiov.) S.M. Phillips are closely related and



there spread introgression between them. However, Salimath (1995) found *E. floccifolia* (along with *E. compressa* Forssk.) to be the most distinct among the species examined, while Neves *et al*. (2005) contradicts Bisht and Mukai's (2002) assertion that *E. floccifolia* is the second genome donor (along with *E. indica*) to *E. coracana*, which raises a question over the position of this taxon in the gene pool.

Based on the most recent study of the infrageneric relationships in *Eleusine* (see Neves *et al*., 2005), we have classified *E. africana, E. indica,* and *E. kigeziensis* S.M. Phillips as the primary wild relatives of *E. coracana* (which together form the phylogenetic 'CAIK' clade) and *E. tristachya* secondary wild relative status on the basis that it is sister to the 'CAIK' clade (together forming the 'CAIKT' clade). We should point out, however, that Neves *et al*. (2005) mention that attempts to produce artificial hybrids between *E. indica* and *E. coracana* have resulted in sterile plants, which suggests that this taxon may be better placed in the secondary wild relative group. The authors note that E. indica seems to be genetically isolated from the tetraploid taxa (which includes *E. coracana* and *E. africana*), but that *E. indica* and *E. africana* derive from a common ancestor. However, earlier studies by Bisht and Mukai (2002) found free genetic flow between *E. indica* and *E. africana* (and other taxa – see above); therefore, further crossing experiments are needed to confirm the status of this taxon. Note that Neves *et al*. (2005) support the view of some other authors that *E. africana* should only be afforded subspecific rank (i.e., *E. coracana* subsp. *africana*); however, we have maintained specific status for this taxon in this study because there is currently no consensus.

Neves *et al*. (2005) suggest that *E. floccifolia* and *E. intermedia* are closely related and sister to the 'CAIKT' clade, but that further analysis is required to confirm this. Since earlier studies showed these two species to be closely related to the primary wild relatives, we have included them in the secondary wild relative group, along with *E. tristachya*. Neves *et al*. (2005) note that *E. multiflora* Hochst. ex A. Rich is distantly related to the 'CAIK' clade; therefore, *E. multiflora* has been classified in this study as a tertiary wild relative, along with *Octhochloa compressa* (Forssk.) Hilu, previously classified as *E. compressa* (Bisht and Mukai, 2002). The position of *E. multiflora* is supported by Phillips (1972) who concluded that the taxon is totally different from the rest of the diploid species of *Eleusine* and shares some similarities with the genus *Acrachne*.

The genetic relationship of *E. jaegeri* Pilger with *E. coracana* is not clear. Bisht and Mukai (2001) found that the genomic DNA of *E. jaegeri* (and *E. multiflora*) did not show any hybridization signals with the chromosomes of *E. coracana*, while Neves *et al*. (2005) found that E. jaegeri (along with *E. multiflora*) form the earliest diverging lineage in the genus. Bisht and Mukai (2002) also designated E. jaegeri as having a different genome to the primary and secondary wild relatives (as classified in this study). On this basis, we have also afforded *E. jaegeri* with tertiary wild relative status. However, further genetic studies are needed to confirm these assumptions.

Primary wild relatives

- *Eleusine africana* K.-O'Byrne
- *E. indica* (L.) Gaertn.
- *E. kigeziensis* S.M. Phillips

Secondary wild relatives

- *E. tristachya* (Lam.) Lam.
- *E. floccifolia* (Forssk.) Spreng.
- *E. intermedia* (Chiov.) S.M. Phillips

Tertiary wild relatives

- *E. jaegeri* Pilger
- *E. multiflora* Hochst. ex A. Rich
- *Octhochloa compressa* (Forssk.) Hilu (syn. *E. compressa* Forssk.)

Distribution and centre of diversity

The species of *Eleusine* are distributed in the tropical and subtropical parts of Africa, Asia and South America (Phillips, 1972). In Africa, most species have a restricted distribution (Neves *et al*., 2005). East Africa is considered the centre of diversity of the genus and eight species (*E. africana, E. coracana, E. kigeziensis, E. indica, E. floccifolia, E. intermedia, E. multiflora* and *E. jaegeri*) occur in this region (Mehra, 1963; Phillips, 1972). *E. coracana* is present in archaeological records of early African agriculture in Ethiopia that date back 5 000 years, and it probably originated somewhere in the area that today is Uganda (National Research Council, 1996). De Wet (1995a) believes that finger millet was domesticated in an area extending from western Uganda to the Ethiopian highlands where *E. coracana* subsp. *africana* (syn. *E. africana*) is particularly abundant.

Known uses of wild relatives in crop improvement

All references found regarding breeding for improvement in finger millet have focused on genetic characterization and use of *E. coracana* cultivars and landraces—we have found no specific records of uses of *E. coracana* wild relatives for crop improvement. However, despite its recognized value as an important staple crop, particularly for many poor people in arid and semi-arid areas, finger millet has been neglected in mainstream crop improvement research (Upadhyaya *et al*., 2006). Much of the research in finger millet has focused on resistance to blast disease (*Pyricularia grisea* Sacc.).

One of the most notable recent research projects aiming to develop high yielding, disease resistant and drought tolerant genotypes was led by the University of Agricultural Sciences (UASB), GKVK, Bangalore, India (see http://mcknight.ccrp.cornell.edu/projects/INTL_fingermillet/ fingermillet_project.html); however, only cultivated varieties were reported to have been used. A current project, 'genetic improvement of chloridoid cereals', led by the Ethiopian Agricultural Research Organization (EARO) (see http://mcknight.ccrp.cornell.edu/projects/INTL_tef/ tef_project.html) also does not report the use of wild relatives in finger millet improvement. Nonetheless, this does not negate the need to conserve finger millet wild relatives, which may be important for future breeding research, particularly in the light of climate change and the associated need for germplasm suited to extreme environmental conditions.

Priority taxa

High priority taxa

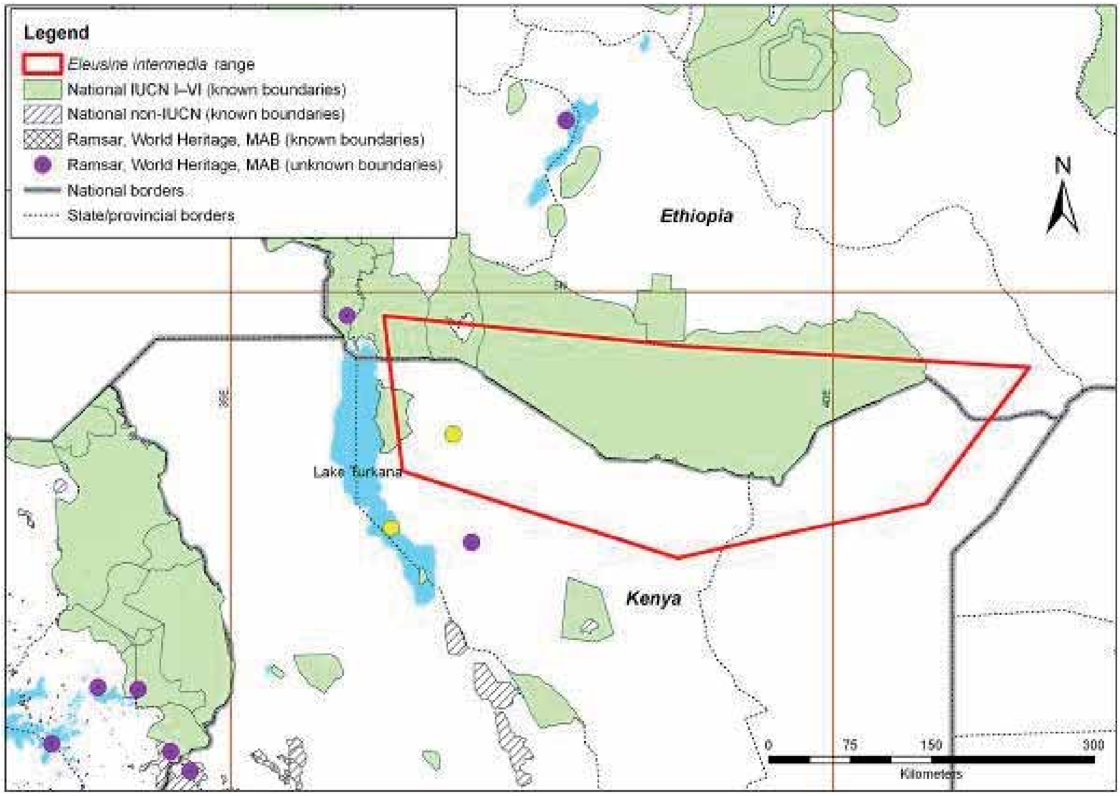
- *E. intermedia*, which is confined to the uplands of northern Kenya and adjacent parts of southern Ethiopia (Bisht and Mukai, 2002).
- *E. kigeziensis*, which was reported by Phillips (1972) to be localized in mountainous regions extending from Kigezi Province, Uganda and adjacent parts of the Congo and Rwanda southwards into Burundi. However, Phillips later reported the taxon to occur in Kivu Province (Democratic Republic of Congo, formerly Zaire), Rwanda and Burundi only (Phillips, 1974). Bisht and Mukai (2002) themselves report the taxon as only occurring in Burundi; however, it is not clear where they obtained this information. The International Livestock Research Institute (ILRI) has three collection records of the taxon: one from Burundi and two from the Democratic Republic of Congo (data accessed via GBIF).

Other priority taxa

- *E. africana*
- *E. floccifolia* (Forssk.) Spreng.
- *E. indica*
- *E. tristachya* (Lam.) Lam.

FIGURE 1

Distribution of *Eleusine intermedia*. The taxon is confined to the uplands of northern Kenya and adjacent parts of southern Ethiopia (Bisht and Mukai, 2002). The range of the taxon is indicated by the (red) polygon



Priority sites (high priority taxa)

Based on the *E. intermedia* data presented in Figure 1, within the area encompassing the most likely range of the taxon, the following protected areas occur:

Ethiopia

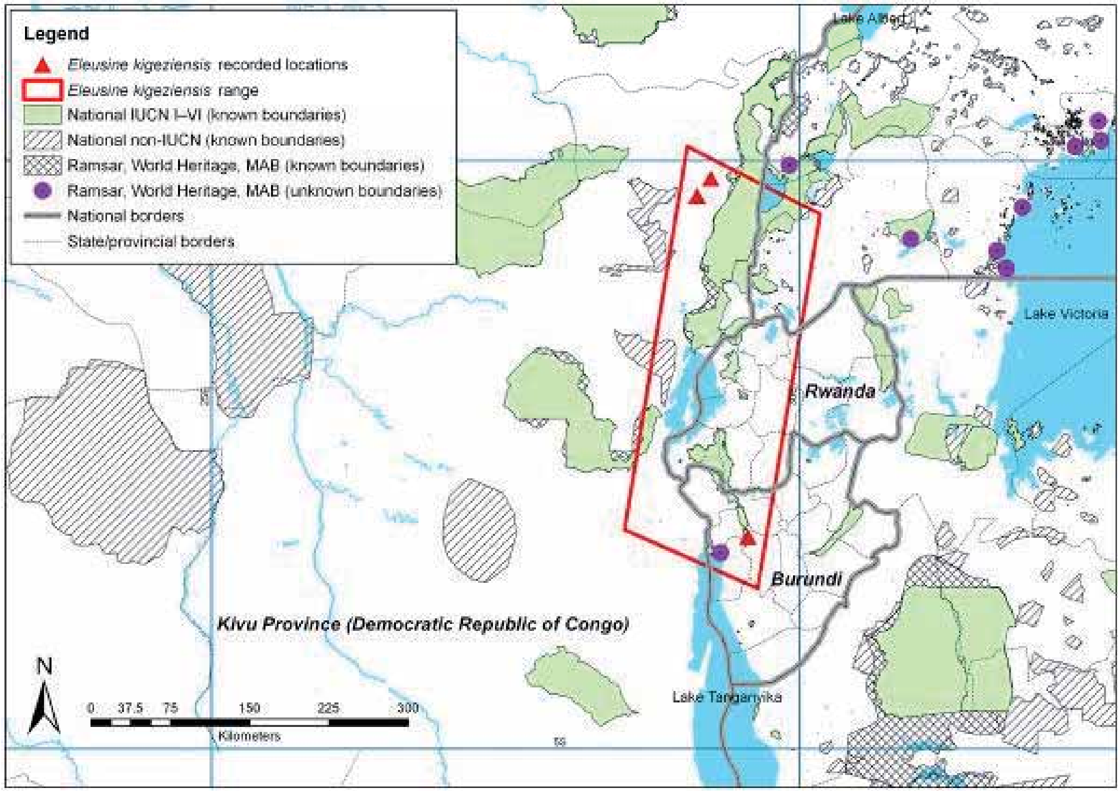
- Chelbi Wildlife Reserve (IUCN category IV)
- Borana Controlled Hunting Area (IUCN category VI)
- Murle Controlled Hunting Area (IUCN category VI)

Kenya

- Sibiloi National Park (IUCN Category II)
- Lake Turkana National Parks (World Heritage Natural (World Heritage Convention)

FIGURE 2

Distribution of *Eleusine kigeziensis*. Locations recorded by the System-wide Information Network for Genetic Resources (SINGER) (accessed through GBIF data portal, http://data.gbif.org/datasets/resource/1430 03/07/2008) are shown by the (red) triangles. The likely range of the taxon is indicated by the (red) polygon, which encompasses the mountainous area extending from Kigezi Province, Uganda, and adjacent parts of the Congo and Rwanda, southwards into Burundi. The map shows four protected area designations within the likely distribution range of the taxon (see legend)



Based on the *E. kigeziensis* data presented in Figure 2, it is likely that the three locations of *E. kigeziensis* recorded by SINGER are not protected. This GIS analysis indicates that one location is just outside the boundaries of the IUCN category IV protected area, Kibira National Park, Burundi. This requires verification. Within the area encompassing the most likely range of the taxon, the following protected areas occur:

Burundi

- Kibira National Park (IUCN category IV)
- Rusizi National Park (IUCN category IV)
- Democratic Republic of Congo:
- Virunga National Park (IUCN category II, World Heritage in Danger List (World Heritage Convention) and Ramsar)
- Rutshuru Hunting Reserve (IUCN Category VI)
- Sud Masisi/Quest Lac Kivu Forest Reserve

Rwanda

- Volcans National Park (IUCN category II, UNESCO–MAB Biosphere Reserve)
- Gishwati Forest Reserve (IUCN category IV)
- Mukura Forest Reserve (IUCN category IV)
- Nyungwe National Park (IUCN category IV)

Uganda

- Rwenzori Mountains National Park (IUCN Category II)
- Kigezi Game Reserve (IUCN category IV)
- North Maramagambo National Forest Reserve
- South Maramagambo National Forest Reserve

Recommendations

- The managers of the protected areas identified under 'priority sites' should be contacted to try to ascertain whether *E. kigeziensis* and *E. intermedia* are found within any of these predicted sites. Field visits may be necessary to verify presence or absence of the taxa. CWR genetic reserves should be established within the protected areas in which they are found.
- A detailed ecogeographic survey of *E. kigeziensis* and *E. intermedia* should be undertaken to verify location data and establish ecogeographic preferences. Once *in situ* locations have been verified, a full gap analysis (both *in situ* and *ex situ*) should be carried out. Based on a detailed *in situ* gap analysis, recommendations should be made for the establishment of CWR genetic reserves (within and/or outside existing protected areas).
- Apart from *E. kigeziensis* and *E. intermedia*, all other primary and secondary wild relatives occur as relatively widespread, weedy, naturalized populations, often in fields, roadsides and other disturbed ground. *E. tristachya* is the only species that is native outside Africa (native to South America). The current status of *E. africana, E indica, E. tristachya* and *E. floccifolia* therefore does not demand urgent conservation action. However, individual populations of these taxa could harbour important adaptive traits; therefore, selected populations should be actively conserved throughout their range, ensuring that populations representing the extremes of the range (both geographically and topographically) are conserved. The taxa should also be included in monitoring activities at national level throughout their range, both within and outside protected areas.
- Since the genetic relationships between *Eleusine* species are not certain and there is currently no evidence of wild species being trialled in breeding programs, populations of *E. jaegeri* and *E. multiflora* should also be earmarked for conservation action. *E. jaegeri* is reported by Bisht and Mukai (2002) as only occurring in Tanzania and by Phillips (1972) as restricted to a small area of the East African highlands. *E. multiflora* occurs in both Kenya and Tanzania (Bisht and Mukai, 2002). These taxa should be included in monitoring activities and their *in situ* and *ex situ* conservation status ascertained.

2.2 Barley

Scientific name

Hordeum vulgare L. (*Poaceae*)

Principle synonyms

H. hexastichum L., *H. polystichon* Haller f., *H. vulgare* subsp. *hexastichon* (L.) Husn.

Global, regional and local importance

Barley was one of the first domesticated cereal grains, originating in the Fertile Crescent over 10,000 years ago (IBSC, no date). Used for animal feed, brewing malts and human food, Ii is a short-season, early maturing grain with high yield potential and is often found on the fringes of agriculture growing in places where other crops are not adapted (Harlan, 1995). Major production areas are Europe, the Mediterranean fringe of North Africa, Ethiopia, the Near East, the former USSR, China, India, Canada and the USA; however, barley appears little in world trade statistics because it is mainly consumed locally (Harlan, 1995). Despite this, barley ranks fourth among the cereals in worldwide production, and in addition to its geographic adaptability, barley is particularly noted for its tolerance to cold, drought, alkalinity and salinity (IBSC, no date).

Barley is the fourth most important cereal after wheat, rice and maize, with an estimated world production of approximately 138.6 million tonnes planted on approximately 55 million ha in 2006 (FAO, 2008). The six countries with highest barley production are the Russian Federation (18.1MT), Germany (12.0 MT), Ukraine (11.3MT), France (10.4MT), Canada (10.0MT) and Turkey (9.6MT). Figure 3 indicates a slight increase in global production and a decline in the area cultivated over the last 40 years, while over the same time period yields have increased from 1694.46 kg/Ha in 1967 to 2497.30 kg/Ha in 2006 (FAO, 2008).

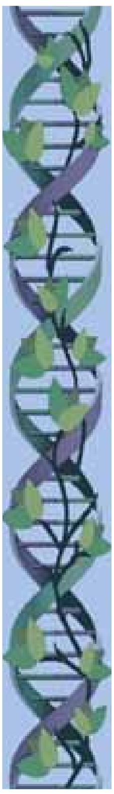
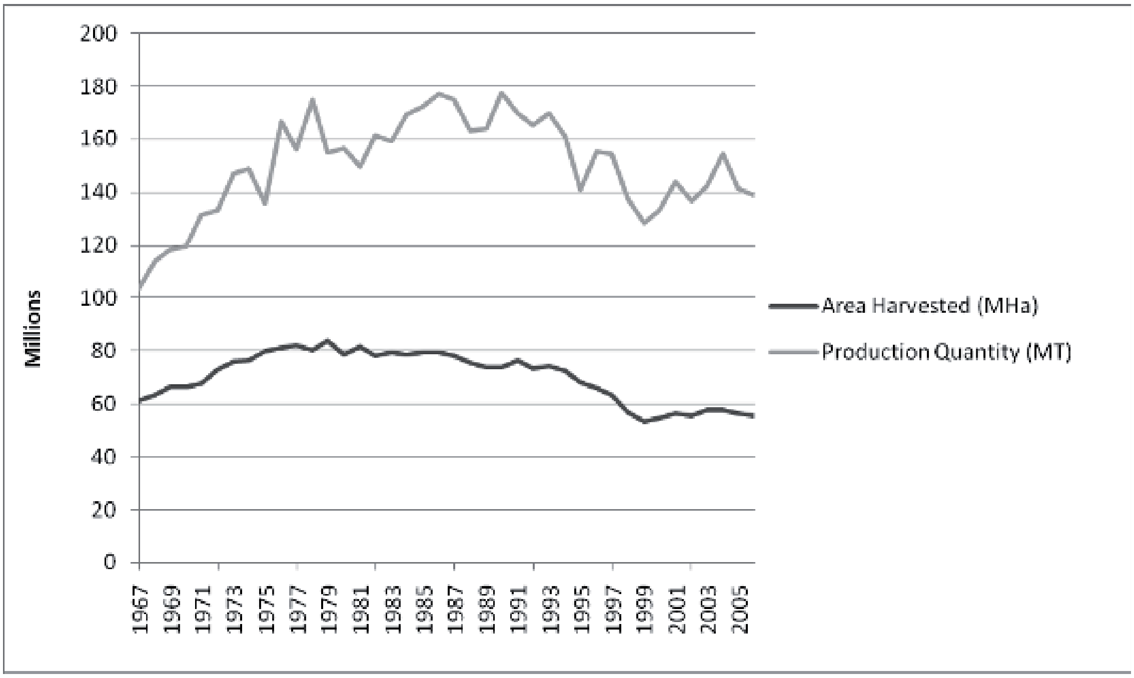


FIGURE 3

World area harvested and production quantity for barley (FAO, 2008)



Taxonomic classification

The genus *Hordeum* contains 16 species and 11 subspecies (USDA, 2008), though von Bothmer *et al*. (1995) note that the sub-generic delimitation of *Hordeum* is the subject of much debate. Cultivated barley *H. vulgare* and its closest wild relative *H. spontaneum* were originally placed in a single section—either *Hordeum* sect. *Crithe* Doell or sect. Cerealia Ands.—with the other annual species being separated into sect. *Hordeastrum* Doell). However, Nevski (1941) treated the perennial species in more detail and placed the long-awned, perennial, American species in sect. *Critesion* (Raf.) Nevski, the short-awned perennial South American species in sect. *Anisolepis* Nevski, the European, Asiatic and North American perennial species in sect. *Stenostachys* Nevski, and *H. bulbosum* in the monospecific sect. *Bulbohordeum* Nevski. Subsequently, based on a morphological study, von Bothmer and Jacobsen (1985) recognized four sections: *Hordeum, Anisolepis, Stenostachys* and *Critesion*. Although von Bothmer *et al*. (1995) recognize that adjustments are required due to novel cytogenetic, biochemical and molecular data becoming available, the von Bothmer and Jacobsen (1985) classification remains the standard for the genus.

Wild relatives[17]

Primary wild relatives

- *Hordeum vulgare* subsp. *spontaneum* (C. Koch.) Thell. (syn. *H. spontaneum* K. Koch)

Secondary wild relatives

- *H. bulbosum* L.

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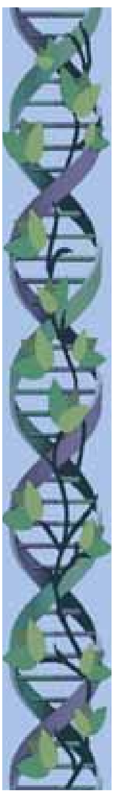
[17] von Bothmer et al. (1995)

Tertiary wild relatives

- *H. murinum* L.
- *H. intercedens* Nevski
- *H. flexuosum* Steudal
- *H. chilense* Roemer & Schultes
- *H. stenostachys* Godron
- *H. halophilum* Grisebach
- *H. jubatum* L.
- *H. procerum* Nevski
- *H. marinum* Hudson
- *H. capense* Thunberg
- *H. roshevitzii* Bowden
- *H. brachyantherum* Nevski
- *H. guatemalense* Bothmer, Jacobsen & Jørgensen
- *H. tetraploidum* Covas
- *H. parodii* Covas
- *H. pusillum* Nuttal
- *H. euclaston* Steudal
- *H. muticum* Presl
- *H. cordobense* Bothmer, Jacobsen & Nicora
- *H. pubiflorum* Hooker f.
- *H. comosum* Presl
- *H. arizonicum* Covas
- *H. lechleri* (Steudal) Schenck
- *H. secalinum* Schreber
- *H. bogdanii* Wilensky
- *H. brevisubulatum* (Trinius) Link
- *H. depressum* (Scribner & Smith) Rydberg
- *H. erectifolium* Bothmer, Jacobsen & Jørgensen
- *H. fuegianum* Bothmer, Jacobsen & Jørgensen
- *H. patagonicum* (Haumann) Covas



Distribution and centre of diversity

Hordeum is widely distributed in temperate areas in the northern and southern hemispheres, reaching subtropical areas in central South America and arctic areas in North America and Central Asia (von Bothmer *et al*., 1995). Barley was domesticated from wild species found today in South-western Asia (Harlan, 1995) but there are three other centres of diversity of *Hordeum*: Central Asia, western North America and southern South America (von Bothmer *et al*., 1995).

Known uses of wild relatives in crop improvement

H. vulgare subsp. *spontaneum* (syn. *H. spontaneum*) contains several traits of interest for transfer to cultivated barley, particularly disease resistant genes (Fischbeck *et al*., 1976; Moseman *et al*., 1983; Lehmann and von Bothmer, 1988) and has been used as a source of resistance to *Erysiphe graminis*, the cause of powdery mildew (Prescott-Allen and Prescott-Allen, 1988). Eglinton *et al*. (2001) proposed that *H. vulgare* subsp. *spontaneum* may be a source of useful genes related to adaptation and stress responses due to its broad adaptation in the wild and relationship between genetic diversity and ecogeographic parameters. Mano and Takeda (1998) found that most wild *Hordeum* species are good sources of germplasm for salt tolerance breeding. Several characters in *H. bulbosum* are of interest for transfer to cultivated barley, including resistance to powdery mildew (Jones and Pickering, 1978; Szigat and Pohler, 1982; Gustafsson and Claësson, 1988; Xu and Snape, 1988).

H. chilense also has a number of characteristics of interest for breeding, and also has potential for use in wheat and triticale improvement (Martín and Cabrera, 2005). Of particular interest is that *H. chilense* has been found to have high resistance to barley leaf rust, *Puccinia hordei* Otth (Patto *et al*., 2001). Kindler and Springer (1991) evaluated several wild *Hordeum* species for resistance to Russian wheat aphid, *Diuraphis noxia*, a serious pest of barley. They found the highest levels of resistance in *H. bulbosum* and *H. brevisubulatum* (Trin.) Link subsp. *violaceum* Boiss. & Hohen and suggested that broadening the genetic base of barley by introducing resistant alien genes may provide additional protection from new virulent strains or biotypes of the pest. However, the use of wild species in barley breeding has not been as successful as for other grain crops, such as wheat (von Bothmer *et al*., 1995) and the potential for exploiting wild barley as a source of novel genes for crop improvement remains untapped (Eglinton *et al*., 2001).

Priority taxa

High priority taxa

- *H. chilense*: although classified in GP3, *H. chilense* has a number of characteristics of interest for breeding, and has potential for use in wheat and triticale improvement (Martín and Cabrera, 2005). Of particular interest is that *H. chilense* has been found to have high resistance to barley leaf rust, *Puccinia hordei* Otth (Patto *et al*., 2001). The species is distributed in central Chile and the westernmost parts of the provinces of Neuquen and Rio Negro, Argentina (von Bothmer *et al*., 1995). Although it is recorded by von Bothmer *et al*. (1995) as "rather common within the distribution area", its overall distribution is narrow relative to many other taxa in the genus. Furthermore, it is thought that there are three distinct ecotypes of the species that exhibit differing levels of avoidance to rust fungi (Patto *et al*., 2001). Based on morphological and molecular (AFLP) variation within the species, the authors believe *H. chilense* warrants classification into three subspecies corresponding to the distinct ecotypes—they found that one of these has a high level of avoidance of infection with barley leaf rust. The level of avoidance has not been shown to be associated with geographic location or altitude, but is associated with populations that grow in humid habitats.

Other priority taxa

- *H. bulbosum*
- *H. vulgare* subsp. *spontaneum*

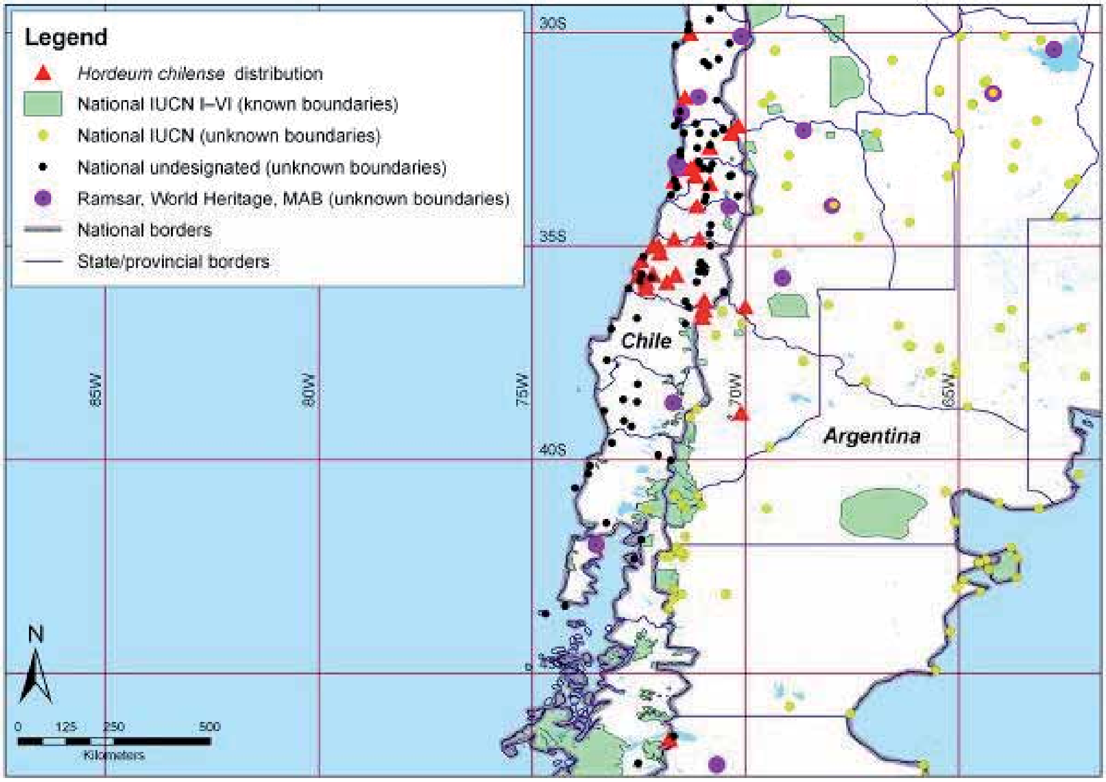
Priority sites (high priority taxa)

Data analysis indicates that few, if any of the recorded populations of *H. chilense* fall within existing protected areas (Figure 4); however, proximity indicates that the following sites may contain populations of the taxon:

- Ciudad de Coquimbo, Coquimbo, Chile (national undesignated – unknown boundaries)
- Cerro Tabasco, Valparaiso, Chile (national undesignated – unknown boundaries)
- Quebrada de Córdoba, Valparaiso, Chile (national undesignated – unknown boundaries)
- Peñaflor, Region Metropolitana, Chile (national undesignated – unknown boundaries)
- Roblería del Cobre de Loncha National Reserve, Region Metropolitana, Chile (IUCN category IV)
- El Junquillar, Maule, Chile (national undesignated – unknown boundaries)
- La Estrella, Maule, Chile (national undesignated – unknown boundaries)
- Río Reloca, Maule, Chile (national undesignated – unknown boundaries)
- Lago Jeinimeni National Reserve, Aisen del General Carlos Ibanez del Campo, Chile (IUCN category IV)

FIGURE 4

Distribution of *Hordeum chilense*. Locations recorded by EURISCO and the Nordic Gene Bank (accessed through GBIF data portal, http://data.gbif.org/datasets/resource/1396 25/10/2007) are shown by the (red) triangles



Recommendations

- Populations of all three ecotypes of *H. chilense* recognized by Patto *et al*. (2001) require active *in situ* conservation with adequate *ex situ* back-up. Based on the data presented in Figure 4, it is likely that few, if any of the known locations of *H. chilense* are within the boundaries of existing protected areas. This requires verification, but it is likely that new protected areas will need to be established. Establishment of genetic reserves for this taxon should take into account populations that grow in both humid and dry habitats to ensure that all three ecotypes are conserved. Additional efforts should be made to ensure that the ecotype that is most resistant to barley leaf rust is adequately conserved *ex situ*.
- An investigation should be conducted to establish how many accessions of the three ecotypes identified by Patto *et al*. (2001) are collected and stored independently of each other in *ex situ* collections. The passport data associated with these accessions should be scrutinized to establish whether it is of sufficient quality to assist in conservation and characterization of the taxon. Further collections may be required.
- The primary and secondary wild relatives, *H. vulgare* subsp. *spontaneum* and *H. bulbosum* are both widespread and locally common species (von Bothmer *et al*., 1995). Their current status therefore does not demand urgent conservation action. However, individual populations of these taxa could harbour important adaptive traits; therefore, selected populations should be actively conserved throughout their range, ensuring that populations representing the extremes of the range (both geographically and topographically) are conserved. The taxa should also be included in monitoring activities at national level throughout their range, both within and outside protected areas.
- Although we have not found any record of the following tertiary wild relatives being of potential use in crop breeding, they have narrow geographical distributions and their populations should therefore be monitored *in situ* and a review of their *ex situ* conservation status undertaken:
- *H. cordobense*: limited to central and northern Argentina, where it is recorded by von Bothmer *et al*. (1995) as "scattered within the distribution area".
- *H. arizonica*: has a restricted distribution in southern Arizona, with a few known locations in the southeastern part of California and northern Mexico (von Bothmer *et al*., 1995). The authors believe the taxon may be threatened with extinction because its habitats are being destroyed or converted.
- *H. procerum*: recorded by von Bothmer *et al*. (1995) as "not common in central Argentina; but it sometimes occurs in large stands".
- *H. erectifolium*: known only from a single location in the western part of Buenos Aires, Argentina (von Bothmer *et al*., 1995).
- *H. guatemalense*: known only from a few locations in the mountainous region of Cuchumatanes in northern Guatemala (von Bothmer *et al*., 1995). Although the authors report that the taxon may not be rare in the area, they also note that heavy sheep grazing could be a threat to populations and further investigation into its status is required.
- *H. capense*: recorded as occurring in South Africa and Lesotho, mainly in highland areas. While von Bothmer *et al*. (1995) believe the taxon to be rather common within its distribution area, they point out that no field study has been undertaken to support this assumption.
- The detailed study by von Bothmer *et al*. (1995) was published more than ten years ago; therefore, the distributions of the taxa recorded by the authors as having the narrowest ranges require re-checking.

2.3 Sweet potato

Scientific name

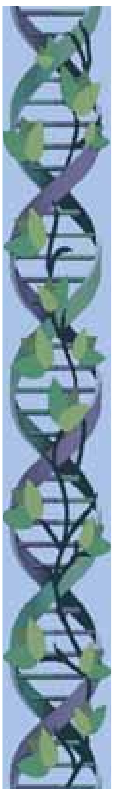
Ipomoea batatas (L.) Lamarck (Convolvulaceae)

Principle synonym

Convolvulus batatas L.

Global, regional and local importance

Sweet potato is the world's seventh largest food crop in terms of production (Bohac and Dukes, 1995). As well as being used for human consumption, it is an important industrial crop for production of starch and ethanol fuels, while the roots and vines are used for animal feed (Bohac and Dukes, 1995). It can grow in high temperatures and with low input of water and fertilizer and is thus a staple crop in the tropics (Bohac and Dukes, 1995). Sweet potato is grown in more

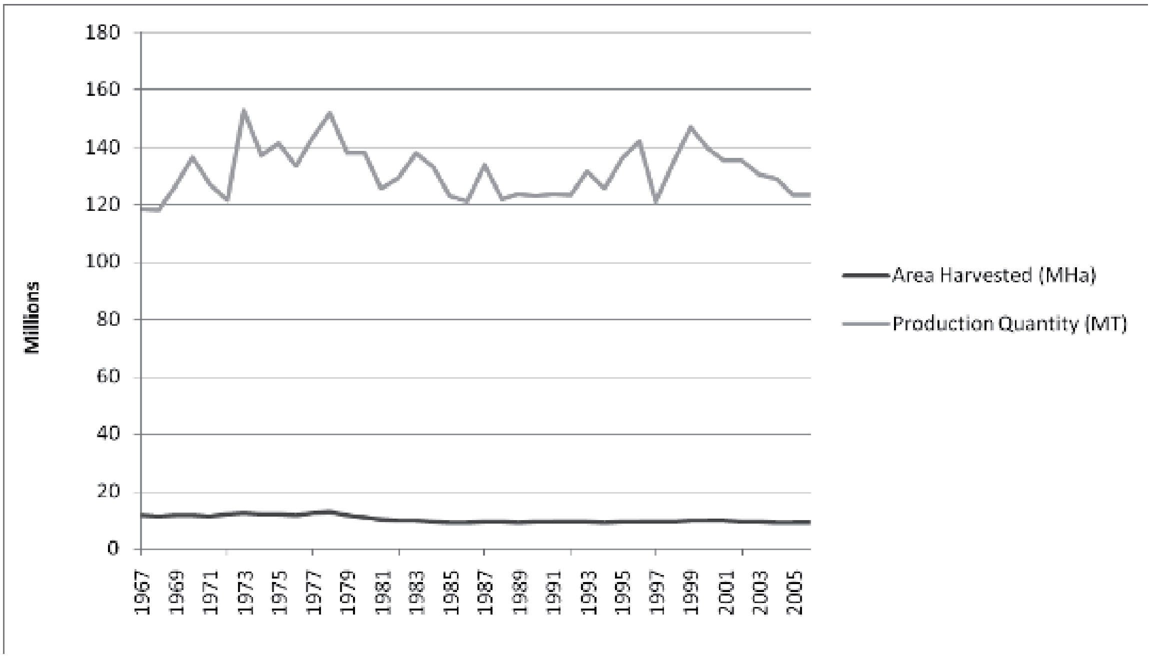


than 100 tropical countries, although China accounts for 90% of worldwide production (CIP, no date). In Asia, nearly half of the crop produced is used for animal feed, while in Africa, where production is much lower, the crop is used primarily for human consumption (CIP, no date).

Sweet potato had an estimated world production of approximately 123.5 million tonnes planted on approximately 9 million ha in 2006 (FAO, 2008). The six countries with highest sweet potato production are China (100.2MT), Nigeria (3.5MT), Uganda (2.6MT), Indonesia (1.9MT), Viet Nam (1.5MT) and Tanzania (1.1MT). Figure 5 shows a slight increase in global production and a slight decline in the area cultivated over the last 40 years, while over the same time period yields have increased from 10 332.08 kg/Ha in 1967 to 13 728.69 kg/Ha in 2006 (FAO, 2008).

FIGURE 5

World area harvested and production quantity for sweet potato (FAO, 2008)



Taxonomic classification

Ipomoea is a large genus thought to contain 600–700 species (Austin, 1997). The taxonomic relationships between sweet potato and its wild relatives have not yet been fully elucidated (Hu *et al*., 2003). However, the genus has historically been subdivided into three subgenera (*Ipomoea* L., *Eriospermum* (Hallier f.) Verdcourt ex Austin and *Quamoclit* (Moench) Clarke)[18] and nine sections, with *I. batatas* and close allies placed in subgenus *Eriospermum*, section *Eriospermum* Hallier f., series *Batatas* (Choisy) D. F. Austin (Austin, 1997). According to Austin (1997), the following 14 American taxa occur in series *Batatas* (in addition to I. batatas): *I. batatas* var. *apiculata* (Martens & Galeotti) McDonald & Austin; *I. cordatotriloba* Dennstedt; *I. cynanchifolia* Meisner; *I. grandifolia* (Dammer) O'Donell; *I. lacunosa* L.; I. *leucantha* Jacquin; *I. littoralis* Blume; *I. ramosissima* (Poiret) Choisy; *I. tabascana* McDonald & Austin; *I. tenuissima* Choisy; *I. tiliacea* (Willdenow) Choisy in D.C.; *I. trifida* (H.B.K.) G. Don.; *I. triloba* L.; *I. umbraticola* House.

Wild relatives

Jarret and Austin (1994) concluded that *I. batatas* var. *apiculata*, *I. trifida* (generally thought to be the progenitor of sweet potato) and *I. tabascana* were the species most closely related to *I. batatas*. This is supported by a phylogenetic study of series *Batatas* in which *I. batatas*, *I. trifida* and *I. tabascana* were found to form a monophyletic group (Rajapakse *et al*., 2004). We have therefore included *I. batatas* var. *apiculata, I. trifida* and *I. tabascana* in the primary wild relative group.

Bohac and Dukes (1995) report that *I. triloba*, along with *I. trifida*, is thought to be the closest extant relative of sweet potato, but they do not provide references to support this hypothesis. Furthermore, Jarret and Austin (1994) concluded

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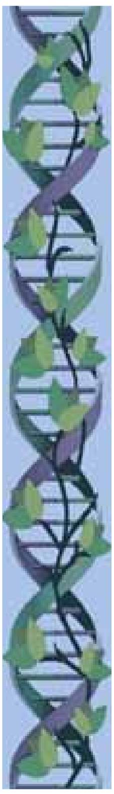
[18] Later, Miller et al. (1999) proposed that the genus should be divided further, into four subgenera.

that phenetic analysis clearly delineates *I. triloba* (along with four other species included in the study: *I. grandiflora, I. lacunosa, I. cordatotriloba* and *I. tenuissima*) from the primary wild relative group (as defined in the current study). This is supported by Rajapakse *et al*. (2004), who showed *I. triloba* to be grouped with taxa possessing the A genome, while *I. batatas, I. trifida, I. tabascana* (and *I. littoralis*) are shown to be more closely related and all possessing the B genome. Therefore, all taxa in series *Batatas* (other than the three designated as primary wild relatives) belong in Taxon Group 2 and we have thus classified them as secondary wild relatives. All remaining taxa in the genus belong in the tertiary group.



Primary wild relatives

- *Ipomoea batatas* var. *apiculata* (Martens & Galeotti) McDonald & Austin
- *I. trifida* (H.B.K.) G.Don.
- *I. tabascana* McDonald & Austin

Secondary wild relatives

- *I. triloba* L.
- *I. cynanchifolia* Meisner
- *I. littoralis* Blume
- *I. tenuissima* Choisy
- *I. grandiflora* (Dammer) O'Donell
- *I. umbraticola* House
- *I. cordatotriloba* Dennstedt
- *I. lacunosa* L.
- *I. ramosissima* (Poiret) Choisy
- *I. tiliacea* (Willdenow) Choisy in D.C.
- *I. leucantha* Jacquin

Tertiary wild relatives

The closest tertiary wild relatives are those taxa within the remaining series of section Eriospermum, which are defined by Austin (1997) as follows:

- *Eriospermum* (Hallier f.) D. F. Austin (64 taxa)
- *Anisomeres* (House) D. F. Austin (3 species)
- *Arborescentes* (Choisy) D. F. Austin (12 taxa)
- *Bombycospermum* (Presl) D. F. Austin (1 species)
- *Jalapae* (House) D. F. Austin (35 species)
- *Mirandinae* D. F. Austin (7 species)
- *Setosae* (House) D. F. Austin (7 species)
- ser. ? (59 species)

Distribution and centre of diversity

Sweet potato originated in north-western South America, which is the major centre of diversity of the crop (Collins, 1995). However, other centres of diversity exist in sub-Saharan Africa (Collins, 1995), Papua New Guinea and Indonesia (Jarret and Austin, 1994; Collins, 1995). The majority of *Ipomoea* species are native to the Americas (Austin, 1997).

Known uses of wild relatives in crop improvement

Bohac and Dukes (1995) note that the germplasm used in sweet potato breeding programs represents only a fraction of the genetic diversity available in the wild and that there is a need to increase the genetic diversity in the crop to meet future needs. However, according to Collins (1995), introgression of traits from related species is usually prevented by crossing barriers. The author reports that there has been some success through the use of "massive" numbers of crosses and embryo culture. However, even though some traits of interest have been identified in related species, introducing genes using this method is generally not viable in breeding programs (Collins, 1995). Recent and ongoing sweet potato improvement research programs under the Collaborative Crop Research Program (CCRP) of the McKnight Foundation do not report the use of wild relatives (see http://mcknight.ccrp.cornell.edu/projects/INTL_spbreeding/sweetpotato_breeding_project.html and http://mcknight.ccrp.cornell.edu/projects/INTL_spdiversity/sweetpotato_diversity_project.html). Nonetheless, Komaki (2001) concluded that wild *Ipomoea* species are an important reservoir of useful genes for crop improvement.

Priority taxa

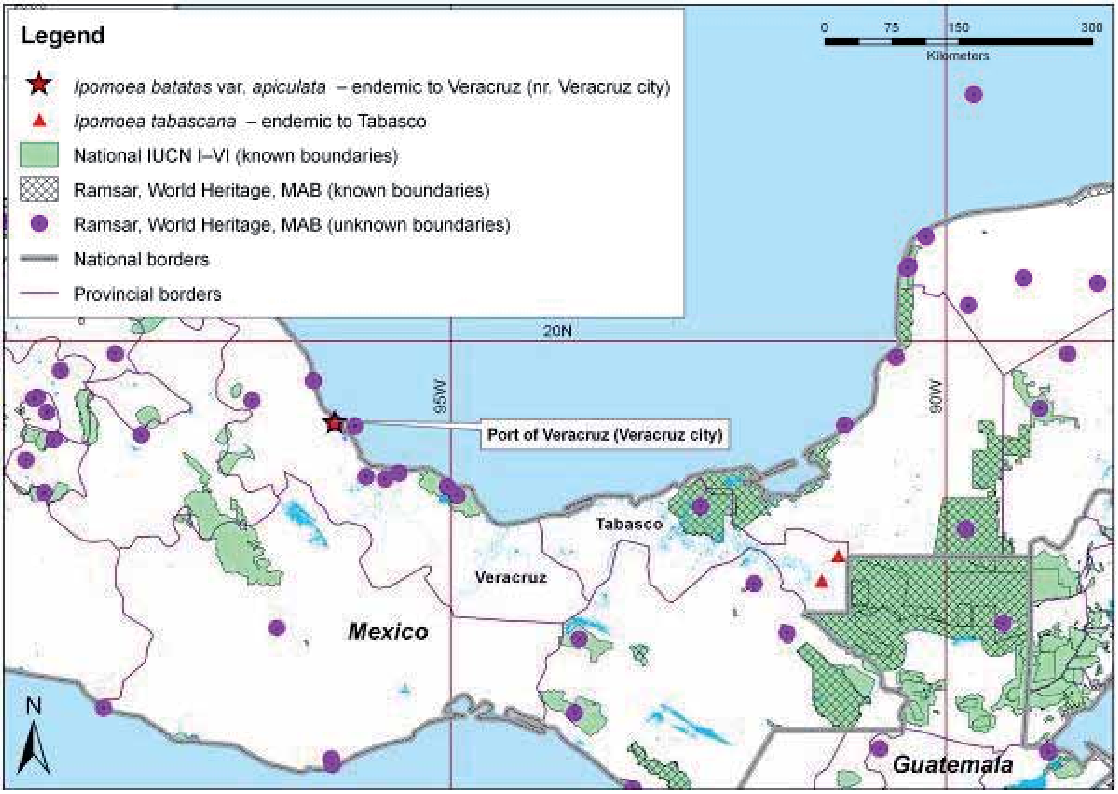
- *I. batatas* var. *apiculata*: endemic to Veracruz, Mexico (MacDonald and Austin, 1990). MacDonald and Austin only found this ecotype near the Port of Veracruz, where it is a littoral plant growing in dunes.
- *I. tabascana*: endemic to Tabasco, Mexico, where it is endangered (Austin *et al*., 1991).

Priority sites (priority taxa)

Based on the data presented in Figure 6, it is possible that *I. batatas* var. *apiculata* occurs within the Sistema de Lagunas Interdunarias de la Ciudad de Veracruz (Ramsar site) and/or the Sistema Arrecifal Veracruzano (UNESCO–MAB Biosphere Reserve). However, this requires verification. The two recorded locations of *I. tabascana* appear not to be protected; therefore, new sites may need to be established to protect these populations.

FIGURE 6

Locations of *Ipomoea batatas* var. *apiculata* and *I. tabascana*. The (red) star indicates the only known location of I. batatas var. apiculata, which was found near the Port of Veracruz by MacDonald and Austin (1990). Locations of I. tabascana recorded by SINGER (accessed through GBIF data portal, http://data.gbif.org/datasets/resource/1430 28/03/2008) and the United States National Plant Germplasm System Collection (NPGS) (accessed through GBIF data portal, http://data.gbif.org/datasets/resource/1429 28/03/2008) are shown by the (red) triangles

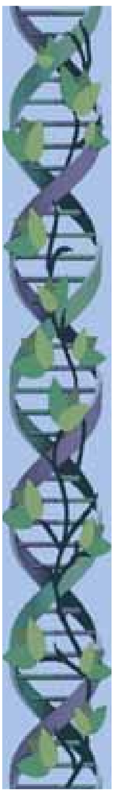


Recommendations

- Populations of *I. batatas* var. *apiculata* and *I. tabascana* require active *in situ* conservation with adequate *ex situ* back-up. As already indicated, some degree of protection of *I. batatas* var. *apiculata* may already be afforded within the designated Ramsar and MAB sites. This requires verification locally. However, if the taxon is found to occur within one or both of these sites it cannot be assumed that it is protected. Active monitoring and management of the population(s) are required in order to ensure its/their survival. *I. tabascana* is likely to be unprotected *in situ*. A detailed ecogeographic survey of the taxon is needed, but if it is found only to occur in the east of Tabasco, the available protected area data indicate no designated sites occur in this area. However, to the east of these sites (across the border into Guatemala) is the Laguna del Tigre National Park (IUCN category II and UNESCO–MAB

Biosphere Reserve). If the ecogeographic survey reveals that the taxon could occur within this site, populations here should immediately be actively monitored and managed. If the taxon does only occur within the borders of Tabasco, Mexico, one or more genetic reserves should be established to protect these populations *in situ*. The possibility of extending the boundaries of Guatemala's Laguna del Tigre National Park into Mexico should also be investigated.

- GBIF reports only two accessions of *I. tabascana* in *ex situ* collections. A comprehensive *ex situ* gap analysis should be undertaken to ascertain whether further collections are required. The *ex situ* status of *I. batatas* var. *apiculata* requires further investigation.
- According to collection records available via GBIF, the primary wild relative, *I. trifida*, is widely distributed throughout Central and South America. Austin (1997) records the taxon as occurring in Mexico, Guatemala, Nicaragua, Costa Rica, Panama, Colombia, Venezuela and Cuba. Therefore, this taxon's current status does not demand urgent conservation action. However, individual populations could harbour important adaptive traits; therefore, selected populations should be actively conserved throughout their range, ensuring that populations representing the extremes of the range (both geographically and topographically) are conserved. The taxon should also be included in monitoring activities at national level throughout its range, both within and outside protected areas.
- Most of the secondary wild relatives are recorded as weeds in 'A Global Compendium of Weeds' (http://www.hear.org/gcw/index.html): *I. triloba, I. cordatotriloba, I. cynanchifolia, I. grandiflora, I. lacunosa, I. littoralis, I. ramosissima, I. tenuissima, I. tiliacea* and *I. leucantha*. However, the status of these taxa within their native ranges requires further investigation. For example, *I. cynanchifolia* was recorded by Austin (1997) as occurring in Guyana and Brazil, but GBIF only reveals a few accessions collected in Bolivia. *I. grandiflora* is recorded by Austin (1997) as occurring in Brazil, Paraguay, Argentina and Uruguay, but collection records available via GBIF only record a few accessions collected in Bolivia and Peru.



2.4 Cassava

Scientific name

Manihot esculenta Crantz (Euphorbiaceae)

Principle synonyms

M. ultissima Phol; *M. aipi* Phol

Global, regional and local importance

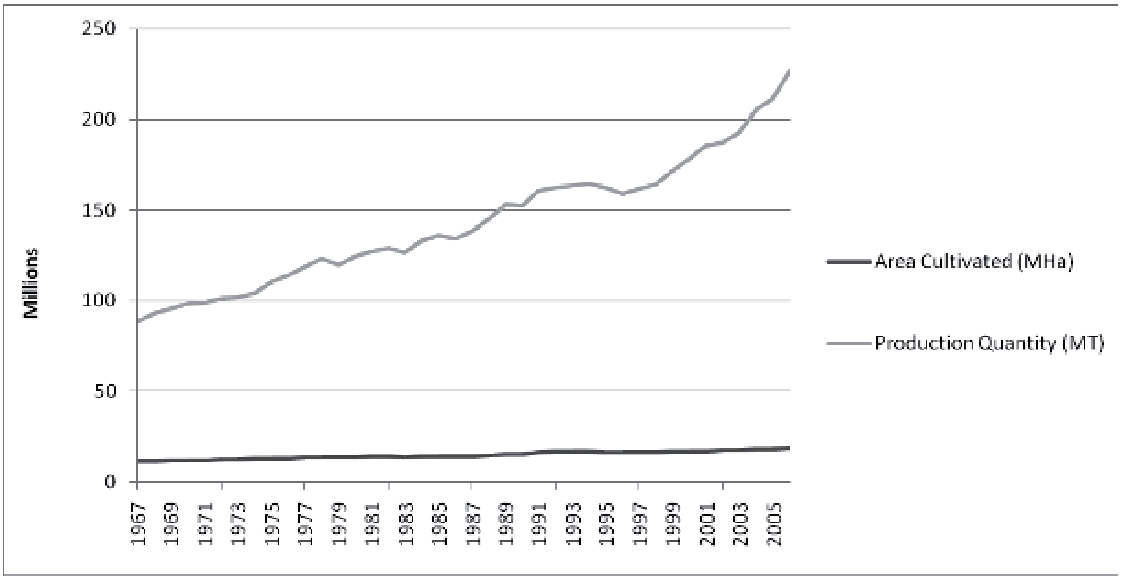
Cassava is grown for its enlarged starch-filled roots, which contain nearly the maximum theoretical concentration of starch on a dry weight basis among food crops (O'Hair, 1995). It is an important food crop for more than 900 million people in the tropics and subtropics (Nassar, 2006) and one of the two most important staples in sub-Saharan Africa (Nassar *et al*., 2008), where its resilience in marginal environments is particularly important for the rural poor (Ortiz, 2007). In sub-Saharan Africa and Latin America, the crop is mainly grown for human consumption, while in Asia and parts of Latin America; it is also used for animal feed and starch-based products (Nassar *et al*., 2008)

Nair and Unnikrishnan (2007) report that cassava is rapidly emerging as an important crop in India, where it produces a large amount of calories per unit area, has the ability to adapt to erratic climatic conditions, is resistant to several pests and diseases, is easy to cultivate, is not labour intensive, and has low production costs. As well as being important for human consumption in India, cassava also provides a cheap and nutritious feed for livestock (Nair and Unnikrishnan, 2007).

Cassava had an estimated world production of approximately 226.3 million tonnes planted on approximately 18.6 million ha in 2006 (FAO, 2008). The six countries with highest cassava production are Nigeria (45.7MT), Brazil (26.7MT), Thailand (22.6MT), Indonesia (19.9MT), Democratic Republic of Congo (15.0MT) and Mozambique (11.5MT). Figure 7 indicates a significant increase in global production and steady increase in the area cultivated over the last 40 years, while over the same time period yields have increased from 8020.84 kg/Ha in 1967 to 12163.23 kg/Ha in 2006 (FAO, 2008).

FIGURE 7

World area harvested and production quantity for cassava (FAO, 2008)



Taxonomic classification

The classification of Rogers and Appan (1973) recognized 98 *Manihot* species and classified these into 19 sections, is widely accepted. Allem (1989) described four further species and later, one more species from the Brazilian Amazon (Allem, 1999), bringing the total to 103. However, recent publications by Nagib Nassar and colleagues at the University of Brazil continue to make reference to the 98 species recognized by Rogers and Appan (1973). Allem *et al*. (2001) proposed a classification of cassava and 17 wild taxa into GP1 and GP2 (see below); however, in terms of cassava breeding, the gene pool concept may be of less importance than it is for other crop complexes because *M. esculenta* hybridizes naturally with many of the wild species (Nassar, 2003). Jennings (1995) reported that all species within the *Fruticosae* section of *Manihot* can be crossed with cassava and various authors report the use of species in other sections of the genus in breeding programmes.

Wild relatives

Primary wild relatives (Allem *et al*., 2001)

- *Manihot esculenta* Crantz subsp. flabellifolia (Pohl) Cif.
- *M. esculenta* Crantz subsp. *peruviana* (Müll. Arg.) Allem
- *M. pruinosa* Pohl

Secondary wild relatives (Allem *et al*., 2001)

• *M. aesculifolia* Pohl	• *M. anomala* Pohl
• *M. brachyloba* Müll. Arg.	• *M. chlorosticta* Standl. & Goldman
• *M. dichotoma* Ule	• *M. epruinosa* Pax & K. Hoffm.
• *M. glaziovii* Müll. Arg.	• *M. gracilis* Pohl
• *M. leptophylla* Pax & K. Hoffm.	• *M. pilosa* Pohl
• *M. pohlii* Wawra	• *M. tripartita* Müll. Arg.
• *M. triphylla* Pohl	

Tertiary wild relatives

All other species in the genus—83 species recognized by Rogers and Appan (1973) and five further species recognized by Allem (1989, 1999).

Distribution and centre of diversity

All species in the genus are native to tropical regions of the New World and are particularly concentrated in Brazil and Mexico (Nassar *et al*., 2008)—species found in other tropical regions are introductions (Nassar, 2007). Nassar (1978a) defined four centres of diversity of *Manihot*: 1) central Brazil, 2) north-eastern Brazil, 3) south-western Mexico, and 4) western Mato Grosso (Brazil) and Bolivia. Three micro-centres of diversity (areas where concentrations of 6–8 species occur in an area of no more than 200km diameter) were defined by Nassar (1978b) in central Brazil—Chapada de Veiadeiros, Corumba de Goias-Pirenopolis and Goias Velho. Later, Nassar *et al*. (2008) redefined these micro-centres as areas of <50km diameter where large numbers of species are found, such as Goiás Velho and Corumbá de Goiás. Thirty-eight of the 98 *Manihot* species are found in Central Brazil (southern Goiás and eastern Minas Gerais), 17 in Mexico, 16 in Northeast Brazil, and six in South Mato Grosso and Bolivia (Nassar *et al*., 2008).

Known uses of wild relatives in crop improvement

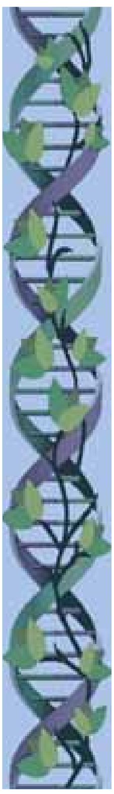
Cassava wild relatives have long been used as a source of useful characters for crop improvement—such as high protein content, apomixis (production of seed without fertilization), resistance to mealybug and mosaic disease, drought tolerance (Nassar, 2007; Nassar *et al*., 2008) and seed fertility (Nassar *et al*., 2008). Notable successes include the use of *M. glaziovii* to transfer resistance to mosaic disease in Tanzania in the 1930s (Nassar, 2007), *M. oligantha* Pax & K. Hoffm. to improve protein content (Nassar and Dorea, 1982) and *M. neusana* N.M.A. Nassar for transfer of apomixis genes (Nassar, 2000; Nassar *et al*., 2000). However, according to Nair and Unnikrishnan (2007), cassava breeders have "not yet scratched the surface" in utilization of the wild relatives and there is an urgent need for international cooperation in the collection, maintenance, evaluation and exploitation of the vast diversity available in the gene pool of this crop.

Jennings (1995) reports that the genes of several species may offer resistance to environmental stresses (e.g., *M. aesculifolia* – greater robustness, particularly on limestone soils; *M. rubricaulis* I.M. Johnst. – high altitudes and cool temperatures; *M. davisiae* Croizat and *M. angustiloba* Müll. Arg. – drought tolerance). Bonierbale *et al*. (1997) have used cassava wild relatives in breeding programs at the International Centre for Tropical Agriculture (CIAT) and the International Institute of Tropical Agriculture (IITA); particularly for high protein content and insect resistance. The same authors compiled a list of reported desirable characteristics of 50 cassava wild relatives.

Recently, CIAT (2006) reported success in using *M. walkerae* Croizat to introduce post-harvest physiological deterioration (PPD) tolerance. Interspecific hybridization of cassava with several wild relatives (including *M. caerulescens* Pohl, *M. tristis* Müll. Arg., *M. glaziovii, M. epruinosa, M. esculenta* var. *flabellifolia, M. esculenta* var. *peruviana, M. catingae* Ule, *M. dichotoma* and *M. pseudoglaziovii* Pax & K. Hoffm.) is also reported by Unnikrishnan *et al*. (2007) for cassava mosaic disease resistance at the Central Tuber Crops Research Institute (CTCRI). *M. caerulescens* was found to exhibit high levels of resistance and accessions have been used as donor parents for transferring resistance to elite Indian cultivars (Nair and Unnikrishnan, 2007).

Priority taxa

As already noted, the Gene Pool concept as applied to cassava wild relatives is of less significance in terms of prioritizing taxa for conservation than for some other crop complexes because *M. esculenta* hybridizes naturally with many of the wild species and a number of species in GP2 and GP3 have already been used in breeding programmes. Therefore, we have selected priority taxa based on a summary of the "most important species from an economic viewpoint" by Nassar *et al*. (2008), who rank *Manihot* species according to their "danger of extinction/conservation" in four categories: 1) almost extinct (one species—*M. neusana*), 2) endangered, 3) medium and 4) abundant. In this study, we have given species in categories 1 and 2 high priority status and species in category 3 'other priority species status.



High priority taxa

- Section *Foetidae*
  - *M. foetida* Pohl. Distribution: Mexico.
- Section *Heterophyllae*
  - *M. leptopoda* (Müll. Arg.) D.J. Rogers & Appan. Distribution: Rio de Janeiro (Brazil)
  - *M. pilosa*. Distribution: Minas Gerais, São Paulo and Rio de Janeiro (Brazil)
  - *M. tristis*. Distribution: Amapá and Roraima (Brazil), Venezuela and Suriname
- Section *Parvibractae*
  - *M. pringlei* S. Watson. Distribution: Tamaulipas and San Luis Potosí (Mexico)
- Section *Peltatae*
  - *M. peltata* Pohl. Distribution: Goiás (Brazil)

- Section *Quinquelobae*
    - *M. alutacea* D.J. Rogers & Appan. Distribution: Goiás (Brazil)
- Section *Stipulares*
    - *M. oligantha*. Distribution: Goiás (Brazil)
- Section *Tripartitae*
    - *M. neusana*. Distribution: Paraná (Brazil)

Other priority taxa

- Section *Graciles*
    - *M. fruticulosa* (Pax) D.J. Rogers & Appan. Distribution: Goiás, Minas Gerais and Distrito Federal (Brazil)
    - *M. pentaphylla* Pohl. Distribution: Pará, Goiás and Minas Gerais (Brazil)
- Section *Stipulares*
    - *M. stipularis* Pax & K. Hoffm. Distribution: Goiás and Distrito Federal (Brazil)

Priority sites (high priority taxa)

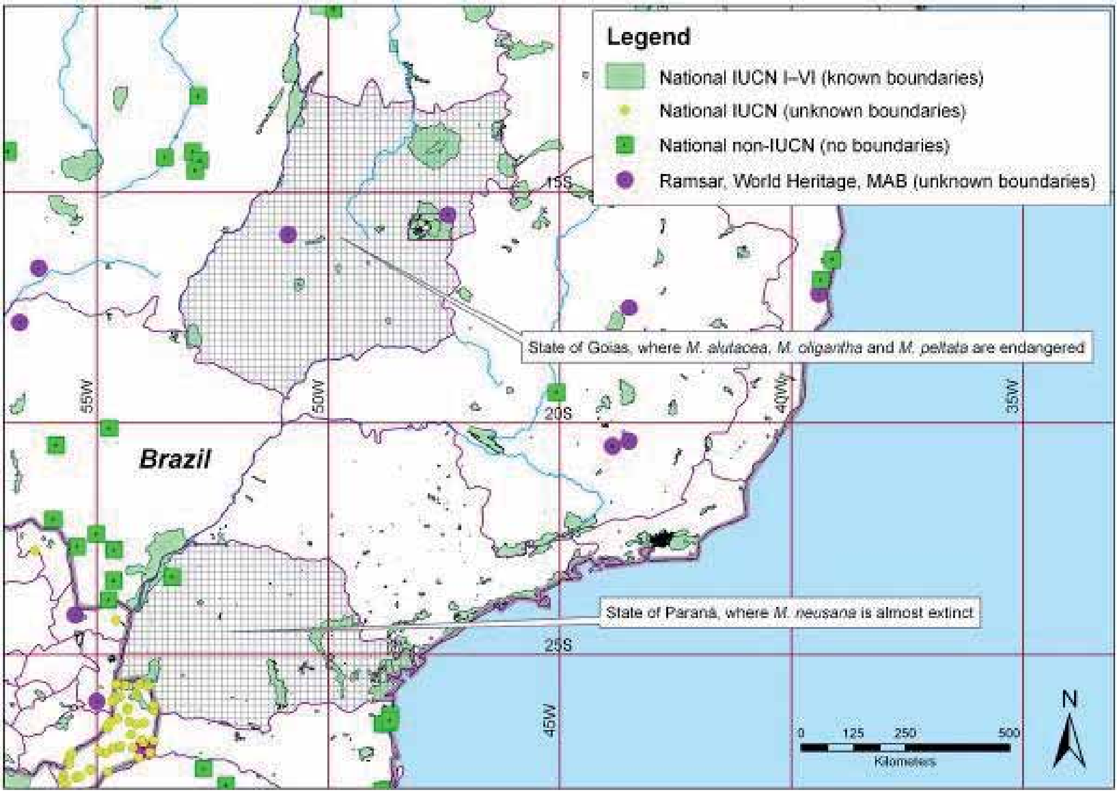
Distribution data for most of the high priority taxa are not readily available via online sources; therefore, before priority sites can be identified, comprehensive ecogeographic surveys of these taxa are needed. Although all the taxa listed have been classified as endangered by Nassar *et al*. (2008), those that are only found in one administrative unit should be given highest priority status (see Figure 8). In particular, *M. neusana*, which is "almost extinct" in Paraná, Brazil (Nassar *et al*., 2008) should be given urgent attention.

Recommendations

- There is an urgent need for a detailed study of the conservation status of the priority taxa and for immediate action to secure their conservation *in situ*. Nassar (2006) reports that in 2001, at least 18 *Manihot* taxa were no longer found at locations originally recorded in the 1960s and 70s, and appeals for action to conserve the remaining populations *in situ*. In particular, the three micro-centres of diversity (Chapada de Veiadeiros, Corumba de Goias-Pirenopolis and Goias Velho) are under threat from tourism (Nassar, 2006).
- Nassar *et al*. (2008) recorded the following economically important species as 'abundant': *M. gracilis, M. anomala, M. glaziovii, M. pseudoglaziovii, M. dichotoma, M. procumbens, M. reptans, M. caerulescens, M. leptophylla, M. aesculifolia, M. angustiloba, M. subspicata* and *M. carthaginensis*. Due to their importance as gene donors, a detailed study of their conservation status should be carried out and a selection of populations throughout their range should also be included in the CWR genetic reserve network. Further *ex situ* collections of these species may also be necessary. These species should be included in monitoring activities at national level throughout their range, both within and outside protected areas.
- A review of *ex situ* conservation of *Manihot* wild relatives should be undertaken, with a special focus on the priority species. Representative samples from extant populations should be conserved, ensuring adequate duplication.

FIGURE 8

High priority areas for *in situ* conservation of the cassava wild relatives, *Manihot neusana, M. alutacea, M. oligantha* and *M. peltata*



2.5 Banana/plantain

Scientific name

Musa acuminata Colla (Cavendish banana), *Musa balbisiana* Colla, *Musa basjoo* Siebold & Zucc. Ex Iinuma (Japanese banana), *Musa xparadisiaca* L. (banana, plantain), *Musa troglodytarum* L. (fe'l banana).

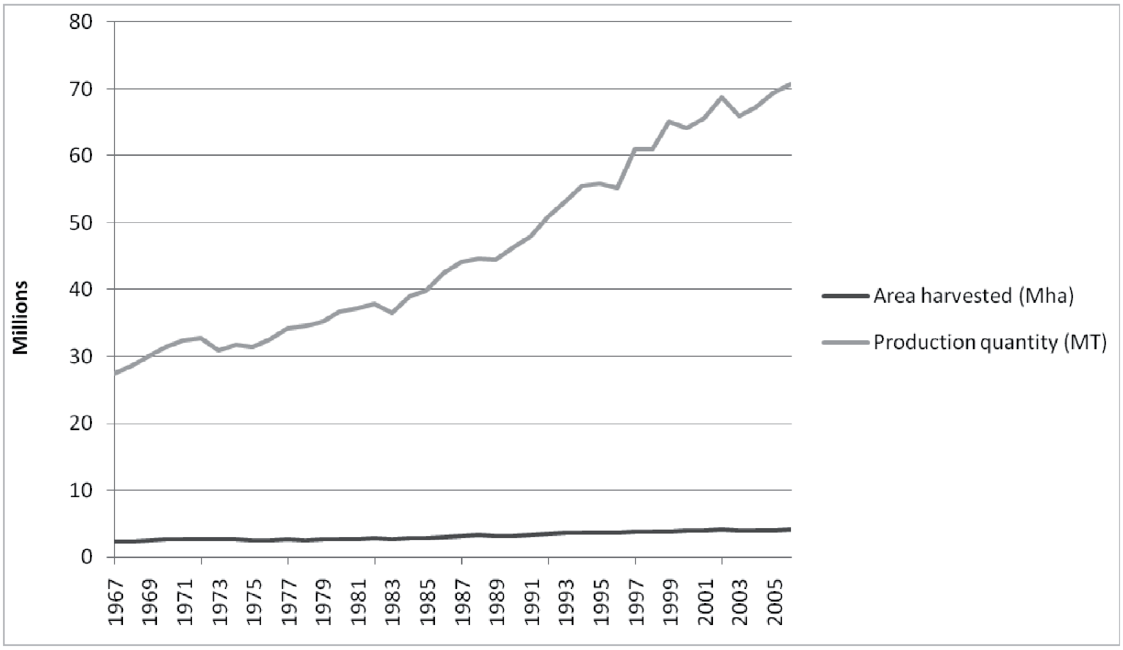
Global, regional and local importance

Bananas, plantains and cooking bananas are crops that are tropical in origin and intolerant of frost; therefore, their cultivation is restricted to tropical countries from 40°N and 40°S, where 5% of production is for domestic consumption (Simmonds, 1995). Bananas and plantains have been widely cultivated throughout the tropics since the sixteenth century. Although bananas are generally intolerant of cold, it is thought that the B genome has conferred a degree of hardiness and resistance to seasonal drought in the monsoon climates north of the primary centre of origin in Southeast Asia (Simmonds, 1995). Plantains are generally less sweet than desert bananas and tend to be cooked before being eaten. They are high in carbohydrates and fibre, with not insignificant protein content. The export banana industry rates very highly in the economies of a number of developing countries across the world, earning significant hard currency as a commodity (FAO, 2008). Cultivated bananas produce fruit parthenocarpically without fertilization. The edible diploid forms are commonly sterile and are reproduced by vegetative propagation. Most edible bananas are triploid and do not produce seeds (Horry *et al*., 1997). If seeds are produced, the fruit becomes practically inedible, because the seeds are relatively large and very hard. Conservation of *Musa* diversity has thus to involve methods other than seed storage—primarily field gene banks and *in vitro* storage (Hawkes *et al*., 2000).

The six countries with highest banana and plantain production in 2006 were: India (11.7 MT), Brazil (7.1 MT), China (7.1 MT), Philippines (6.8 MT), Ecuador (6.1 MT) and Indonesia (5.2 MT) (FAO, 2008). Figure 9 indicates an impressive global increase in banana and plantain production. While the area cultivated has only increased slightly over the last 40 years, over the same time period, yields have increased from 11 335.33 kg/Ha in 1967 to 16 927.20 kg/Ha in 2006 (FAO, 2008).

FIGURE 9

World area harvested and production quantity for banana and plantain (FAO, 2008)



Taxonomic classification

The family *Musaceae* is formed by two genera: *Ensete* and *Musa* (Simmonds, 1995). Within the genus *Musa*, four sections are recognized (see Table 1)—the great majority of cultivated forms have originated from only one of these sections, *Eumusa* (Simmonds, 1962). This section is the largest and includes 11 species (Horry *et al*., 1997). The edible forms have principally evolved within two of these species: *Musa acuminata* and *M. balbisiana*, but rare cultivars are derived from hybridizations with *M. schizocarpa* (S genome) (Shepherd and Ferreira, 1982), and *M. balbisiana* and *M. textilis* (T genome) (Carreel *et al*., 1994). *Musa acuminata* is the most widespread and most diverse species, with nine subspecies recognized (Horry *et al*., 1997). These edible forms have three different ploidy levels—2n=22, 3n=33 and 4n=44). The triploid cultivars are most numerous and widely cultivated, while diploid forms are more locally important and tetraploids are rare. It is estimated that there are at least 1000 recognizable *Musa* cultivars distributed pantropically and *Musa acuminata* subsp. *banksii* is believed to be the ancestral parent of the majority of edible banana cultivars (INIBAP/IPGRI, 2006). The two species, *M. acuminata* and *M. balbisiana* are designated as having different genomes, which are referred to in the Simmonds and Shepherd (1955) genome nomenclature as being AA and BB respectively in the diploids, while the triploids can have various combinations of these genomes; such as AAA (export dessert bananas exemplified by the 'Cavendish' type and East African cooking and beer bananas), AAB (plantains, e.g. 'Horn' and 'French' and local dessert bananas), and ABB (cooking bananas), and likewise the tetraploids AAAA, AAAB, AABB and ABBB. Edibility of mature fruits of diploid *Musa acuminata* (AA) came about as a result of female sterility and parthenocarpy, but would no doubt have been selected and maintained by humans (Daniells *et al*., 2001). Molecular analyses of a large number of plantain landraces using various techniques indicate that most plantains have a very high level of genetic identity to one another (Carreel *et al*., 1994; Crouch *et al*., 1998; Howell *et al*., 1994). This supports the suggestion that somatic mutations are responsible for the diversity of 'morphotypes' of plantains now found in West Africa.

The bananas of section *Australimusa* are the most poorly understood group; collectively known as Fe'i cultivars, they are distinguished from other cultivated bananas by their erect fruit bunches and generally red sap. Fe'i bananas were originally distributed from the Molluccas to Hawaii and Tahiti (Daniells *et al*., 2001). They not only provide a source of food, but are also used to provide fibre for ropes and weaving and a dark red dye. Little is known about the origins of this crop, although various authors have speculated about possible wild ancestors. Simmonds (1956) suggests that *M. maclayi* is the most likely ancestor, while Cheesman (1950) notes their similarity to *M. lolodensis*—a view supported by RFLP analysis (Jarret *et al*., 1992). However, an interspecific origin for Fe'i bananas has been suggested and the Fe'i's origin still requires clarification (Carreel, 1994).

Wild relatives

As the two cultivated species, *M. acuminata* and *M. balbisiana* are members of section *Eumusa*, the close wild relatives are the other species of this section. However, as *M. textilis* of section *Australimusa* is known to forms natural hybrids with *M. acuminata* (Carreel *et al*., 1994) it should also be considered a primary wild relative.

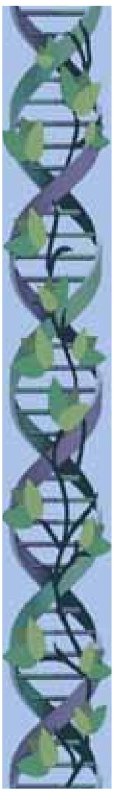
Primary wild relatives

- *Musa schizocarpa* N.W. Simmonds
- *M. itinerans* Cheesman
- *M. sikkimensis* Kurz
- *M. nagensium* Prain
- *M. ochracea* K. Sheph.
- *M. basjoo* Siebold & Zucc. Ex Iinuma
- *M. flaviflora* N.W. Simmonds
- *M. cheesmani* N.W. Simmonds
- *M. halabanensis* Meijer
- *M. textilis* Nee

TABLE 1

Classification and distribution of *Musa* (Daniells *et al*., 2001)

Genus	Section	Species	Subspecific groups	Distribution
Musa	*Eumusa* (2n=22)	*acuminata*	subsp. *banksii* subsp. *burmannica* subsp. *burmannicoides* subsp. *malaccensis* subsp. *microcarpa* subsp. *truncata* subsp. *siamea* subsp. *zebrina* subsp. *errans*	New Guinea, Australia, Samoa Myanmar, Thailand Myanmar, Thailand Malaysia Indonesia, Malaysia, Thailand Malaysia Indonesia, Malaysia, Thailand Indonesia
		balbisiana		India to Philippines
		schizocarpa		Papua New Guinea
		basjoo		Japan[19]
		itinerans		China, India, Myanmar, Thailand, Vietnam
		flaviflora		Bhutan
		sikkimensis		India, Bhutan
		cheesmani		India
		nagensium		India
		halabanensis		Sumatra
		ochracea		India
	Rhodochlamys (2n=22)	*laterita*		Myanmar, Thailand
		ornata		N India, Myanmar, Thailand
		sanguinea		N India
		velutina		N India
	Callimusa (2n=20)	*coccinea*		China, Indonesia, Thailand
		violascens		Malaysia
		gracilis		Malaysia, Thailand
		borneensis		Sarawak, Brunei
		beccarii		Sabah
		salaccensis		Java, Sumatra
	Australimusa (2n=20)	*maclayi*	subsp. *maclayi* var. *maclayi* subsp. *maclayi* var. *namatani* subsp. *maclayi* var. *erecta* subsp. *ailuluai*	Papua New Guinea New Ireland Papua New Guinea Papua New Guinea
		peekelii	subsp. *peekelii* subsp. *angustigemma*	New Ireland Papua New Guinea



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[19] Constantine and Rossel (2008) believe this species is introduced in Japan and is in fact native to China

Genus	Section	Species	Subspecific groups	Distribution
		jackeyi		Australia
		lododensis		Indonesia, Papua New Guinea
		textilis		Philippines
		bukensis		Papua New Guinea
	Incertae sedis	*ingens*		Papua New Guinea
		boman		Papua New Guinea
		lasiocarpa		China, Vietnam, Laos, Myanmar

Secondary wild relatives

- *M. laterita* Cheesman
- *M. sanguinea* Hook. f.
- *M. coccinea* Andrews
- *M. gracilis* Holttum
- *M. beccarii* N.W. Simmonds
- *M. maclayi* F. Muell.
- *M. jackeyi* W. Hill
- *M. bukensis* Argent
- *M. ornata* Roxb.
- *M. velutina* H. Wendl. & Drude
- *M. violascens* Ridl.
- *M. borneensis* Becc.
- *M. salaccensis* Zoll.
- *M. peekelii* Lauterb.
- *M. lododensis* Cheesman

Tertiary wild relatives

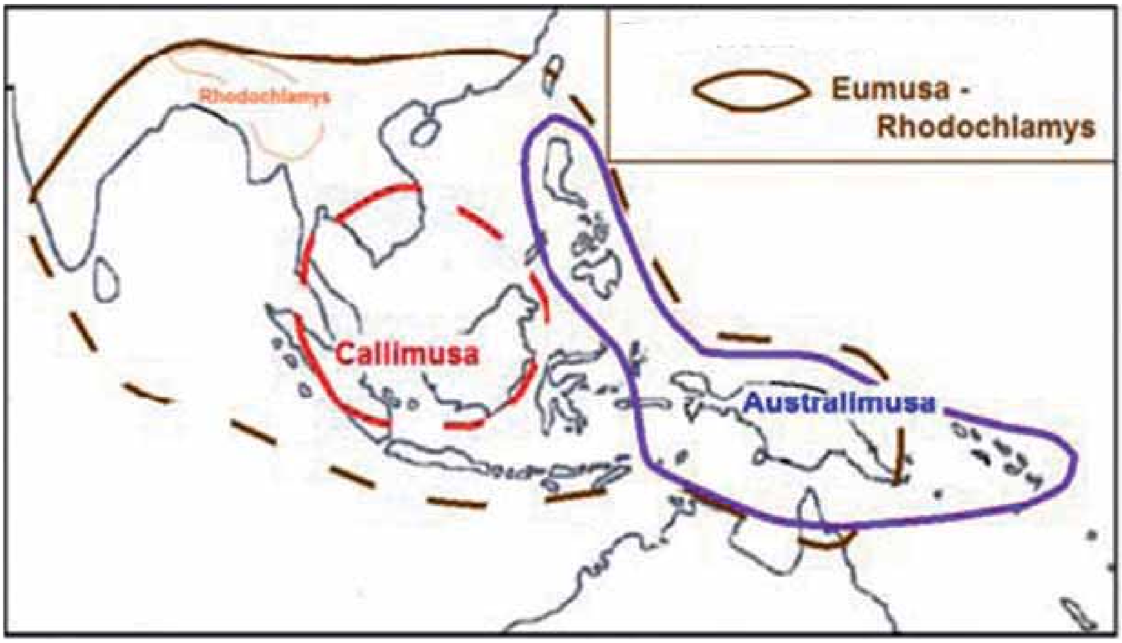
- *Ensete* species (including *E. ventricosum* which is cultivated in Ethiopia).

Distribution and centre of diversity

In cultivation, bananas are distributed throughout the warmer countries of the world, and are more or less confined within latitudes 40°N and 40°S (Simmonds, 1995). In terms of the origins and diversity of the various cultivated forms, the AA cultivars' origins are probably Malaysia, with Papua New Guinea as the centre of greatest diversity (Novak, 1992). The primary origin for the triploid AAA cultivars, which arose from the diploids, is again Malaysia, but there is also significant diversity occurring in the highlands of East Africa. For the AAB forms, the primary centre is India, with a second centre in the Pacific Islands. Again, for ABB types, the major centre is India with possibly a minor centre in eastern Malaysia. In most parts of Southeast Asia, these triploids, which are more vigorous and have larger fruit, have replaced the original AA diploids. However, in Papua New Guinea, AA diploids remain agriculturally significant and a wide range of diversity is still found in cultivation (Daniells *et al*., 2001). *Musa acuminata* is the most widespread of the *Eumusa* species, with its centre of diversity in either Malaysia (Simmonds, 1962) or Indonesia (Nasution, 1991; Horry *et al*., 1997). The diploid and triploid *M. acuminata* cultivars are thought to have been taken to areas where *M. balbisiana* is native (India, Myanmar, Thailand, Philippines) and natural hybridizations resulted in the formation of hybrid progeny with the genomes AB, AAB, and ABB. The Indian subcontinent is the major centre for hybridization of *acuminata* types with the indigenous *M. balbisiana*, and the region is noted for the wide variety of AAB and ABB cultivars. It is thought that subsequent dispersal of edible bananas outside Asia is human mediated (Simmonds, 1962) and therefore the history of banana cultivation is closely linked to patterns of human migration leading to the development of distinct sub-groups of varieties in different geographic locations (e.g., the distinct AAB Maia Maoli/Popoulu bananas of the Pacific Islands) (De Langhe, 1996; De Langhe and De Maret, 1999) or cooking banana (plantain AAB) in the wet tropical zones of West and Central Africa.

The distribution of the wild species is entirely southern and eastern Asian and northern Australasian, with obvious centres of species diversity in Papua New Guinea and Indonesia and a secondary centre in northern India/Bhutan (see Table 1 and Figure 10). The wild species of section *Eumusa* are distributed throughout the range of the genus from India to the Philippines and China, while section *Rhodochlamys* species are found on the western distributional fringe in northern India, Myanmar and Thailand. Section *Callimusa* species are primarily distributed further east in Malaysia and Indonesia and species in section *Australimusa* are distributed from the Philippines to northern Australia with several taxa being restricted to Papua New Guinea or New Ireland.

FIGURE 10
Distribution of the four sections of the genus *Musa* (INIBAP/IPGRI, 2006)



Known uses of wild relatives in crop improvement

Progress in the formal breeding of plantain and banana has been restricted by the complex genetic structure and behaviour of cultivated polyploid *Musa* species. Genetic improvement has been hindered due to the large amount of space required for growth and maintenance of plant populations, in addition to the long growth cycle and the low levels of fertility and seed viability characteristic of cultivated genotypes (Crouch *et al*., 1999). However, informally, mutations affecting traits of economic or horticultural interest have been selected by farmers over the years and multiplied by vegetative propagation to produce a diverse range of morphotypes (Daniells *et al*., 2001). *M. balbisiana* is considered more robust than *M. acuminata*, and characteristics such as drought and disease resistance have been transferred from the B genome to cultivars. Hybridization would have given rise to a wide range of edible types of banana, some of which would have survived and been multiplied under domestication. Consequently, a diverse selection of cultivars of Musa is thought to have arisen in Southeast Asia along with the earliest developments of agriculture many thousands of years ago (Price, 1995). Most interspecific breeding has focused on crossing *M. acuminata* and *M. balbisiana*, but recently introduced *Musa* hybrids, bred for improved yield and resistance to diseases, have been found to be widely infected with banana streak virus (BSV), the causal agent of banana streak disease (BSD). Data indicate that a genetic mechanism is involved in BSV appearance, which unless resolved will seriously limit hybrids involving *M. balbisiana* (Lheureux *et al*., 2003). IITA (2008) report the use of *M. acuminata* and *M. balbisiana* hybrids in breeding for black sigatoka resistance.

Bananas and plantains suffer from a number of highly significant pests and diseases (Sagi *et al*., 1998), some most significant examples of which are Panama disease (banana wilt: caused by *Fusarium oxysporum*), sigatoka (leaf spot: caused by *Mycosphaerella musicola*), black sigatoka (black leaf streak: caused by *Mycosphaerella fijiensis*), bacterial wilt (caused by *Pseudomonas solanacearum*), banana bunchy top virus and burrowing nematodes. Because of the difficulties of undertaking conventional breeding in bananas due to sterility, mutation breeding and somaclonal approaches have been used for developing new cultivars (Novak, 1992)—as a consequence there has been limited use of wild germplasm to date. Nevertheless, sources of resistance amongst germplasm of *Musa* are still important, with resistance to bacterial and fusarial wilt, sigatoka, and burrowing nematodes having been found in the various diploid subspecies of *M. acuminate*; such as *malaccensis, banksii, errans* and *burmannica* (Novak, 1992).

The Global Conservation Strategy for *Musa* (Banana and Plantain) (INIBAP/IPGRI, 2006) states that there has been insufficient use of wild species diversity in banana breeding; for example, for in improving fruit pulp quality, resistance to abiotic stress such as tolerance to cold (*M. sikkimensis, M. basjoo*), water-logging (*M. itinerans*), and drought (*M. balbisiana, M. nagensium*). The difference in ploidy level between many *Musa* taxa may be responsible for the limited success of interspecific breeding (Oselebe *et al*., 2006). Due to the difficulty of breeding bananas conventionally, genetic engineering to confer disease resistance qualities to new cultivars is perhaps a greater priority than for many other crops (Crouch *et al*., 1998).

Priority taxa

- *M. basjoo* – distribution: China (Fujian, Gansu, Guandong, Guangxi, Guizhou, Hubei, Hunan, Jiangsu, Jiangxi, Sichuan, Yunnan and Zhejiang), Japan (introduced).
- *M. cheesmani* – distribution: India (Assam)
- *M. flaviflora* – distribution: Bhutan
- *M. halabanensis* – distribution: Sumatra
- *M. itinerans* – distribution: China, India, Myanmar, Thailand, Vietnam
- *M. nagensium* – distribution: India (Naga Mountains, Assam)
- *M. ochracea* – distribution: India
- *M. schizocarpa* – distribution: Papua New Guinea
- *M. sikkimensis* – distribution: Northeast India and Bhutan
- *M. textilis* – distribution: Philippines

Priority sites

Occurrence data for the priority taxa are not readily available via online sources; therefore, distribution mapping has not been possible in this study. However, the general distribution information given above provides an indication of the priority areas for *in situ* conservation; namely, Assam (India), Bhutan, Papua New Guinea, Sumatra and the Philippines.

Recommendations

- Detailed ecogeographic surveys of the priority taxa are needed in order to ascertain their *in situ* and *ex situ* conservation status. Genetic reserve sites should be identified based on further work.
- When Bioversity International was established in 2006, the International Network for the Improvement of Banana and Plantain (INIBAP) ceased to exist as a distinct entity and became a network of collections, curators and information scientists whose responsibility it is to take care of the world's genetic resources of banana (Bioversity International, 2008). At the heart of the Network is the INIBAP Transit Centre at the Catholic University of Leuven in Belgium, which hosts major collections of banana germplasm in the form of tissue culture and cryopreserved in liquid nitrogen. However, the majority of regional and national banana and plantain collections are held as field gene banks due to the lack of seed for the majority of cultivars. Leuven currently holds over 1 168 accessions made up of 15% wild relatives, 75% land races and 10% advanced cultivars, covering most of the genetic diversity within the genus *Musa* (INIBAP, 2008). INIBAP has, as one of its main objectives, the organization and coordination of research on bananas and plantains, to include the development, evaluation and dissemination of improved cultivars, as well as the conservation and use of *Musa* genetic diversity (Bioversity International, 2008). A major component of these activities is represented in the Global Conservation Strategy for Musa (Banana and Plantain) (INIBAP/IPGRI, 2006) and the Musa Germplasm Information System (http://195.220.148.3:8013/mgis_2/homepage.htm). The Global Conservation Strategy for *Musa* concludes that although about 60 *Musa* collections exist, they do not effectively meet the users' demand for germplasm and many of the collections are threatened by funding instability. It also identifies the following priorities:
- genetic diversity is comprehensively characterized and documented, taxonomy is harmonized, and collections are rationalized
- the global system for the safe exchange of germplasm is strengthened, the entire gene pool is conserved in perpetuity, and the use of genetic diversity is maximized.
- Despite the third and fourth priorities of the Global Conservation Strategy it does not address *in situ* conservation of wild *Musa* diversity. Given the restricted distribution of several species and the likely genetic erosion they are suffering due to habitat destruction, stochastic events (substantial losses due to typhoons etc.) and likely impact of climate change, it would appear urgent that an *in situ* conservation strategy is developed and implemented. As the Musa community are used to working together so effectively, the actual strategy implemented will need to be developed by INIBAP.

2.6 Rice

Scientific name

Oryza sativa L.

Principle synonyms

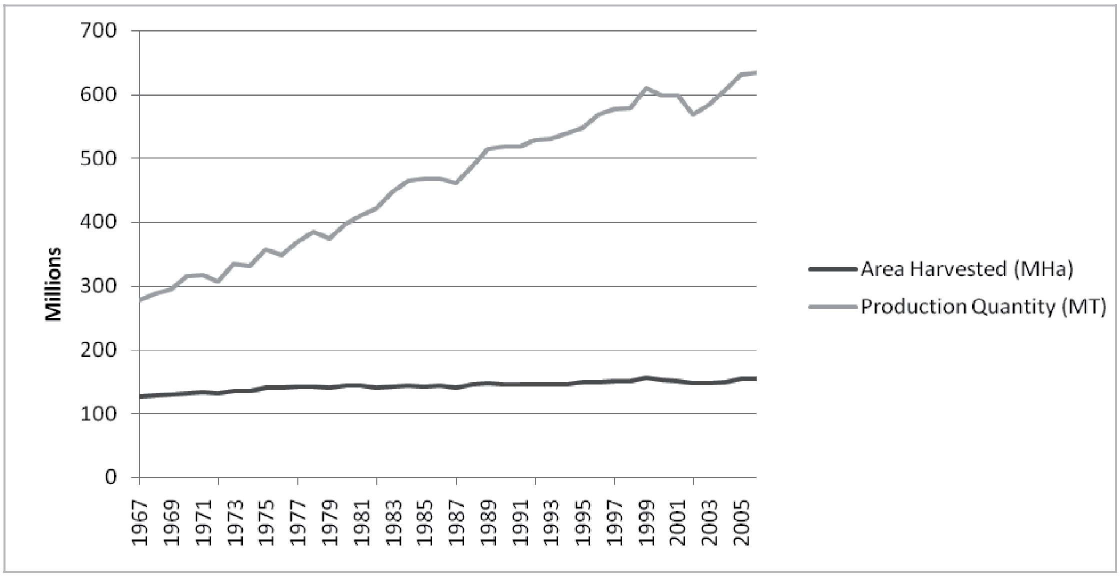
Padia meyeriana Zoll. & Moritzi, *Oryza formosana* Masamune & Suzuki

Global, regional and local importance

Rice feeds half the world's people—mainly in Asia (Jackson *et al*., 1997)—and is the second highest production crop (after maize) in terms of total production (634.6M Mt in 2006) (FAO, 2008). 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 (29.4MHa or 19.0%/184.0MT or 29.0%), India (43.7MHa or 28.3%/136.5MT or 21.5%), Indonesia (11.4MHa or 7.4%/54.4MT or 8.6%), Bangladesh (11.2MHa or 7.3%/43.7MT or 6.9), Vietnam (7.3MHa or 4.7%/35.8MT or 5.6%) and Thailand (10.1MHa or 6.5%/29.2MT or 4.6%) (FAO, 2008). Figure 11 indicates an impressive global increase in production of paddy rice based on a less significant increase in the area cultivated, indicating yields have increased from 2175 kg/Ha in 1967 to 4112 kg/Ha in 2006 (FAO, 2008).

FIGURE 11

World area harvested and production quantity for rice (FAO, 2008)



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 (Table 2), 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 indica rice and group VI encompasses the japonica and javanica (tropical japonica) types.

TABLE 2

Section, species and species complexes in the genus *Oryza*, with designated genome groups (after Vaughan, 1994; Aggarwal et al., 1997; Kurata, 2008)

Section	Species	Genome group	2n =	Distribution
Oryza	*O. sativa* complex:			
	O. sativa	AA	24	Worldwide
	O. nivara	AA	24	South and East Asia
	O. rufipogon	AA	24	South, East and Southeast Asia, Australia, Central and South America
	O. glaberrima	AA	24	West Africa, Pemba and Zanzibar
	O. barthii	AA	24	West, Central and southern Africa
	O. longistaminata	AA	24	West, Central and southern Africa
	O. meridionalis	AA	24	Northern Australia (Northern Territory, Queensland, Western Australia)
	O. glumaepatula	AA	24	Central and South America
	O. officinalis complex:			
	O. officinalis	CC	24	South, East and Southeast Asia
	O. minuta	BBCC	48	Philippines, Papua New Guinea
	O. rhizomatis	CC	24	Sri Lanka
	O. eichingeri	CC	24	West and Central Africa, Sri Lanka
	O. punctata	BB, BBCC	48	West, Central and southern Africa
	O. latifolia	CCDD	48	Central and South America
	O. alta	CCDD	48	Central and South America
	O. grandiglumis	CCDD	48	South America
	O. australiensis	EE	24	Northern Australia (Northern Territory, Queensland, Western Australia)
Ridleyanae	*O. brachyantha*	FF	24	West and Central Africa
	O. schlechteri	?	24	Irian Jaya, Papua New Guinea
	O. ridleyi complex:			
	O. ridleyi	HHJJ	48	Southeast Asia
	O. longiglumis	HHJJ	48	Irian Jaya, Papua New Guinea
Granulata	*O. meyeriana* complex:			
	O. meyeriana	GG	24	Southeast Asia
	O. granulata	GG	24	South, East and Southeast Asia

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

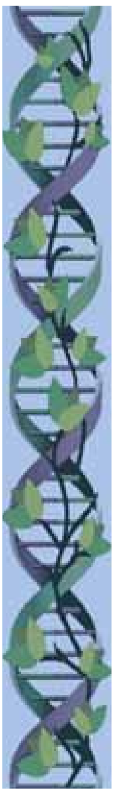
- *Oryza sativa* L. f. *spontanea* Roshev.
- *O. nivara* S.D. Sharma & Shastry
- *O. rufipogon* Griff.
- *O. glaberrima* Steud.
- *O. barthii* A. Chev.
- *O. longistaminata* A. Chev. & Roehrich
- *O. glumaepatula* Steud.
- *O. meridionalis* N.Q. Ng

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, and now plays a vital role in the food security of Asia, West Africa, the Caribbean and South America (FAO, 1998). The major distribution areas for all the species are given in Table 2. 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.

O. sativa can be ecologically subdivided into dryland, deep water and very deep water rice (Huke and Huke, 1990). Dryland rice is dependent on rainfall for moisture and is therefore common along river banks as water recedes at the end of the rainy season. Deep water rainfed rice (50–100cm) is associated with greater water depth, and occurs at sites such as the major river deltas of South and Southeast Asia, as well as the foot of mountain ranges. Very deep water rice is grown in depths of at least one metre, while in parts of Bangladesh and the deltas of the Mekong and Chao Phraya, depths may exceed 5 metres. (Huke and Huke, 1990)

As far as the wild species are concerned, ecological requirements range from full sun (e.g., *O. australiensis*) to partial shade (e.g., *O. eichingeri*), and many grow in wet habitats (e.g., *O. alta, O. granulata*) or standing water (e.g., *O. brachyantha, O. barthii*). They are adapted to a broad range of ecosystems from open savannah to shady forests, but are most often associated with swamps, ditches or damp areas within these ecosystems; for example, the high-humidity Himalayan foothills, Asian river deltas, tropical Caribbean islands, the Amazon Basin, and the inland swamplands of southern and western Africa, as well as in temporary pools of the arid savannas of the tropics (Vaughan, 1994).

Known uses of wild relatives in crop improvement

The classification of *O. sativa* into six crossability groups (Glaszmann, 1987) has greatly facilitated the use of diverse germplasm because they reflect the potential for making crosses: fertilities of within-subspecific crosses average approximately 69%, whereas hybrids formed between different groups are substantially less fertile (e.g., the average fertility of japonica x indica crosses is only about 14%). There are many barriers to hybridization in the A-genome *Oryza* species (Oka, 1988), but natural hybrids between *O. sativa* and its wild relatives do occur when the species are coincident and flowering at the same time. In Asia, introgression between the various A-genome *Oryza* species is common (Chen *et al*., 2004; Kuroda *et al*., 2005), while in Africa, introgression and hybrids have been found between introduced *O. sativa* and wild and cultivated A-genome African species (Chu and Oka, 1970; Semon *et al*., 2005), and in Latin America the A-genome *O. glumaepatula* commonly hybridizes with *O. sativa* in Venezuela (Dr. Zaida Lentini, CIAT; reported by Vaughan *et al*., 2008). With this level of natural hybridization, it is not surprising that wild relatives 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). Even wild species that appear phenotypically inferior have been used to enhance yield (Xiao *et al*., 1998). Direct crosses and embryo rescue techniques have been used to successfully produce hybrids between Asian rice and all other wild species (except *O. schlechteri*). Brar (2005) provides a detailed summary of the uses of CWR for Asian rice breeding at IRRI, which clearly shows that wild species of *Oryza* are important sources of useful genes for resistance to major biotic and abiotic stresses (Table 3). 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 3

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

Trait	Donor species	Genome	Accession number
Grassy stunt resistance	*O. nivara*	AA	101508
Bacterial blight resistance	*O. longistaminata* *O. officinalis* *O. minuta* *O. latifolia* *O. australiensis* *O. brachyantha*		
Blast resistance	*O. minuta*	BBCC	101141
Brown plant hopper resistance	*O. officinalis* *O. minuta* *O. latifolia* *O. australiensis*	CC BBCC CCDD EE	100896 101141 100914 100882
White-backed plant hopper resistance	*O. officinalis*	CC	100896
Cytoplasmic male sterility	*O. perennis* *O. glumaepatula*	AA AA	104823 100969
Tungro resistance	*O. rufipogon* *O. rufipogon* *O. rufipogon*	AA AA AA	106423 105909 105908
Introgression lines under evaluation			
Yellow stem borer	*O. longistaminata* *O. rufipogon*	AA AA	110404 -
Sheath blight resistance	*O. minuta* *O. rufipogon*	BBCC AA	101141 -
Increased elongation ability	*O. rufipogon*	AA	CB751
Tolerance of acidity and iron and aluminium toxicity	*O. glaberrima* *O. rufipogon* *O. rufipogon*	AA AA AA	Many 106412 106423
Resistance to nematodes	*O. glaberrima*	AA	Many

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)

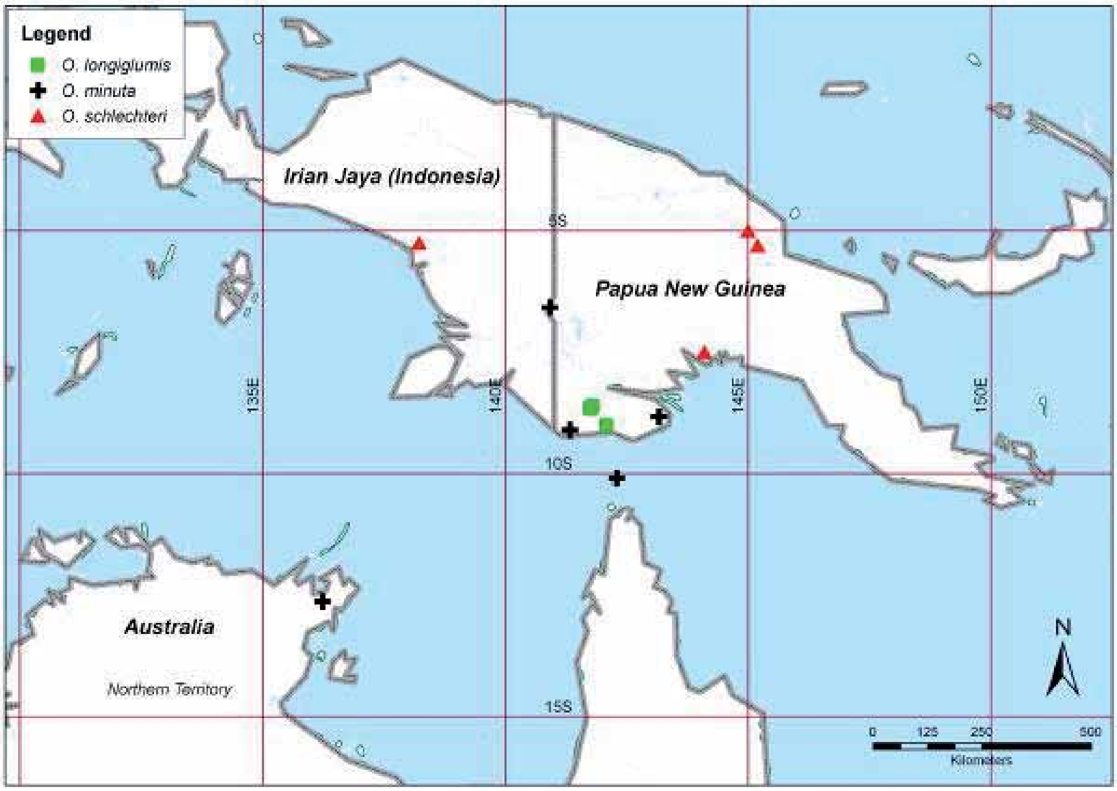
Based on the analysis presented in Figures 12 and 13, the following locations should be investigated further as potential sites for *in situ* conservation of the highest priority rice wild relatives:

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 12

Distribution of high priority rice wild relatives, *O. longiglumis, O. minuta*[20] and *O. schlechteri*[21]



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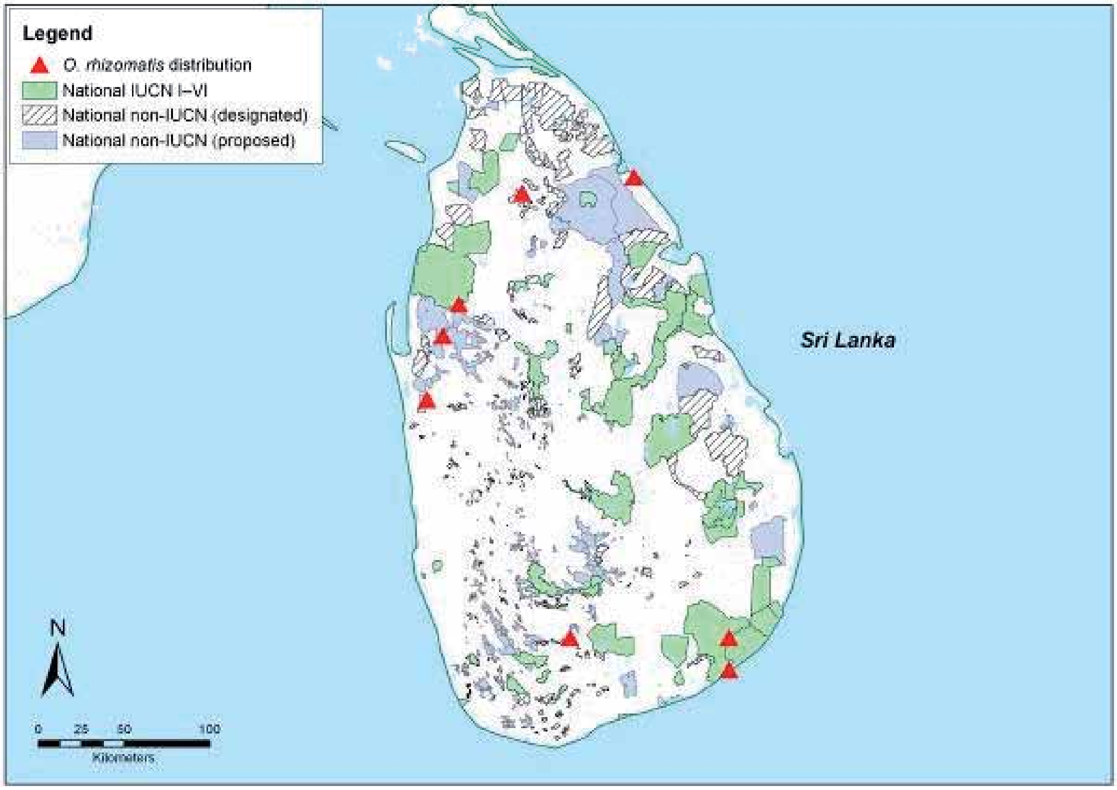
[20] *O. minuta* is also distributed in the Philippines, but coordinate data were not available for this study.

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

FIGURE 13

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[21].
- Wilpattu National Park (IUCN category II). *O. rhizomatis* has been recorded within the boundaries of this protected area[22].
- 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.

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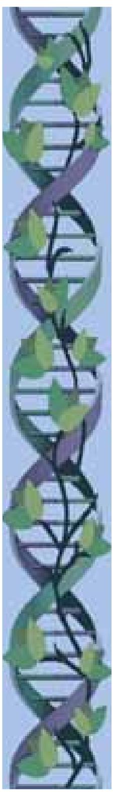
[21] *O. eichingeri* has also been recorded within this protected area (coordinates not available) [Data source: Australian National Herbarium (CANB) (accessed through GBIF data portal, http://data.gbif.org/datasets/resource/47 05/08/2008)].

[22] *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

- In recent years, the *in situ* conservation of rice landraces on-farm has received some attention (Bellon *et al*., 1997; Carpenter, 2005; Fukuoka *et al*., 2006; Joshi and Bauer, 2006; Agnihotri and Palni, 2007; Virk and Witcombe, 2007). However, despite Vaughan and Chang's (1992) warning of the loss of rice diversity through habitat destruction and the need for systematic *in situ* conservation with the establishment of protected areas, there remain no genetic reserves that conserve wild *Oryza* diversity. Another warning was provided by Akimoto's *et al*. (1999) study of *Oryza rufipogon* in Thailand. The authors sampled populations in 1985 and 1994 and compared genetic diversity using allozymes. They found a severe decline in diversity and significant introgression of the wild species from Asian rice, and what is even more concerning is that each of the original populations was extinct when revisited in 1996. A similar picture has also emerged in China (Fan *et al*., 2000; Gao *et al*., 2000), which means there is real concern for maintenance of the wild rice genome. Gao (2003) distinguish between the extinction of entire populations and the drastic change of genetic structure of populations from introgression with cultivated rice, both of which have a serious impact on wild rice gene pool diversity. Therefore, implementation of a network of wild rice genetic reserves will be 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 and 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 focussed 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 (though further studies are required to obtain the most recent occurrence data and to collect fresh data where gaps exist in order to obtain a clear picture of their current distribution), this does not mean that they are not under threat of genetic erosion. On the contrary, as already noted, 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. 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, there is a requirement to ensure the full geographic range is reflected in the wild rice germplasm conserved *ex situ* and as such a full *ex situ* gap analysis study is needed. However, parallel to this action there is a need to streamline existing collections in relation to duplicate identification and particularly to develop a 'core' collection (Ford-Lloyd *et al*., 1997; Jackson *et al*., 1997).
- The situation for wild species is different. Far fewer samples of wild species are being conserved *ex situ*. There are 4 370 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, despite the fact that valuable genes are known to exist and could be transferred from these species to the cultigens (Brar and Khush, 1997). 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).



2.7 Pearl millet

Scientific name

Pennisetum glaucum (L.) R. Br. (*Poaceae*)

Principal synonyms[23]

Pennisetum americanum L., *Pennisetum typhoides* auct. non. (Burm.) Stapf & C.E. Hubbard, *Chaetochloa glauca* (L.) Scribn., *Chaetochloa lutescens* (Weigel) Stuntz, *Panicum americanum* L., *Panicum glaucum* L., *Setaria glauca* (L.) Beauv., *Setaria lutescens* (Weigel) F.T. Hubbard

Global, regional and local importance

Pearl millet is a staple food grain and source of feed, fodder, fuel and construction material (ICRISAT, 2008). It is the fifth most important cereal crop and most important millet (more than 55% of global millet production) grown in over 40 countries, predominantly in Africa and Asia (ICRISAT, 2008). In West Africa, it is one of two main staple food crops[24] grown by smallholder farmers in marginal agricultural environments in semi-arid to arid regions (CCRP, 2008). Pearl millet is cultivated across 29 million ha and supports more than 100 million people. The major producing countries are Senegal, Mali, Burkina Faso, Niger, Nigeria, Chad, Sudan and India (India being the largest producer, both in terms of area and production), but the crop is most important to national food security in Namibia and Niger. It is also grown in Oceania and the Americas, predominantly as a forage and/or mulch component of minimum tillage-based cropping systems (ICRISAT, 2008). The secondary wild relative, *P. purpureum* Schum., is grown as a forage grass throughout the wet tropics (Brunken, 1977).

Taxonomic classification

Brunken (1977) (citing Pilger, 1940), states that *Pennisetum* L. Rich. is one of the largest genera in the tribe Paniceae (of subfamily Panicoideae), containing over 140 species; however, Watson and Dallwitz (1992) consider the genus to contain only about 80 species. The number of species in the genus remains uncertain. The genus was divided into five sections by Stapf and Hubbard (1934) based on morphological characters: *Gymnothrix, Eu-Pennisetum, Penicillaria, Heterostachya* and *Brevivalvula*. *P. glaucum* belongs to section *Penicillaria* (Martel *et al*., 2004), which is synonymous with section *Pennisetum* (Brunken, 1977). While *P. glaucum* is now generally accepted as the name of the crop, Terrell (1976) argued that the correct name for pearl millet is *P. americanum* (L.) Leeke. Brunken (1977) refers to the crop as *P. americanum* (L.) Leeke subsp. *americanum* and its closest wild relatives as *P. americanum* subsp. *monodii* (Maire) Brunken and *P. americanum* subsp. *stenostachyum* (Klotzsch ex A. Br. & Bouché) Brunken[25] Together with *P. purpureum*, these taxa comprise *Pennisetum* sect. *Pennisetum* (Brunken, 1977).

Wild relatives

Studies of the genetic relationships within *Pennisetum* have classified *P. glaucum* subsp. *monodii* and *P. glaucum* subsp. *stenostachyum* in GP1, *P. purpureum* as the only species in GP2 and the remaining species in GP3. However, recently, Akiyama *et al*. (2006) suggested the placement of *P. squamulatum* in the secondary gene pool, along with *P. purpureum*.

Primary wild relatives

- *Pennisetum glaucum* subsp. *monodii* (Maire) Brunken
- *P. glaucum* subsp. *stenostachyum* Kloyzcsh ex. A. Br. and Bouche

Secondary wild relatives

- *P. purpureum* Schum.
- *P. squamulatum* Fresen.[26]

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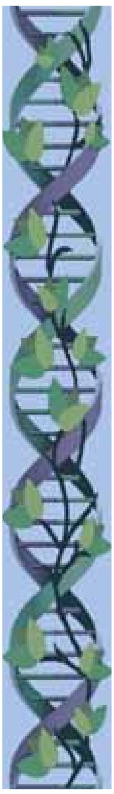
[23] ITIS (2007).

[24] The other main staple in these areas is sorghum.

[25] Index Kewensis recognizes the following authorities: *P. americanum* (L.) K. Schum., *P. americanum* subsp. *monodii* (Maire) J.N. Brunken, *P. americanum* subsp. *stenostachyum* (Klotzsch ex A. Braun & Bouche) J.N. Brunken.

[26] As suggested by Akiyama et al. (2006)



Tertiary wild relatives

All other species in the genus.

Distribution and centre of diversity

Pearl millet originated in western Africa and was introduced to eastern Africa and the Indian subcontinent around 2000 years ago (ICRISAT, 2008). The closest wild relatives are found in arid regions of West and East Africa (de Wet, 1995b).

Known uses of wild relatives in crop improvement

Due to the large amount of genetic variation available in *P. glaucum* landraces and breeding materials (Bhattacharjee *et al*., 2007), wild species have not been used extensively in breeding programs. However, there have been some successful targeted attempts (Rai *et al*., 1997); such as the use of *P. glaucum* subsp. *monodii* for resistance to leaf diseases, *P. purpureum* for forage traits, stiff stalk and restorer genes of the A_1 CMS (cytoplasmic-nuclear male sterility) system, and *P. squamulatum* for apomictic genes (Hanna, 1992). Wilson *et al*. (2004) found resistance to the hemi-parasitic weed, *Striga hermonthica* in accessions of the wild relative, *P. glaucum* subsp. *monodii*, while Mariac *et al*. (2006) report that, contrary to an earlier study, cultivated pearl millet accessions in Niger contain a significantly lower number of alleles and lower gene diversity than *P. glaucum* subsp. *monodii*, which showed marked variation between accessions. Mariac *et al*. (2006) concluded that "wild populations may be an interesting source of new alleles and new allele combinations, which could be useful to broaden the genetic basis of cultivated accessions". Wilson and Hanna (1992) note that in their evaluation of disease resistance in the primary and tertiary *Pennisetum* gene pool, resistance was more commonly found and more effective in wild species than in landraces.

In a study to investigate the potential of using wild relatives for genetic enhancement of some semi-arid food crops (including pearl millet), Kameswara Rao *et al*. (2003) note that although the use of wild species in the secondary and tertiary gene pools has generally been limited due to sterility, restricted recombination or cross incompatibility, these species are "extremely important" because they contain high levels of resistance to several important biotic and abiotic stresses. The authors note that while sources of resistance to diseases affecting pearl millet[27] have been identified in cultivated germplasm, when inoculum levels are high, the resistance can be overcome. In their review of the uses of pearl millet wild relatives, Kameswara Rao *et al*. (2003) found that several taxa in the tertiary gene pool have shown promise for crop improvement; including: *P. pedicellatum, P. polystachion, P. subangustum, P. schweinfurthii, P. setaceum, P. orientale* and *P. squamulatum*. As a result of hybridization experiments between pearl millet and some wild relatives, Marchais and Tostain (1997) concluded that the gene pool could be considerably enlarged using germplasm from a range of species using embryo rescue techniques.

Priority taxa

High priority taxa

- *P. schweinfurthii*, which is of limited distribution, occurring only in Ethiopia and Sudan (USDA, ARS, National Genetic Resources Program, 2008).

Other priority taxa

- *P. americanum* subsp. *monodii* (syn. *P. glaucum* subsp. *monodii*) – according to Brunken (1977), this primary wild relative occurs in the Sahel zone of West Africa "from the docks at Dakar to central Sudan". Specimens have also been collected in northern Ethiopia and the taxon is also "very common" in the foothills of the mountains of the central Sahara. The subspecies is a colonizer of sandy soils and disturbed habitats, such as seasonal stream beds and roadsides, and as a weed near human habitations (Brunken, 1977).
- *P. americanum* subsp. *stenostachyum* (syn. *P. glaucum* subsp. *stenostachyum*) – this primary wild relative is found "within and below" the Sahel region, from Senegal to Sudan, is especially common in western Senegal and has also been found in Angola and northern Southwest Africa (Brunken, 1977). Throughout its distribution, the taxon occurs as an agricultural weed in cultivated and recently abandoned pearl millet fields (Brunken, 1977).
- *P. purpureum* – the natural distribution range of this secondary wild relative is from "Guinea in the west, through the forest belt of West Africa, south through Angola and Rhodesia and in East Africa from Mozambique to southern

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[27] The four major diseases of pearl millet are downy mildew (*Sclerospora graminicola* (Sacc.) J. Schröt), smut (*Moesziomyces penicillariae* (Bref.) K. Vánky), ergot (*Claviceps fusiformis* Loveless) and rust (*Puccinia substriata* var. *indica* (Ellis & Barth.) Ramachar & Cummins) (Kameswara Rao et al., 2003).

Kenya" (Brunken, 1977). *P. purpureum* has been introduced to most of the world's wet tropics as a forage crop and has become naturalized in many places. It is a colonizing species preferring wet, disturbed sites, such as stream banks and roadsides. (Brunken, 1977)

- *P. squamulatum* – native to Northeast and East tropical Africa (Clayton *et al*., 2008; USDA, ARS, National Genetic Resources Program, 2008); specifically, Eritrea, Ethiopia, Kenya and Tanzania (USDA, ARS, National Genetic Resources Program, 2008).

Priority sites (High priority taxa)

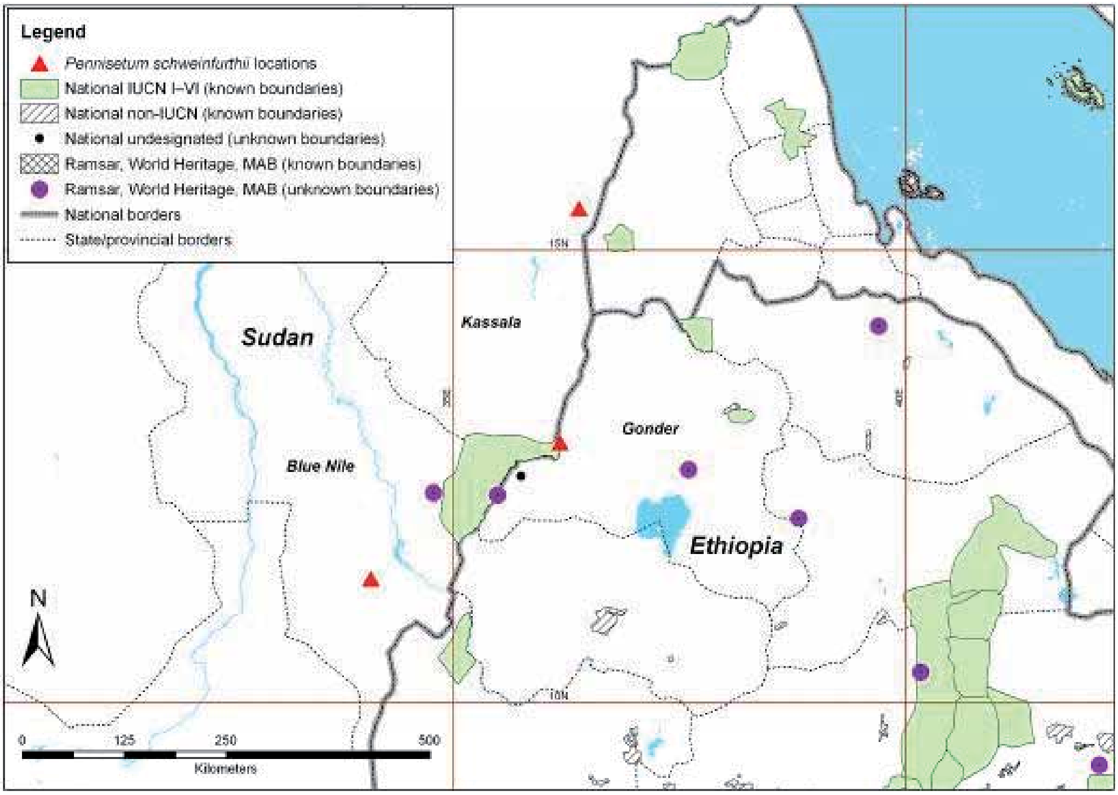
Pennisetum schweinfurthii is recorded as occurring in Sudan and Ethiopia. Ethiopian records are on the Sudan–Ethiopia border only (see Figure 14).

Recommendations

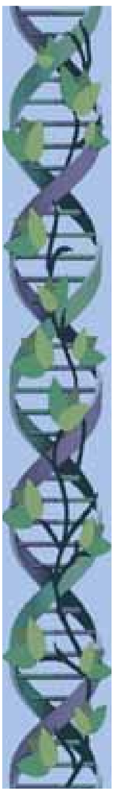
- An ecogeographic survey of *P. schweinfurthii* is needed in order to ascertain its current distribution and conservation status; however, based on our analysis, it is likely that the taxon is in need of immediate conservation action, both *in situ* and *ex situ*. Occurrences of the taxon near the towns of Gallabat (Sudan) and Metema (Ethiopia) could be inside the boundaries of Dinder National Park, Sudan (IUCN category II). The manager of this site should be contacted to try to ascertain whether the taxon can be found there. The analysis presented in Figure 14 indicates that the locations of other populations of the taxon (to the north in Kassala and to the southwest in Blue Nile, Sudan) are not protected.

FIGURE 14

Locations of *Pennisetum schweinfurthii*. Data recorded by SINGER (accessed through GBIF data portal, http://data.gbif.org/datasets/resource/1430 15/07/2008) and extrapolated from Herbarium W (Natural History Museum, Vienna) (accessed through GBIF data portal, http://data.gbif.org/datasets/resource/1479 15/07/2008)



- A detailed ecogeographic survey of *P. squamulatum* is required in order to establish its current distribution and to identify priority sites for its conservation *in situ*.
- Due to the wide range and colonizing habit of *P. americanum* subsp. *monodii*, *P. americanum* subsp. *stenostachyum* and *P. purpureum*, these taxa are not a high priority for inclusion in the genetic reserve network. However, detailed ecogeographic surveys may reveal distinct genetic diversity in some populations; in which case, representative populations should eventually be included in the network.
- All of the tertiary wild relatives listed by Kameswara Rao *et al*. (2003) as having shown promise for crop improvement, apart from *P. schweinfurthii* (i.e., *P. pedicellatum, P. polystachion, P. subangustum, P. setaceum* and *P. orientale*) are relatively widely distributed and therefore not of immediate conservation concern. *P. pedicellatum* and *P. polystachion* are both widely distributed in Africa and *P. pedicellatum* is also native to India (USDA, ARS, National Genetic Resources Program, 2008). The taxa are also naturalized elsewhere and are both declared as noxious weeds by the USDA Animal and Plant Health Inspection Service (USDA–APHIS) (USDA, ARS, National Genetic Resources Program, 2008). *P. subangustum* is native to and widely distributed in West and West–Central Tropical Africa (USDA, ARS, National Genetic Resources Program, 2008). *P. setaceum* is widely distributed in Africa, temperate Asia, Australasia, the Pacific and southeastern Europe (Clayton *et al*., 2008) and is declared a noxious weed in the United States (USDA, ARS, National Genetic Resources Program, 2008). *P. orientale* is distributed in North and Northeast tropical Africa, temperate and tropical Asia, the Pacific and the Caribbean (Clayton *et al*., 2008). Although these taxa may not be under threat throughout their range, efforts to collect and conserve genetically representative samples *ex situ* should be made to ensure that material is readily available for use in breeding programs.
- Bhattacharjee *et al*. (2007) note that the available genetic diversity in ICRISAT's pearl millet germplasm collection (which includes 750 accessions of a number of wild relatives) has not been adequately utilized due to a lack of proper evaluation data. Although the authors report that they have recently established an evaluated core collection of pearl millet germplasm, wild relatives are not included in this core collection. An *ex situ* gap analysis of the wild relatives of *P. glaucum* should be undertaken, fresh collections made as necessary and wild germplasm characterized and evaluated to aid use in breeding programs in the future.



2.8 Garden pea

Scientific name

Pisum sativum L.

Principle synonyms

Lathyrus oleraceus Lam., *Pisum vulgare* Jundz.

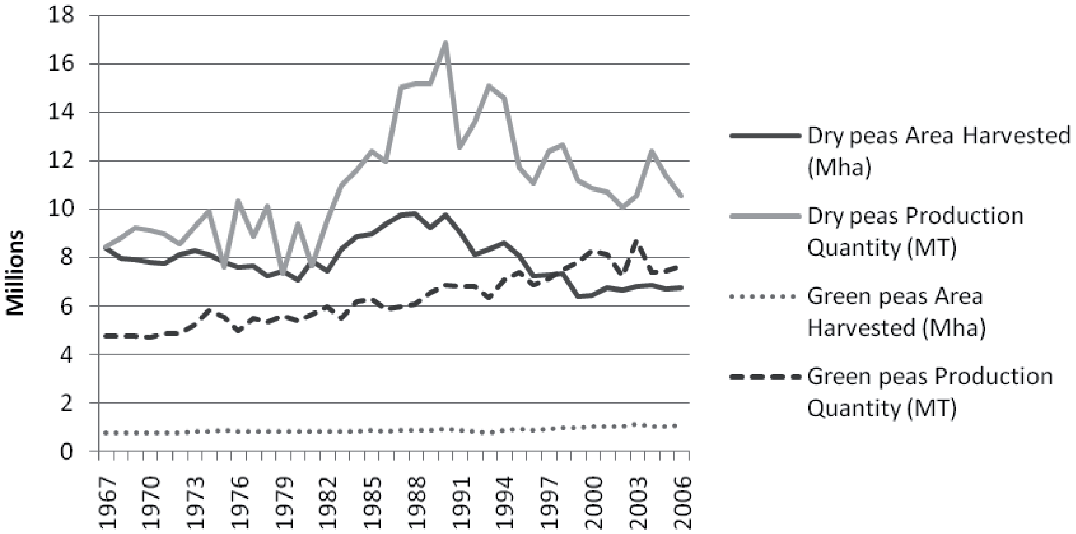
Global, regional and local importance

The garden or field pea is a diverse crop with relatively high intra-specific variation. It is cultivated across temperate regions of Asia, Europe and America and as a winter crop in highland tropical Africa. Pea has been cultivated for millennia, possibly because of the low levels of toxins in the seed (Liener, 1982) and the relatively high protein content of 25% (Monti, 1983). Peas remain today one of the most important temperate pulse, fodder and vegetable crops. Garden peas (*P. sativum* L. var. *sativum*) are produced primarily for human consumption; as a vegetable they are harvested and eaten either as immature pods (e.g., 'mangetout'), or as a green pea with seeds shelled from the pods and eaten fresh. In a number of developed countries, a significant proportion of the crop is now harvested in an immature state and frozen to make a convenience food or harvested as dry pea and canned. Field peas (*P. sativum* var. *arvense* (L.) Poiret) are usually harvested as dried seeds and are predominantly utilized as a fodder for domestic farm animals. They are also often used traditionally as a green manure or for enhancing soil fertility in a crop rotation.

Garden or field peas are the fourth most important legume pulse, with an estimated world production of approximately 10.5 Million tonnes for dry peas and 7.6 Mt for green peas, planted on approximately 7 million ha (6.7 m/ha dry peas and 1.0 m/ha green peas) in 2006 (FAO, 2008). The majority are used for pulse production and the remainder are largely frozen for convenience food production. Figure 15 indicates a steady global production of green peas, but dry pea production peaked in the early 1990s (FAO, 2008). Peas are well placed to meet increased global demand for high protein human and animal feed and to act as a leguminous break crop in diverse farming systems (Ambrose *et al*., 1997). It is therefore important to ensure that pea genetic resources are conserved and available for further exploitation and crop development.

FIGURE 15

World area harvested and production quantity for dry and green peas (FAO, 2008)



Taxonomic classification

Pisum sativum is taxonomically isolated from other cultivated legumes and is placed in a small genus with its wild relative, *P. fulvum* Sibth. & Sm. and *P. abyssinicum* A. Br. (Maxted and Ambrose, 2001). However, the diversity of the genus *Pisum* is not well understood, conserved or utilized, even though its conservation was given priority by the International Board for Plant Genetic Resources (IBPGR, 1985). The genus *Pisum* is a member of the legume tribe Vicieae of subfamily Papilionoideae, along with *Lathyrus* L., *Lens* Mill., *Vavilovia* A. Fedorov and *Vicia* L. The genus is distinguished from related genera by the presence of relatively large, leafy stipules, which are semi-amplexical around the terete stem. The genus is most closely related to the monospecific genus Vavilovia, which contains the one dwarf, perennial, alpine species, *V. formosa* (Stev.) A. Fed. (formerly regarded as the *Pisum* species, *P. formosum* (Stev.) Boiss.), an endemic of high altitude areas in the Middle East.

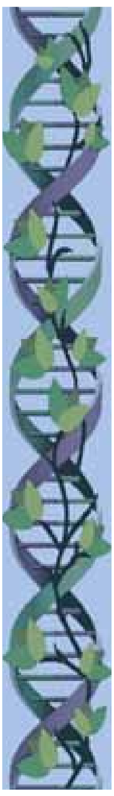
There has been some agreement in the literature over the number of taxa in the genus but much dispute over their rank. Boissier (1872) recognized four annual species: *P. elatius* Bieb., *P. humile* Boissier and Noë, *P. fulvum* and *P. formosanum* (Stev.) Alef. (syn. *V. formosa*). The former three have subsequently remained key taxa within the genus. Their inter-relationships and taxonomic position was partially clarified by breeding experiments undertaken by Ben-Ze'ev and Zohary (1973). They found when crossing the putative species, *P. sativum, P. elatius, P. humile* and *P. fulvum*, that *P. sativum, P. elatius* and *P. humile* were completely inter-fertile and only *P. fulvum* was more isolated, and thus deserving of specific distinction from *P. sativum*. Therefore, the classification proposed by Davis (1970), which recognized two species and multiple subspecific taxa within *P. sativum*, has largely been adopted. The classification produced by Davis (1970) resulted from a national flora so does not include taxa found outside of the Middle East; therefore, it is not fully comprehensive. Importantly, the primarily Ethiopian taxon, *P. abyssinicum* A. Br., was not considered and on the basis of diverse sources of evidence (Kloz, 1971; Przybylska *et al*., 1983; Parzysz and Przybylska, 1984; Ambrose, 1992; Ellis *et al*., 1998), this species also deserves specific rank.

Smartt (1990) makes the point that widely cultivated species often suffer highly disrupted selection pressures, which leads to the production of extreme morphological variants. These are often subsequently given taxonomic rank (e.g., 'mangetout' pea has been given specific status as *P. macrocarpum* Ser. ex Schur, but it is known that pod size is under simple genetic control and therefore this rank would appear unwarranted). Thus, within *P. sativum*, the description of subspecies and varieties has proliferated. Maxted and Ambrose (2001), following their review of the literature, proposed the adoption of a simple infra-specific classification of two subspecies and varieties (see Table 4). Subsequently, as a result of a study of plastid, mitochondrial and nuclear genomes, Kosterin and Bogdanova (2008) identified a third *P. sativum* subspecies, subsp. *jomardii* (Schrank) Kosterin; but this taxa has still to be generally accepted.

TABLE 4

Classification of *Pisum* taxa (Maxted and Ambrose, 2001)

Species	Subspecies	Varieties
P. sativum L.	*sativum*	*sativum*
		arvense (L.) Poiret
	elatius (Bieb.) Aschers. & Graebn.	*elatius*
		brevipedunculatum Davis & Meikle
		pumilio Meikle (syn. P. humile Boiss. & Noë)
P. abyssinicum A. Br.		
P. fulvum Sibth. & Sm.		



Wild relatives

Qualitative and quantitative characterization data (Ambrose, 1992; Amurrio *et al*., 1995) and molecular techniques are being used to identify taxonomic groupings (Hoey *et al*., 1996; Lu *et al*., 1996; Ambrose *et al*., 1997; Kosterin and Bogdanova, 2008) and this is providing insight into the phylogenetic relationship both between *Pisum* species and within *P. sativum*. All *Pisum* taxa are inbreeders with a diploid number of 2n=14 (Ben-Ze'ev and Zohary, 1973). The taxa within *P. sativum* are fully inter-fertile and crosses between *P. sativum* and *P. fulvum* are possible (Ben-Ze'ev and Zohary, 1973; Ochatt *et al*., 2004), particularly if *P. sativum* is the female parent (Ben-Ze'ev and Zohary, 1973). A small number of crosses between *Pisum* and *V. formosa* made at the N.I. Vavilov Institute of Plant Industry (St. Petersburg, Russia) have also proven successful if *P. fulvum* is the female parent; however, the two resultant F_1 hybrid plants were not viable (A. Golubev, pers. comm.).

Primary wild relatives

- *Pisum sativum* L. subsp. *arvense*
- *P. sativum* subsp. *elatius* var. *elatius*
- *P. sativum* subsp. *elatius* var. *brevipedunculatum*
- *P. sativum* subsp. *elatius* var. *pumilio* (syn. *P. humile*)

Secondary wild relatives

- *P. abyssinicum* A. Br.
- *P. fulvum*

Tertiary wild relatives

- *Vavilovia formosa*

Distribution and centre of diversity

P. sativum is naturally found in Europe, Northwest Asia and extending south to temperate East Africa, while *P. fulvum* is more restricted to the Middle East and *P. abyssinicum* is an endemic of Ethiopia and Yemen. Maxted and Ambrose (2001) summarized the ecogeographic distribution and cultivation status for *Pisum* taxa (see Table 5). It is difficult to provide precise details for the centre of diversity for the crop taxa because their range has been modified significantly by human activities during the millennia it has been cultivated. Its cultivation is mentioned by Greek and Roman writers in the 500 BC (Roy Davies, 1995). Carbonized peas are found during excavations of Neolithic sites from c. 7 000 BC. Zohary and Hopf (2000) conclude that cultivation of peas pre-dates wheat and barley. Vavilov (1949) considered the centre of origin for peas was Ethiopia, the Mediterranean and central Asia, with a secondary centre in the Near East. Archaeological evidence suggests that this was the area of crop domestication (Zohary and Hopf, 1973).

Known uses of wild relatives in crop improvement

All taxa within *P. sativum* are fully inter-fertile and crosses between *P. sativum* and *P. fulvum* are possible, though difficult (Ben-Ze'ev and Zohary, 1973; Ochatt *et al*., 2004). Crosses between *Pisum* taxa and *V. formosa* have shown limited success as the F1 hybrid plants were not viable (A. Golubev, pers. comm.). Thus, most use of CWR has been in using the *P. sativum* subsp. *elatius* varieties (Hance *et al*., 2004), with much more limited use of *P. fulvum*. Forster *et al*. (1999) used a mutant line of *P. fulvum* that lacked seed lipoxygenase-2 (LOX-2) to introgress with *Pisum sativum* cv. Birte and produce near-isogenic lines with or without seed LOX-2, which in turn generated relatively less 13-hydroperoxides and produced relatively more hydroxy and ketoacid compounds that have implications for the fresh-frozen pea industry of increased disease (*Ascocyta pisi* and *Erysipi pisi*) and pest resistance (bruchids). Fondevilla *et al*. (2007) also found a new gene for resistance to powdery mildew (*Erysipi pisi*) in accessions of *P. fulvum*. Pea weevil, *Bruchus pisorum* L. (*Coleoptera: Bruchidae*) remains one of the most intractable pest problems of cultivated pea, but significant weevil resistance has been found in *P. fulvum* that could be used to endow pea cultivars with pod and/or seed resistance to *B. pisorum* (Clement *et al*., 2002). Crosses between *P. fulvum* as the pollen parent with *P. sativum* cv. Wirrega, using wild type *P. sativum* JI 252 as a bridging cross, identified two sources of partial resistance to ascochyta blight (*Mycosphaerella pinodes*), which together significantly reduced foliage infection (Wroth, 1998). Pea bacterial blight (*Pseudomonas syringae* cv. Pisi) occurs worldwide and can cause severe damage under cool and wet conditions, but resistance to all seven blight races has been found in *P. abyssinicum* and this resistance is now used in commercial cultivars (Elvira-Recuenco, 2000; Elvira-Recuenco *et al*., 2003). This finding has been further explored by Hollaway *et al*. (2007) who describe attempts to commercialize race non-specific resistance identified from *P. abyssinicum* into field pea. Elvira-Recuenco (2000) also showed that endophytic bacteria (predominantly Gram-negative bacteria, including *Pseudomonas* sp., *Pantoea agglomerans*, *Arthrobacter* sp. and *Curtobacterium* sp.) offer a source of biological control via their ability to suppress bacterial blight.

TABLE 5

Geographic distribution of Pisum and *Vavilovia* taxa (Maxted and Ambrose, 2001)

Taxon	Geographic distribution	Cultivation status	Ecological preferences
P. sativum subsp. *sativum* var. *sativum*	Pan-temperate	Crop	Cultivated & spontaneous
P. sativum subsp. *sativum* var. *arvense*	Europe and Southwest Asia	Crop	Cultivated & spontaneous
P. sativum subsp. *elatius* var. *elatius*	Eastern Mediterranean and Southwest Asia	Wild	Rocky & grassy slopes, forest & field margins, scrub, ruins, 0 – 1,700m
P. sativum subsp. *elatius* var. *brevipedunculatum*	Cyprus and Turkey	Wild	Fields, vineyards & roadsides, 700 – 1,000m
P. sativum subsp. *elatius* var. *pumilio*	Eastern Mediterranean and Southwest Asia	Wild	Open scrub, rocky slopes & fallow fields, 700 –1 ,800m
P. abyssinicum	Ethiopia and Yemen	Crop/wild	Cultivated & spontaneous
P. fulvum	Eastern Mediterranean and Southwest Asia	Wild	Rocky limestone slopes, & dwarf shrubland, 30 – 1,500m
V. formosa	Caucasus and Southwest Asia	Wild	Loose limestone scree, > 1,500m

Priority taxa

High priority taxa

- *P. abyssinicum*
- *P. sativum* subsp. *elatius* var. *brevipedunculatum*

Other priority taxa

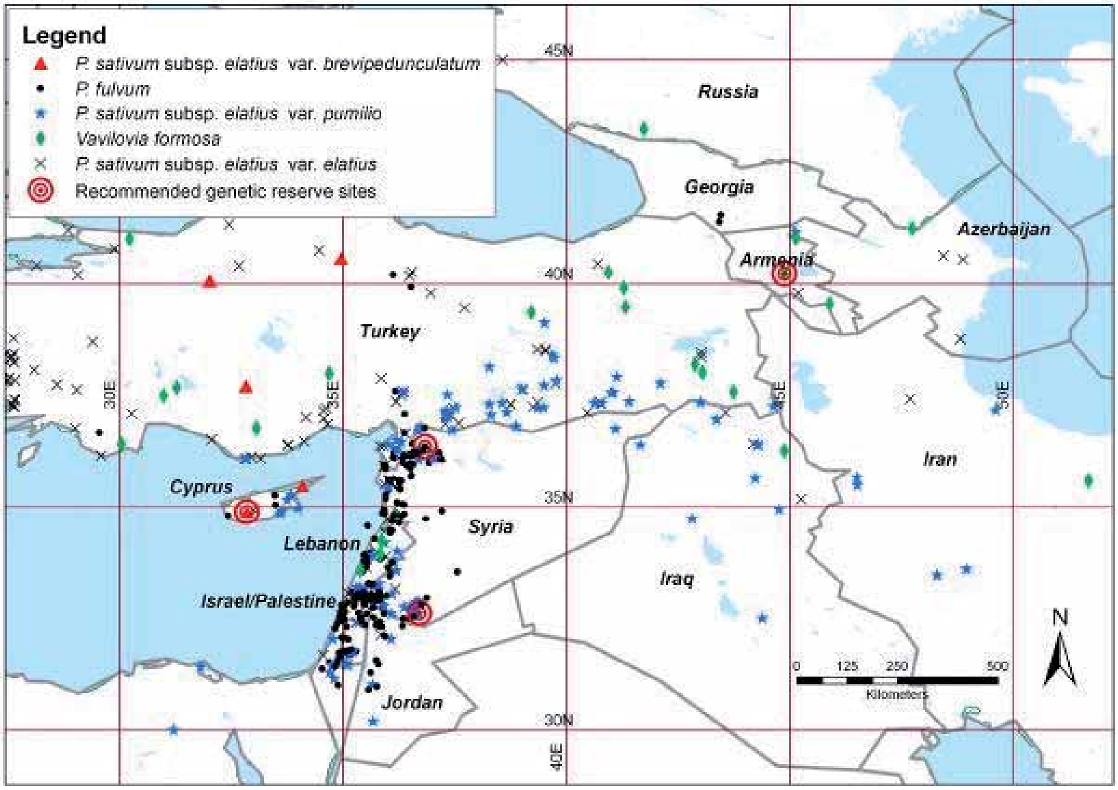
- *P. fulvum*
- *P. sativum* subsp. *elatius* var. *pumilio*
- *Vavilovia formosa*

Priority sites

Wild *Pisum* taxa naturally occur in 21 countries at the junction of Asia, Europe and Africa; but Turkey, Syria, Cyprus and Israel/Palestine harbour the highest number of populations, while *V. formosa* is more restricted, being found in high altitude areas of Turkey, Lebanon, Iraq, Iran, Armenia, Azerbaijan, Georgia and bordering areas of Russia (Figure 16). The high priority taxon, *P. sativum* subsp. *elatius* var. *brevipedunculatum* is only known from a few locations in Cyprus, Turkey and Syria. *P. abyssinicum* is poorly known and rarely studied, being restricted to Ethiopia and Yemen (see Figure 17), at some distance from the main centre of *Pisum* diversity. Mumtaz (2005) undertook complementarity analysis using the Rebelo and Siegfried (1992) methodology via Diva GIS (Hijmans *et al*., 2001) and suggested the establishment of two genetic reserves to conserve *Pisum* diversity—one near the border of Hatay province in southern Turkey and in Aleppo province in Northwest Syria and another in Southwest Syria on the Israel/Palestine and Jordanian border. In a recent review of *V. formosa* in Armenia (Akopian and Gabrielyan, 2008), the perennial species was found to be highly endangered and the establishment of a protected area was recommended.

FIGURE 16

Locations of priority *Pisum* wild relatives, *P. sativum* subsp. *elatius* var. *brevipedunculatum*, *P. fulvum*, *P. sativum* subsp. *elatius* var. *pumilio* and *Vavilovia formosa* (primary data source: Mumtaz, 2005), with additional records for *P. fulvum* accessed via GBIF[28] and additional records for V. formosa from Akopian and Gabrielyan (2008) and EURISCO (accessed through GBIF data portal, http://data.gbif.org/datasets/resource/1905 18/07/2008). Locations of *P. sativum* subsp. *elatius* var. *elatius* are also shown (Mumtaz, 2005). Although this taxon is not a high priority due to its extensive distribution (which extends into western and northern Europe), it may be conserved within the some of the same sites as the priority taxa



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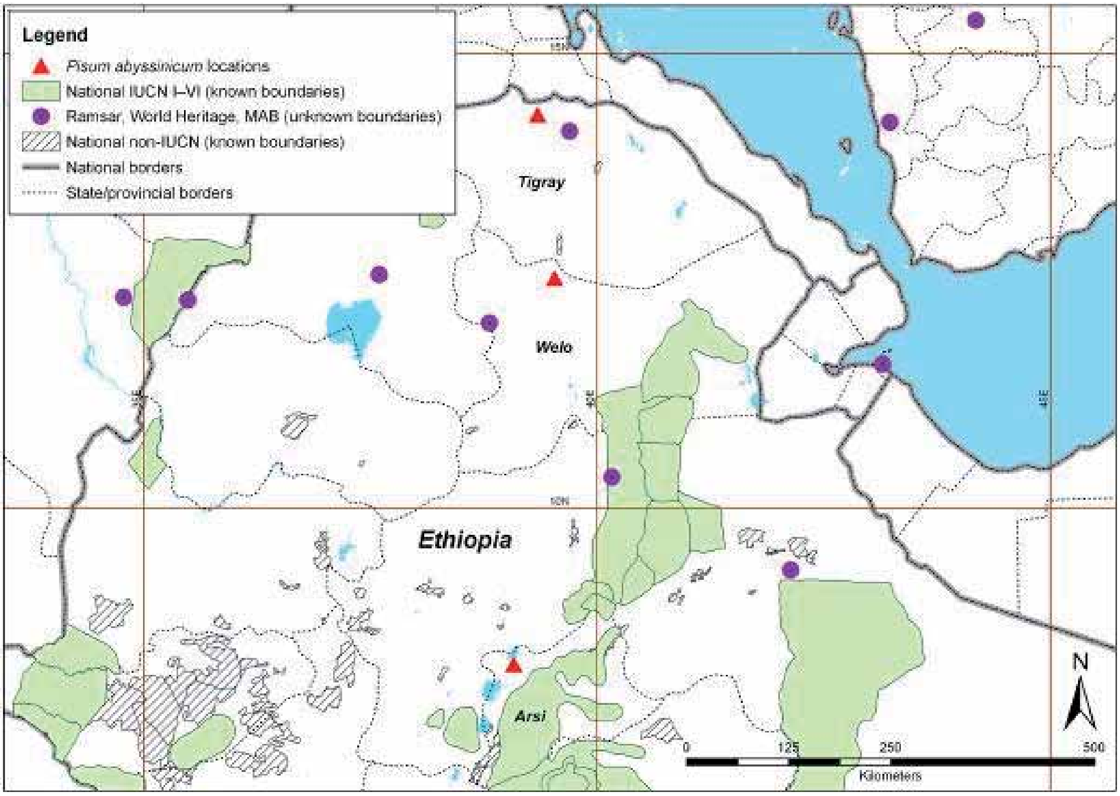
[28] From SINGER (accessed through GBIF data portal, http://data.gbif.org/datasets/resource/1430 18/07/2008), NPGS (http://data.gbif.org/datasets/resource/1429 18/07/2008), Israel Nature and Parks Authority (http://data.gbif.org/datasets/resource/1431 18/07/2008) and CIBIO, Alicante:ABH-GBIF (http://data.gbif.org/datasets/resource/251 18/07/2008).

FIGURE 17

Locations of *Pisum abyssinicum*. Data source: SINGER (accessed through GBIF data portal, http://data.gbif.org/datasets/resource/1430 18/07/2008)



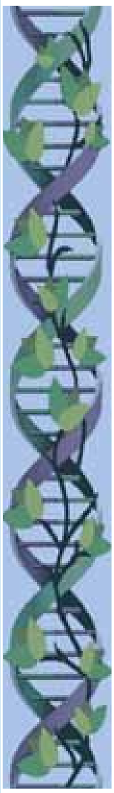
Based on this analysis, specific sites to conserve *Pisum* and *Vavilovia* should be located at:

- Troodos Mountains, Limassol, Cyprus (34.8833N, 32.8547E), near the village of Phini. One of only a few recorded locations of *P. sativum* subsp. *elatius* var. *brevipedunculatum*. This is the only recorded location close to an existing protected area (Troodos National Forest Park, IUCN category II). Further searches may reveal locations within this protected area.
- Jabal Simeon, Aleppo province, Syria (36 20 02.65N, 36 50 37.47E). This would be a good option for a single reserve as there are significant local populations of *P. fulvum* and *P. sativum* subsp. *elatius*, as well as significant populations of other forage legume and cereal CWR present. The local presence of the citadel of St. Simeon means the area already has some level of protection and there is potential of associated eco-tourism, so designation and site protection should be a priority.
- Salkhad, Suweida province, Syria (32 36 25N, 36 43 02E). This is a good general site for *Pisum* with *P. fulvum, P. sativum* subsp. *elatius* var. *elatius* and var. *pumilio*, as well as significant populations of other forage legume and cereal CWR.
- Akna Lich, Geghama mountain ridge, Yerevan province, Armenia (40 13 19.43N, 44 53 17.31E). This location has the largest known population of *V. formosa* in Armenia, with approximately 1200 individuals growing in an area of about 2 ha. The site was identified during the recent UNEP/GEF project, '*In situ* conservation of crop wild relatives through enhanced information management and field application', and thus already has a level of protection.

Recommendations

- *Pisum* CWR are not currently being actively conserved *in situ*, though as noted above the establishment of *V. formosa* genetic reserves in Armenia has been suggested (Akopian and Gabrielyan, 2008). Like many other groups of CWR species, some wild *Pisum* taxa are currently found within existing protected areas (national parks, wildlife reserves, etc.), but here they are being 'passively' conserved (species and genetic diversity is not being actively monitored and managed) and thus they are susceptible to genetic erosion and possible extinction.

- Wild *P. abyssinicum* has only been recorded at three locations in Ethiopia[29] (in Tigray, Welo and Ārsī provinces). This taxon is a high priority for conservation action. Our analysis indicates that it is not found within existing protected areas. On the basis of current knowledge it is not possible to make suggestions regarding an appropriate conservation strategy for this taxon, but given that both cultivated and wild forms are found, it deserves increased attention. Immediate steps should be taken to undertake a comprehensive ecogeographic survey to verify locations and recommendations should be made for genetic reserve establishment at suitable sites.
- *P. sativum* subsp. *elatius* var. *brevipedunculatum* has a very limited distribution and should be targeted for immediate conservation action. Our analysis indicates that none of the known locations of this taxon are found within an existing protected area. However, one population in Southwest Cyprus is near Troodos National Forest Park (IUCN category II). Local searches should be carried out to ascertain whether the taxon may be found within this protected area and if found, the population(s) should be actively monitored and managed.
- Genetic reserves should be established at the two sites in Syria suggested by Mumtaz (2005) (to conserve *P. fulvum*, *P. sativum* subsp. *elatius* var. *pumilio* and *P. sativum* subsp. *elatius* var. *elatius*). The site suggested by Akopian and Gabrielyan (2008) to conserve *V. formosa* should also be established. Further sites for *V. formosa* should be established following a detailed ecogeographic survey of this taxon.
- Our analysis indicates that Lebanon is a hot-spot for all the priority taxa. A detailed study of the distribution of the taxa in Lebanon should be undertaken and reserves established to conserve these western Mediterranean populations.
- Although there are relatively large *ex situ* seed collections of cultivated (76,000—FAO, 1998) and wild (approx. 500—Maxted and Ambrose, 2001) *Pisum* accessions, the collections are not comprehensive in terms of taxon or genetic diversity and there remain numerous gaps in conserved materials—notably for Ethiopian material of *P. abyssinicum* and *V. formosa* (Maxted and Ambrose, 2001). As well as the need to establish genetic reserves and for further germplasm collection, there is a complementary need to take positive steps to ensure *in situ* on-farm conservation of landrace diversity in countries that retain high levels of landrace cultivation; such as Albania, Armenia, Ethiopia, Iran, Morocco, Portugal, Syria, Turkey and Yemen.



2.9 Potato

Scientific name

Solanum tuberosum L.

Principle synonyms

S. esculentum Neck., *S. sinense* Blanco, *S. chilense* (DC.) Berth., *S. cultum* (DC.) Berth., *S. sabinii* (DC.) Berth., *S. maglia* Schlechtd., *S. molinae* Juz., *S. leptostima* Juz.

Global, regional and local importance

Potato production represents roughly half of the world's annual output of all roots and tubers (Hawkes *et al*., 2000). The crop is eaten by over one billion people worldwide and is part of the diet of half a billion consumers in developing countries (FAO/CIP, 1995). Today, potato (*Solanum tuberosum* L.) is widely cultivated in most parts of the world, but was originally restricted to the Andes mountains of South America (Colombia, Venezuela, Ecuador, Peru, Bolivia) and the coastal regions of southern Chile (Hawkes, 1990). The crop was first brought to Europe in the late 16th century and has now become adapted to cool, warm, temperate and many tropical regions of the world (Hawkes, 1990). *S. tuberosum* has an annual production of 315 million tonnes (FAO, 2008). Several other species are cultivated in the Andes and the economic value of these is without doubt high, though impossible to calculate. Potato is however the most important tuber crop, planted on approximately 19 million ha in 2006 (FAO, 2008). Figure 18 indicates a steady global production of potato with an increase since 2000 (FAO, 2008). The five highest producers are China, Russian Federation, India, United States of America and the Ukraine with 70.3, 38.5, 23.9, 19.7 and 19.4 million tonnes of production, respectively in 2006, while Peru, the centre of diversity, grew 3.3 MT (FAO, 2008). Potato originated in the Andes of South America but is important to food security not only in this region but also in North America, Europe and higher altitude regions of Asia (FAO, 2008).

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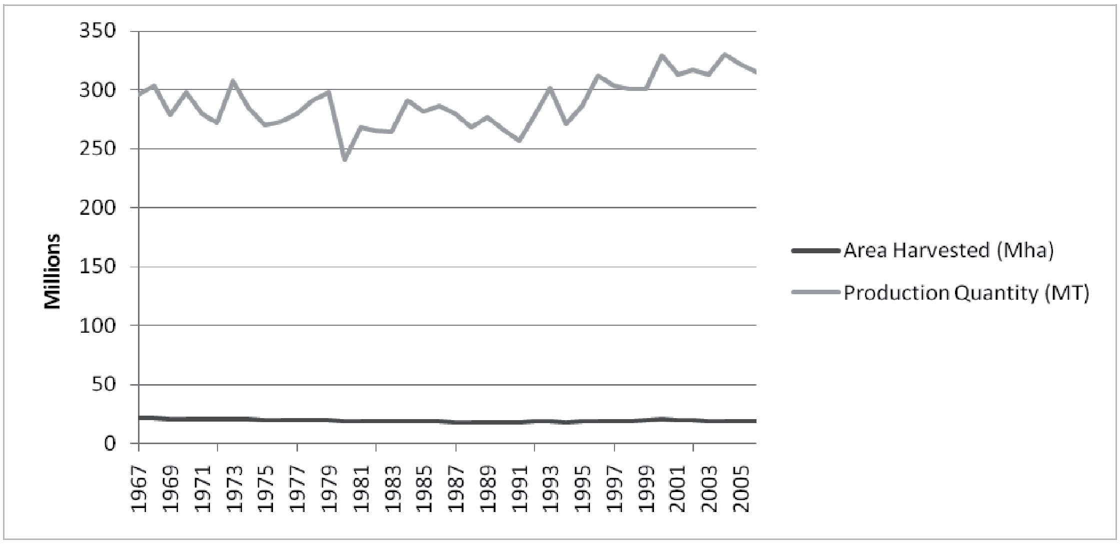
[29] Collections of cultivated material have also been made at other locations (mainly markets) in Ethiopia.

FIGURE 18

World area harvested and production quantity for potato (FAO, 2008)

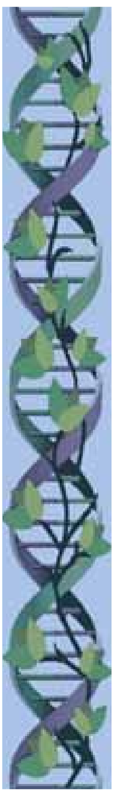


Hawkes (1999) noted that when we talk about the potato, there are in fact seven cultivated taxa known in the Andes (referred to either as species or cultivar groups), with diploid, triploid, tetraploid and pentaploid chromosome numbers, but the tetraploid *S. tuberosum* is the only one to have become a crop of global significance. The other cultivated species are the diploids (2n=24), *S. stenotomum* Juz. and Buk. (thought by Hawkes to be the original cultivated species), *S. phureja* Juz. and Buk. and *S. ajanhuiri* Juz. and Buk., two triploids (2n=36), *S. chaucha* Juz. and Buk. and *S. juzepczukii* Buk., one tetraploid (2n=48), *S. tuberosum*, and one pentaploid (2n=60), *S. curtilobum* Juz. and Buk. Although the cultivated *S. tuberosum* is tetraploid (2n=48), its wild relatives range from diploid (2n=24) to hexaploid (2n=72).

The cultivation of traditional potato cultivars of *S. tuberosum* subsp. *andigena* is most widespread in the highlands of Venezuela, Colombia, Ecuador, Peru, Bolivia and northern Argentina, and to a lesser extent in Mexico and Guatemala, primarily at altitudes of 2 000–4 000 m (Huamán *et al*., 1997). The cultivation of other species is more restricted—ancient cultivars of *S. tuberosum* subsp. *tuberosum* are restricted mainly to Chiloe Island in southern Chile at about sea level, *S. stenotomum, S. goniocalyx* and *S. x chaucha* are primarily cultivated from northern Peru to central Bolivia between 3 000 and 3 900 m, *S. phureja* is the only species cultivated in the warmer Andean valleys of Venezuela, Colombia, Ecuador, Peru and Bolivia from 2 000–3 700 m, while cultivation of other species is rarer and scattered and may have resulted from recent introductions. The hybrids *S.* x *curtilobum*, *S.* x *juzepczukii* and *S.* x *ajanhuiri* are cultivated in restricted areas of Peru, Argentina and Bolivia at 3800–4200m and as a result show excellent frost tolerance (Huamán *et al*., 1997).

Taxonomic classification

In their review of the taxonomy of wild potato, Hijmans *et al*. (2002) refer to *Solanum* as having a dynamic taxonomy, which appears entirely apt as there remain numerous classifications of the potato and its relatives. However, potato belongs to the family Solanaceae, which contains approximately 2 300 species (primarily herbs, with a few shrub or tree species) divided into 96 genera and three subfamilies (D'Arcy, 1986, 1991). The highest concentration of species is in South America, suggesting the family is likely to have originated in that subcontinent (Hawkes *et al*., 2000). The family is composed of a few large genera (*Solanum* – about 1 000 species, *Cestrum* – 175 species, *Lycium* – 75 species, *Physalis* – 75 species, *Nicotiana* – 95 species and *Cyphomandra* –50 species) and many genera with smaller numbers of species (D'Arcy, 1991). The tuber-bearing *Solanum* species are restricted to section *Petota*, which are distributed from south-western United States to Mexico, Central America and the western region of South America. Within the section D'Arcy (1991) recognizes approximately 225 species, but Spooner and Hijmans (2001) have a slightly more restricted circumscription of 196 species, having transferred the non-tuber bearing species to section *Etuberosum*. Section *Petota* is divided into 3 subsections and 19 series (D'Arcy, 1986, 1991) and *S. tuberosum* is placed in subsection *Petotoe* series *Tuberosa* (Nee, 1999). This series contains a differing number of cultivated taxa—21 species (Lechnovich, 1971), 7 species (Hawkes, 1990), 9 species (Ochoa, 1990), or as a single species, *S. tuberosum*, with eight cultivar groups (Huamán and Spooner, 2002). The most comprehensive recent classification of the whole genus *Solanum* is provided by (Nee, 1999).



Wild relatives

The potato gene pool is unusual in terms of a crop/CWR complex in that there is a significant number of both cultivated and relatively closely related wild species, although *S. tuberosum* does predominate in terms of scale of cultivation (Hawkes, 1990). As a result it can be argued that the primary wild relatives of *S. tuberosum* are other cultivated species of *Solanum* in section *Petota* subsection *Potatoe* series *Tuberosa* placed alongside *S. tuberosum*, and the secondary wild relatives are the wild species of the same series. However, Hawkes (1990) divides series *Tuberosa* into four groups of species—the cultivated species are placed in Group iv and the implication is that the closest wild relatives of the cultivated taxa are found in Group iii, so these are the secondary wild relatives, with other *Solanum* species constituting the tertiary wild relatives. Hijmans *et al*. (2002) state that within section *Petota* many of the species at the same ploidy and Endosperm Balance Number levels, even those that are morphologically distinct, freely cross to form fertile hybrids and approximately 13% (26) of the 196 tuber-bearing *Solanum* species have been hypothesized to have arisen by hybrid speciation. Further, Hawkes and Hjerting (1969, 1989) believed that inter-specific hybridization that did not necessarily lead to full speciation was common in section *Petota*, a situation in part confirmed by molecular evidence (Rabinowitz *et al*., 1990; Clauson and Spooner, 1998). Hijmans *et al*. (2002) conclude that the extent and effect of hybridization in wild potatoes is still an open question, which makes the attribution of *Solanum* taxa into the primary, secondary and tertiary gene pool in the conventional Harlan and de Wet (1971) sense premature. Nonetheless, even though the Hawkes (1990) conception is no longer universally accepted, it can be used until such time that further research into the potato gene pool provides us with better knowledge of the genetic relationships between taxa.

Primary wild relatives

Solanum section *Petota* subsection *Potatoe* series *Tuberosa* Group iv:

- *Solanum stenotomum* Juz. and Buk.
- *S. phureja* Juz. and Buk.
- *S. ajanhuiri Juz. and Buk.*
- *S. chaucha* Juz. and Buk.
- *S. juzepczukii* Buk.
- *S. curtilobum* Juz. and Buk.

Secondary wild relatives

Solanum section *Petota* subsection *Potatoe* series *Tuberosa* Group iii:

- *S. achacachense* Cárd.
- *S. alandiae* Cárd.
- *S. avilesii* Hawkes & Hjerting
- *S. berthaultii* Hawkes
- *S. brevicaule* Bitter
- *S. candolleanum* Berth.
- *S. gandarillasii* Cárd.
- *S. gourlayi* Hawkes (syn. *S.* × *bruecheri*)
- *S. hondelmannii* Hawkes & Hjerting
- *S. hoopesii* Hawkes & Okada
- *S. incamayoense* Okada & Clausen
- *S. kurtzianum* Bitter & Wittrn.
- *S. leptophyes* Bitter
- *S. microdontum* Bitter
- *S. neocardenasii* Hawkes & Hjerting
- *S. neorossii* Hawkes & Hjerting
- *S. okadae* Hawkes & Hjerting
- *S. oplocense* Hawkes
- *S. sparsipilum* (Bitter) Juzepczuk & Bukasov, in Buk.
- *S. spegazzinii* Bitter
- *S. ugentii* Hawkes & Okada
- *S. venturii* Hawkes & Hjerting
- *S. vernei* Bitter & Wittrn.
- *S. virgultorum* (Bitter) Cárd. & Hawkes

Tertiary wild relatives

Other *Solanum* species

Distribution and centre of diversity

The genus *Solanum* is geographically widespread; most are tropical, whilst the tuber-bearing species tend towards warm temperate and cool climatic zones (D'Arcy, 1991) from the Southwest United States southwards through Mexico and Central America into the western parts of South America and the region of southern Brazil, Argentina and Chile. The distribution of the taxa of section *Petota* have been extensively mapped by Hijmans *et al*. (2002) and they are found from sea level to 4 500m, with the series *Tuberosa* species showing a correlation with the higher altitude areas of Central and South America. Their main centres of diversity are, however, situated in south–central Mexico in an area lying between approximately 16º and 20º north and in South America where there is a wider area of diversity, lying in the Andes and adjacent regions, from North Peru (5º S) to Northwest Argentina (25º S) (Hawkes, 1990). Wild potato occurs in a wide variety of habitats, including high altitude Andean grasslands (puna and paramo vegetation), dry deciduous forests in Mexico, strand vegetation along Chilean beaches, and cool upland rain forests in the eastern Andes (Hijmans *et al*., 2002). In Mexico and the USA, wild potato is commonly found in such different environments as scrub and cactus vegetation, and pine, fir and oak forests (Hawkes, 1990). Some of the wild species are gathered occasionally for food and many have potential in providing genes for disease and pest resistance for the potato crop.

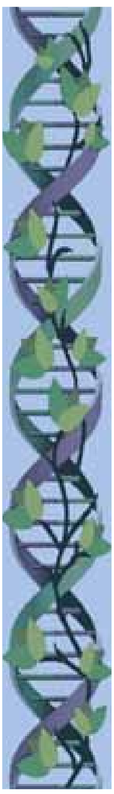
In their GIS analysis of wild potato, Hijmans *et al*. (2002) found that using 50 km2 grid cells, Bolivia, Peru and Argentina had the highest *Solanum* species richness (with 19, 17 and 17 species per grid cell), followed by Mexico (with cells containing 12 species) and Ecuador (with 9 species) (Table 6). Only 6% of the cells have ten or more species, while 46% of the cells only have one species. The highest number of species in a single grid cell was 19, found in the department of Potosi in Bolivia. Other grid cells with high species richness (17 species) are found in the adjacent cell to Potosi in the Peruvian department of Ancash and in Jujuy province of northern Argentina. Peru has the most species overall and although its most species-rich areas are comparable in species richness to those of Bolivia, overall, Peru has the highest number of endemic species.

TABLE 6

Grid-based species richness statistics by country (Hijmans *et al.*, 2002)

Country	No. of grid cells with one or more observation	Mean no. of spp. per grid cell	Mean no. of observations per grid cell	Highest no. of spp. per grid cell	Concentration of species richness
Argentina	288	2.4	16.4	17	65
Bolivia	114	6.4	40.3	19	53
Brazil	60	1.0	1.4	2	67
Chile	11	1.1	2.3	2	100
Colombia	65	1.9	7.3	4	31
Costa Rica	12	1.0	6.5	1	100
Ecuador	36	4.1	12.4	9	56
Guatemala	18	3.4	12.4	6	120
Honduras	5	1.2	1.2	2	100
Mexico	275	3.2	10.7	12	33
Panama	5	1.6	8.2	2	100
Paraguay	24	1.3	2.6	2	100
Peru	230	4.6	19.3	17	19
Uruguay	24	1.2	1.8	2	100
USA	118	1.2	3.9	2	67
Venezuela	11	2.2	7.0	3	100

Apart from *S. tuberosum* subsp. *tuberosum*, all the other cultivated species are confined to the Andes of South America (Hawkes, 1990). Within Peru alone, 90 wild potato species have been described, but 35 are no longer found in the wild (FAO, 1997). The cultivated potato centre of diversity lies in the Andes from about 10º S to about 20º S, with a minor centre in southern Chile (35º S to 45º S) (Hawkes and Hjerting, 1969). Of the two subspecies of *S. tuberosum,* the more primitive subsp. *andigena* is confined to the Andes Cordillera, whilst subsp. *tuberosum* was originally cultivated in the coastal regions of south–central Chile. The other cultivated taxa range from Venezuela southwards through Colombia, Ecuador, Peru, Bolivia and northern Argentina, with a centre of diversity in southern Peru to Central Bolivia, and are not cultivated outside of South America.



Known uses of wild relatives in crop improvement

There has been extensive use of wild relatives in potato breeding[30]; for example, resistance to late blight has been introgressed into cultivated potato from *S. demissum* and *S. stoloniferum* and resistance to viruses has been introgressed from these species, together with *S. chacoense* and *S. acaule* (Ross, 1986; Bradshaw *et al*., 2006). Resistance to potato cyst nematodes has come from *S. multidissectum, S. kurtzianum, S. oplocense, S. vernei* and *S. spegazzinii* (Simmond, 1995; Bradshaw and Ramsey, 2005). Hawkes *et al*. (2000) note that wild diploid species in the Andes and Mexico have contributed many useful genes through plant breeding activities (e.g., *S. acaule* for resistance to frost) and that further screening has revealed resistance to pink rot, common scab, wart, smut and charcoal rot, as well as bacterial soft rot, *Pseudomonas* wilt, potato viruses PVX, PVY, PLRV, and to nematodes (*Globodera* and *Meloidogyne*) and tuber moth (see discussion in Hawkes, 1958). *S. tarnii* has been found to be highly resistant to PVY and Colorado potato beetle and shows a strong hypersensitive reaction to *Phytophthora infestans* (Thieme *et al*., 2008).

Hawkes (1990) notes that there is comparatively extensive genetic diversity in the Andean subspecies of *S. tuberosum*, but he is doubtful if this diversity has resulted from introgression with related wild species, except perhaps for the diploid weed species *S. sparsipilum* and the hybridogenic tetraploid weed species *S. sucrense*. Naturalized forms of *S. tuberosum* subsp. *tuberosum* occur in southern Chile (Guaiticas Archipelago, etc.), but Hawkes (1990) doubts whether they have contributed various useful genes to their cultivated progenitor. This is echoed by Bradshaw *et al*. (2006), who conclude that the introgression of genes from wild species has been fairly limited and that the genetic base of modern cultivars is primarily a relatively small sample of *S. tuberosum* from the Andes and coastal Chile.

The wide distribution of wild potato indicates a wide ecological amplitude and adaptation to extremes of temperature and humidity which far surpasses that of the cultivated species (Hawkes *et al*., 2000)—this is indicative of a wide range of useful traits. Bradshaw *et al*. (2006) note that given the wide range of habitats in which they have evolved, there should be greater use of wild species to improve the resistance of cultivated potatoes to abiotic and biotic stresses. In Mexico, many of the wild species are adapted to hot, dry semi-desert conditions; others, such as *S. demissum*, grow in damp, cool forests where *Phytophthora infestans* is rampant and many resistance genes have evolved. The high Andean wild species such as *S. acaule, S. megistacrolobum* and others are frost resistant and can exist at altitudes of 3 000–4 000 m or more. Others, such as *S. sparsipilum* exist as cultivation weeds and one, *S. morelliforme* is adapted to epiphytic conditions on the mossy branches of high rain forest trees in Mexico (Hawkes, 1990).

Although wild species have been used extensively since the 1980s (Ross, 1986), sources of new resistance genes continue to be located and introduced; such as *S. bulbocastanum*, which provided blight resistance for the cv. Biogold released in 2004 (Hodgkin and Hajjar, 2008). Wild relatives have become a routine part of potato breeding and their use is clearly established within a more general strategy of base broadening for the crop (Bradshaw and Ramsey, 2005). Bradshaw *et al*. (2006) anticipate greater use of wild species in potato breeding in future. They cite various studies that have shown that ploidy manipulation or somatic fusion can be used to overcome crossing barriers, meaning virtually any potato species can be utilized in potato improvement. Improving the ease of use of wild species in potato breeding also continues to be investigated by various authors (e.g., see Voronkova *et al*., 2007; Wang *et al*., 2008; Yermishin *et al*., 2008).

Priority taxa

The relative closeness of the wild species to *S. tuberosum* is probably of less significance in potato than for some other crops because a number of studies have shown that ploidy manipulation or somatic fusion can be used to overcome crossing barriers; therefore, virtually any potato species can be utilized in potato improvement (Bradshaw *et al*., 2006). Prioritizing potato wild relatives on the basis of their relative distribution is also of limited use, since the majority of the species have very narrow distribution ranges. In their Atlas of Wild Potatoes, Hijmans *et al*. (2002) found that only five species accounted for 29% of the observations plotted (*S. acaule, S. leptophyes, S. megistacrolobum, S. bukasovii* and *S. chacoense*), while 3% were accounted for by 72 species, each of which had five or fewer observation records. For 21 species there were only two observations and for 17 species there was only one observation. By consulting the Wild Potato Species Atlas (http://www.cipotato.org/databases/), published online by the International Potato Centre (CIP), we identified 158 species (out of 196 in section *Petota*) that appeared to have 20 or fewer observations. Therefore, we may

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[30] For a review of progress in use of wild species in potato breeding, see Bradshaw et al. (2006).

conclude that the majority of species in section *Petota* are highly restricted and should be considered a priority for *in situ* conservation. A detailed study of the conservation status of these taxa is needed in order to target those species that are under greatest threat and thus in most immediate need of active *in situ* conservation measures. Species that have been highlighted as gene donors or potential gene donors should also be afforded high priority status.

Priority sites

Hijmans *et al*. (2002) mapped all the wild potato species (196 species in *Solanum* section *Petota*) using several data sources. In their study, they grouped the species according to regions (or countries) and series. Individual maps for each of the species can be found by consulting the Wild Potato Species Atlas (http://www.cipotato.org/databases/). Due to the high number of restricted distribution priority species, a detailed study to identify genetic reserve sites for the wild relatives is needed. Access to the most up to date data is required in order to overlay distributions with protected area data. This has not been possible within the confines of this background study. However, the Hijmans *et al*. (2002) study does provide us with some useful pointers with regard to the highest priority areas, as summarized below.

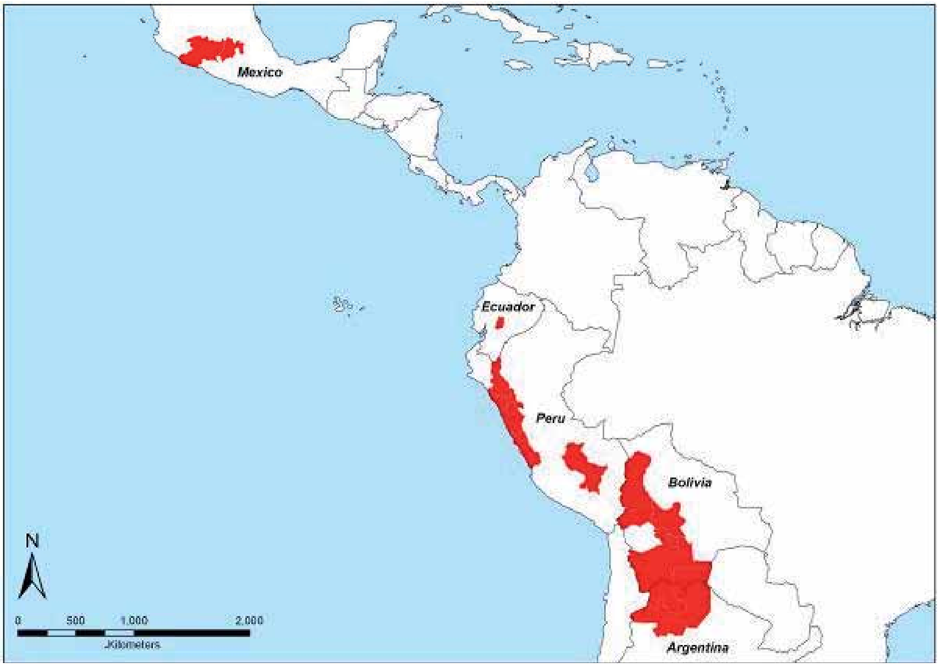
Wild potato species occur in 16 countries, but only four of these (Argentina, Peru, Bolivia and Mexico) harbour 171 (87%) of the species (Hijmans *et al*., 2002). The authors found that Peru has the highest number of species, as well as the highest number of rare species (i.e., those with five or less observation records). Only 35 species occur in two or more countries and there are no species that are found both in North and South America. The authors also analyzed range size and found that for 68 species, the maximum distance between two observations (MaxD) was less than 50 km and for 104 species, it was less than 200 km. Circular area (CAr) was also calculated, which, when compared with the number of observations, can be used to estimate abundance. These range statistics could also be useful for prioritizing taxa for *in situ* conservation (see Hijmans *et al*., 2002, Table 1). The authors also determined the geographic distribution of species richness using 50 x 50 km grid cells. They found that species richness is particularly high in the southern and central Andes and in central Mexico and listed the following areas with high species richness (Figure 19):

- The central Mexican highlands (México and Michoacán states);
- A small area in central Ecuador (Chimborazo province);
- A stretch from northern to central Peru (in Ancash, southern Cajamarca, La Libertad and Lima departments);
- Southern Peru (in Cusco department);
- Central Bolivia (in Cochabamba, Chuquisaca and Potosí and to a lesser extent La Paz and Tarija departments);
- Northern Argentina (Jujuy and Salta provinces).

From the point of view of conserving maximum species diversity, these areas could be targeted for genetic reserve conservation. Further analysis is needed in order to identify the exact locations and to predict whether some sites may occur within existing protected areas. Special attention also needs to be paid to the many rare species that have only been found in five or less locations.

FIGURE 19

Areas identified by Hijmans *et al.* (2002) with high species richness of potato wild relatives



Recommendations

- The establishment of potato parks in centres of potato diversity, such as that in the Cusco region of Peru by the indigenous Quechua people working in collaboration with CIP scientists (www.cipotato.org), has focused attention on the *in situ* protection of landrace diversity, but the continued practice of traditional agriculture will also favour maintenance of wild potato species. Similarly highly diverse cultivars of *S. tuberosum* subsp. *andigena* and related cultivated species are found in the Tiahuanaco region of south of Peru and north of Bolivia and this region may be suitable for establishment of a further potato park.
- It seems likely that although many *Solanum* species have restricted distributions they will be found in existing national parks and other protected areas. *In situ* conservation of potatoes is of considerable importance for the wild species, but since there are a large number of species and they commonly have a restricted distribution, it is clearly impossible to establish reserves for each of them. It would, however, be valuable to establish reserves in the mountains and plains surrounding Mexico City where late blight (*Phytophthora infestans*) resistant species, such as *S. demissum, S. verrucosum* and *S. stoloniferum*, occur. Frost-resistant species, such as S. acaule should also be conserved in southern Peru and northern Bolivia. A thorough review of all current and potential wild species gene donors should be undertaken in order to afford these species high priority status for *in situ* conservation.
- Extensive pest and disease resistant genetic diversity is available amongst wild species in the Andes ranges, from northern Argentina northwards to Ecuador and Central Colombia, as well as Central Mexico. Although *in situ* reserves cannot be established for the whole region, local country agencies should investigate the establishment of national reserves. As the International Centre for the Potato (CIP) in Peru is concerned both with the conservation and breeding of indigenous wild and cultivated species they are ideally situated to coordinate future conservation activities in the centre of diversity and elsewhere.
- A detailed study is required in order to identify high priority locations for the establishment of genetic reserves. This will involve mapping the known distributions of all wild potato species using the most up to date data and overlaying protected area data to predict the occurrence of the species inside the boundaries of existing sites. Those taxa that are found to occur within existing protected areas can immediately be targeted for active genetic reserve conservation. For those that are not found within existing protected areas, the possibility of establishing genetic reserves should be investigated and an *ex situ* gap analysis undertaken to ensure that sufficient genetically representative samples are conserved *ex situ*. It is also worth noting that some wild potato species may be found growing in agricultural landscapes as weeds of cultivated areas. In this case, on-farm conservation strategies may be needed to ensure that these weedy populations are maintained *in situ*.

- FAO (1998) estimate that 40% of wild *Solanum* species have been collected, the CIP collection being the most diverse; however, overall, wild relatives of potato only account for 5% of accessions and a survey of wild potato holdings showed that few wild species are adequately sampled throughout their geographic range (Hawkes *et al*., 2000). The material conserved *ex situ* should be reviewed in terms of coverage of priority taxa and intra-population genetic diversity. Further collections should be made to fill the gaps. Passport data associated with wild species collections should also be looked at to assess the effectiveness of existing collections for conservation and utilization. The question is whether to focus active conservation on the tuber-orientated cultivars, or the seed orientated wild species, or both. Since the tubers of the wild species are small and perishable, if kept for more than one season, the obvious choice here is for these to be conserved using their seed (Hawkes *et al*., 2000). The seed of the wild species is orthodox and will not need immediate regeneration if dried and cooled in the standard way. For the cultivated species, however, if the seed is regenerated the exact genotypes cannot be recovered because different genotypes will result from recombination. Here, then, the option is to conserve the range of genotypes by means of tissue culture and whole plants in field gene banks, unless the genes and genotypes are considered to be of greater importance.
- Potato gene banks have been established in various countries, such as at the CGIAR centre with the responsibility for potato conservation, CIP (Centro Internacional de la Papa) in Peru, Sturgeon Bay, Wisconsin, USA, Dundee, U.K., and also in other countries such as Germany, India, Colombia, Peru, Bolivia, Argentina, etc. The need for safe duplication in at least two banks is paramount. Conservation of cultivar genotypes has been attempted in parts of South America, in some of the larger collections in the afore-mentioned institutes, as well as in the Canary Isles.

2.10 Sorghum

Scientific name

Sorghum bicolor (L.) Moench

Principle synonyms

Holcus bicolor L., *Holcus arduini* Gmel., *Andropogon bicolor* Roxb., *Andropogon sorghum* (L.) Brot., *Sorghum vulgare* Pers., *Andropogon sorghum* subsp. *eu-sorghum* Aschers. et Graebner, *Andropogon halepensis* var. *bicolor* Vines et Druce, in Moris.

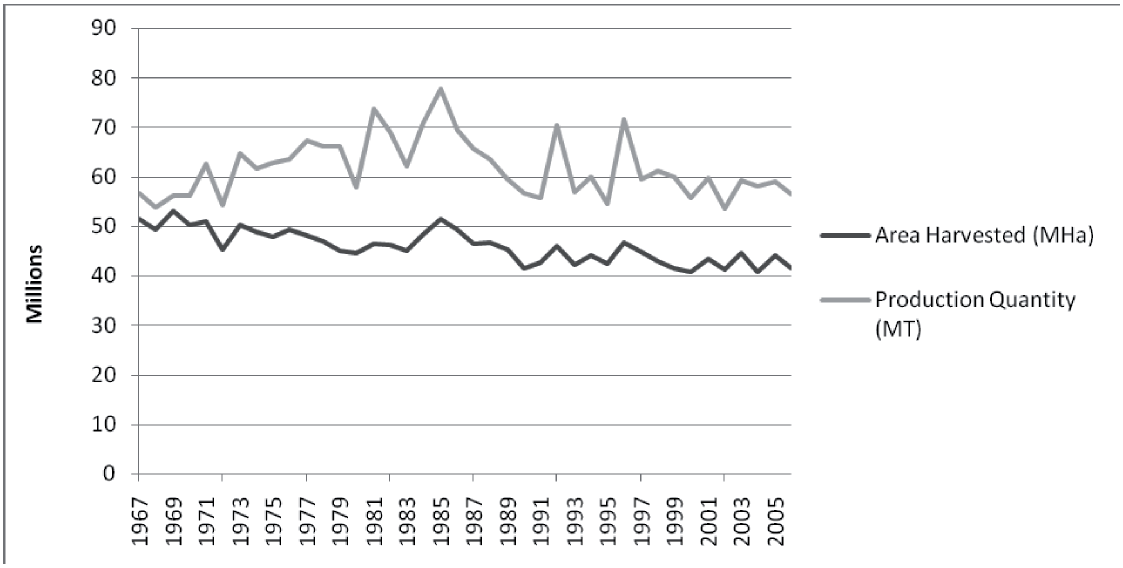
Global, regional and local importance

Sorghum (*Sorghum bicolor* (L.) Moench) is the fifth most important cereal crop in the world, grown across 44 million ha in 99 countries in Africa, Asia, Oceania and the Americas (ICRISAT, 2008). It is a staple food crop of millions of poor in the semi-arid tropics of Africa and Asia and has gained increasing importance as a fodder (green/dry) and feed crop in the last decade. Major producers are the USA, India, Nigeria, China, Mexico, Sudan and Argentina. The crop occupies 25% or more of arable land in Mauritania, Gambia, Mali, Burkina Faso, Ghana, Niger, Somalia and Yemen, and more than 10% of this area in Nigeria, Chad, Sudan, Tanzania and Mozambique. (ICRISAT, 2008)

Sorghum had an estimated world production of approximately 56.5 million tonnes planted on approximately 51.4 million ha in 2006 (FAO, 2008). The six countries with highest sorghum production are Nigeria (9.9MT), India (7.2MT), United States of America 7.1MT), Mexico (5.5MT), Sudan (5.2MT) and China (2.5MT). Although production on a country basis is less intense, sorghum is a significant part of agricultural production in many subsistence agricultural regions; particularly in rain-fed areas of Asia and Africa (Stenhouse *et al*., 1997). In many of these regions the stalks and foliage (used as fodder, fuel, thatching and fencing material) are valued as much as the grain. Figure 20 indicates a stable global production based on a slight decline in the area cultivated over the last 40 years, while over the same time period yields have increased from 1101.79 kg/Ha in 1967 to 1361.09 kg/Ha in 2006 (FAO, 2008).

FIGURE 20

World area harvested and production quantity for sorghum (FAO, 2008)



Taxonomic classification

The genus *Sorghum* Moench is a member of the subtribe *Sorghastrae* of the *Poaceae* tribe *Andropogoneae* (Stapf, 1917). Garber (1950, 1954) and Garber and Snyder (1951) divide subtribe *Sorghastrae* into two main genera and within the genus *Sorghum* the approximate 25 species are split into six subgenera, *Eu-sorghum, Chaetosorghum, Heterosorghum, Sorghastrum, Para-sorghum* and *Stiposorghum*. De Wet (1978) recognizes these as having sectional rank and refers to section *Sorghum* rather than *Eu-sorghum*. The cultivated sorghums are found in section *Sorghum*. *Sorghum bicolor* itself is considered a highly variable crop-weed complex, which contains wild, weedy and cultivated annual forms which are fully inter-fertile (FAO, 1995). Snowden (1936) produced a much dissected classification of 31 domesticated species and this dissection has been expanded further by Ivanjukovich (1981) who recognizes 8 cultivated species and 70 varieties; however, Harlan and de Wet (1972) published a simplified classification based on spikelet morphology and panicle shape, and this is now widely followed. It is now generally accepted that sect. *Sorghum* contains four species and three subspecies within *S. bicolor* (see Table 7), and within subsp. *bicolor* there are five basic races (bicolor, guinea, caudatum, kafir, and durra) and all combinations of their hybrid derivatives, for a total of 15 races. *S. almum, S. halepense* and *S. propinquum* are perennial, while *S. bicolor* is annual.

The cultivated races are thought to have originated from *S. arundinaceum* (Desv.) Stafp (synonym subsp. *verticilliflorum* (Steud.) Piper). The races of subsp. *bicolor* are widely distributed across the African savannah and have been introduced to tropical Australia, parts of India and the Americas. The weedy forms are classified as subsp. *drummondii*, which arose and probably continue to arise from crossing between cultivated grain sorghums and their close wild relatives wherever in Africa they are sympatric. Several hybrids have stabilized and occur as very persistent weeds in abandoned fields and field margins (Stenhouse *et al*., 1997).

TABLE 7

Classification and distribution of *Sorghum* diversity (de Wet, 1978)

Genus	Section	Species	Subspecific groups	Common name	Distribution
Sorghum	*Sorghum*	*S.* x *almum* Parodi (2n=22)		Columbus grass	Argentina (introduced into other tropical countries)
		S. bicolor (L.) Moench (2n=20)	subsp. *bicolor*	grain sorghum	Cultivated
			subsp. *drummondii* (Nees ex Steud.) de Wet & Harlan	Sudan grass	Africa (with introduction to other grain sorghum growing areas)
			subsp. *arundinaceum* (Desv.) de Wet & Harlan	common wild sorghum	Africa (with introduction to other grain sorghum growing areas)
		S. halepense (L.) Pers. (2n=40)		Johnson grass	Southern Eurasia east to India
		S. propinquum (Kunth) Hitchc. (2n=20)			Indian sub-continent to Southeast Asian islands

Wild relatives

The primary genepool of sorghum has been defined by Stenhouse *et al*. (1997) as including the *S. bicolor* complex, with the addition of the wild diploid *S. propinquum* (Kunth) Hitchc. complex found in Southeast Asia. The authors define the secondary genepool as including *S. halepense* (L.) Pers. and the autotetraploid form of *S. propinquum*. The tertiary genepool is defined as including all other sections/subgenera of *Sorghum*.

Primary wild relatives

- *Sorghum bicolor* subsp. *drummondii* (Nees ex Steud.) de Wet & Harlan
- *S. bicolor* subsp. *arundinaceum* (Desv.) de Wet & Harlan
- *S. propinquum* (Kunth) Hitchc. (diploid form)

Secondary wild relatives

- *S.* × *almum* Parodi
- *S. halepense* (L.) Pers

Tertiary wild relatives

All non-section *Sorghum* species

Distribution and centre of diversity

The native distribution of the wild species is outside of Africa in the Indian sub-continent, Southeast Asia and South America, yet the distribution of the two weedy *S. bicolor* subspecies is African (although the native distribution is blurred by extensive introductions throughout the tropics) (see Table 7). Sorghum was domesticated between 5 000 and 7 000 years ago, most likely as a selection from wild sorghum (Purseglove, 1972) in Northeast Africa, which remains the centre of diversity of cultivated and wild sorghum (Doggett, 1988). Alternatively sorghum may have developed from other wild species in western, eastern and eastern–Central Africa (Snowden, 1936; de Wet and Huckabay, 1967). Sorghum first spread across Africa, then was taken to India via the Middle East at least 3 000 years ago (Mann *et al*., 1983). FAO (1995) suggest that sorghum was taken along the Silk Route to China and to Southeast Asia, and to the Americas and Australia from West Africa, North Africa, South Africa and India towards the end of the 19th century. Currently, sorghum is cultivated in the drier areas of Africa, Asia, the Americas and Australia from sea level to 2 200 m and up to 50° N in Russia and 40°S in Argentina (Stenhouse *et al*., 1997).

Known uses of wild relatives in crop improvement

S. bicolor forms an extremely variable, at least partially out-breeding complex, comprising wild, weedy and cultivated plants that are fully inter-fertile (Stenhouse *et al*., 1997). *S.* x *almum, S. halepense* and *S. propinquum* each naturally introgress with cultivated sorghum (Celarier, 1958; de Wet, 1978), making the use of the wild taxa in conventional breeding programmes possible. However, most sorghum improvement has been achieved within grain sorghum races of the same species or closely related species—wider crosses with the wild grassy sorghums of non-sect. *Sorghum* have been unsuccessful (Duncan *et al*., 1991; Rosenow and Dahlberg, 2000), although a successful cross of a species outside of sect. *Sorghum, S. purpureosericeum* subsp. *dimidiatum* has been reported, which offers good resistance to sorghum shoot-fly (Nwanze *et al*., 1990). Price *et al*. (2006) note that the wild Australian *Sorghum* species alone contain resistance to important insects and pathogens, including midge (*Stenodiplosis sorghicola*) and sorghum downy mildew (*Peronosclerospora sorghi*). The strong reproductive barrier to inter-specific hybridization is associated with adverse pollen-pistol interaction leading to abnormal pollen tube growth (Hodnett *et al*., 2005) and hybrid failure (Kuhlman *et al*., 2008). Price *et al*. (2006) overcame the reproductive barrier by using cytoplasmic male-sterile *S. bicolor* plants homozygous for the *iap* (inhibition of alien pollen) allele and three divergent Sorghum species, S. angustum Blake, *S. nitidum* (Vahl) Pers. and *S. macrospermum* Garber, a technique that can now be used to introgress desirable traits into cultivated sorghum. Kuhlman *et al*. (2008) have also recently successfully crossed *S. bicolor* with *S. macrospermum*, further opening the possibility of successful wild species use in sorghum breeding. In conclusion, it appears that the use of wild relatives in sorghum breeding is still in its infancy, but sorghum wild relatives do offer a range of desirable traits and the recent identification of the barriers to hybridization open the opportunity for more systematic exploitation of the secondary and tertiary gene pool.

Priority taxa

The primary and secondary wild relatives of sorghum are all relatively widespread species that are not a high conservation priority. USDA, ARS, National Genetic Resources Program (2008) report the following distributional information: *S. bicolor* subsp. *drummondii* "may occur as a weed wherever sorghum is cultivated"; *S. bicolor* subsp. *arundinaceum* is widely distributed in Africa and naturalized in South, Central and North America; *S. propinquum* is distributed in India, Sri Lanka, Indochina, Myanmar, Thailand, Malaysia and the Philippines[31]; *S.* x *almum* is distributed in Argentina, Paraguay and Uruguay—it is a natural hybrid arising from cultivated and weedy sorghum in Argentina and naturalized elsewhere; *S. halepense* is distributed in northern Africa, western Asia, the Caucasus, Soviet Middle Asia and the Indian Subcontinent and is naturalized in warm-temperate regions, including North America. *S. bicolor* subsp. *drummondii*, *S.* x *almum* and *S. halepense* are also classified as noxious weeds in the United States (USDA, ARS, National Genetic Resources Program, 2008).

Priority sites

As the closest sorghum wild relatives are relatively widespread, the establishment of specific genetic reserves for their conservation *in situ* is not a high priority. However, the species may be found in the some of the same locations as the wild relatives of other crops that have been given high priority status for conservation action *in situ*, in which case they may be conserved as part of a multi-species reserve approach.

Recommendations

- The use of some tertiary wild relatives for sorghum improvement has been reported, although non-conventional breeding methods are needed to overcome crossing barriers. While such techniques are not currently widely accessible to breeders in all sectors, these species may be important gene donors in the future. Therefore, an investigation into the conservation status of the tertiary wild relatives should be undertaken to ensure that priority taxa are adequately conserved, both *in situ* and *ex situ*. For example, of the species utilized by Price *et al*. (2006) and Kuhlman *et al*. (2008) (reported above), *S. angustum* is limited to Queensland and *S. macrospermum* to Northern Territory, Australia.

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[31] We have been unable to source a comprehensive occurrence data set for *S. propinquum* to assess its range within these countries, but its wide country distribution implies that it is not of immediate conservation concern.

- A review of the *ex situ* conservation status of sorghum wild relatives should be undertaken and collection gaps filled as necessary.
- Landraces of sorghum may harbour important genetic diversity for improvement of the crop. A survey and conservation gap analysis of sorghum landraces should be undertaken in order to ensure the maximum genetic diversity within the crop gene pool is adequately conserved.

2.11 Wheat

Scientific name

Triticum aestivum L.

Principle synonyms

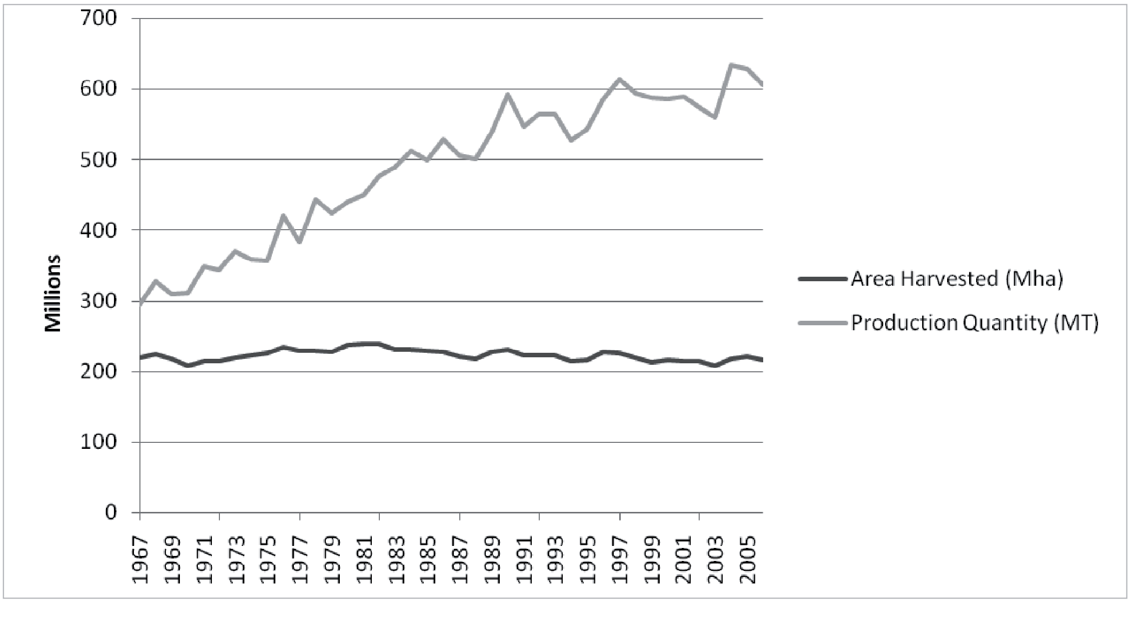
T. hybernum L., *T. macha* Dekap. & Menab., *T. sativum* Lam., *T. sphaerococcum* Percival, *T. vulgare* Vill.

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 the 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*) whose cultivation is primarily 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). Today, bread wheat is cultivated in a wide range of environments from 67° N in Canada, Scandinavia and Russia to 45° S in Argentina, but in the tropics its cultivation is restricted to higher altitudes. The largest wheat-producing countries in 2006 were China (104.5 MT), India (69.4 MT), United States of America (57.3 MT), Russian Federation (45.0 MT), France (35.4 MT) and Canada (27.3 MT) (FAO, 2008). As is shown in Figure 21, the area harvested has remained relatively constant over recent years, but the production has increased markedly, with wheat now cultivated on approximately 200 million hectares and with an annual production of 600 million tonnes worldwide in 2006 (FAO, 2008).

FIGURE 22

World area harvested and production quantity for wheat (FAO, 2008)



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. However, subsequent taxonomists have failed to agree on the precise distinction between the two genera, leading to an abundant and complex synonymy, with some suggesting merging the genera (Stebbins, 1956) and at the other extreme, Löve (1984) arguing for the establishment of 37 genera on the basis of genomically homogeneous taxa. Following a detailed review, van Slageren (1994) argued for the retention of the two options, with the cultivated taxa and their closest wild relatives in *Triticum* and the wild forms in *Aegilops*, though there are those who many consider this strict division rather over-simplistic. The genus *Triticum* is composed of six species—two diploids, two tetraploids and two hexaploids (van Slageren, 1994), while *Aegilops* comprises 22 species, inclusive of ten diploids, ten tetraploids and two hexaploids (Manners and van Slageren, 1998).

Wild relatives

The gene pool of wheat has been defined; however, there remains disagreement between taxonomists over the precise delimitation of GP1, GP2 and GP3. One interpretation of the bread wheat gene pool 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, where the species still cross freely amongst themselves and with *Secale*. 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 man—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) (see Table 8).

Wild *Triticum* species tend to grow in medium to large sized, relatively compact populations, while the diploid *Aegilops* species are usually found in smaller, more dispersed populations (*Ae. speltoides* being the exception) (van Slageren, 1994). The tetraploid species of *Triticum* often occur in massive, dense stands, reflecting their invasive, weedy habit. They are essentially pasture species that tend to occupy poor, thin and rocky, dry soils, but they respond well to better soils. They prefer open steppe-like communities, degraded deciduous forests (e.g., of oaks and pistachio), garrigue and maquis vegetation, wadi beds, roadsides, edges of cultivation and recently disturbed land. 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 2 700 m, but most species are much more specific and are most commonly found from 500–1 200 m (van Slageren, 1994).

Known uses of wild relatives in crop improvement

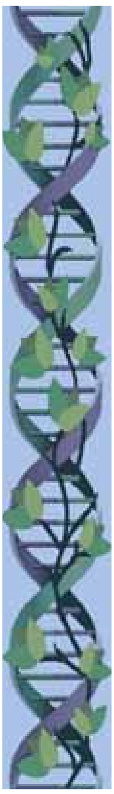
The history and extent of the use of CWR for wheat improvement is unrivalled (Hodgkin and Hajjar, 2008); it is believed this may be partially due to the narrow genetic base of wheat following domestication (Feldman and Sears, 1981; Zohary, 1999). Millet *et al*. (2008) conclude that wheat wild relatives still hold additional potentially useful traits for resistance to biotic stress, abiotic stress resistance (particularly important in times of climate change), and technological and nutritional quality. McFadden (1930) was the first to transfer desirable traits via inter-specific hybridization to wheat when he introduced disease resistance from emmer wheat. The utilization of *Aegilops* species to broaden the genetic base of wheat has recently been reviewed by Schneider *et al*. (2008), who conclude that although many useful traits have been transferred from *Aegilops* species to wheat, there remains much that can be utilized, particularly in *Aegilops* species not previously evaluated and with the aid of advanced molecular characterization. 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), *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).

TABLE 8

Geographic distribution of *Triticum, Aegilops* and *Amblyopyrum* taxa

Taxon	Geographic distribution	Status	Ecological preferences
T. aestivum	Pan-temperate	Crop	Cultivated
T. monococcum	Southern Europe, eastern Mediterranean, Caucasus, West Asia	Crop/wild	Cultivated and spontaneous
T. timopheevii	Eastern Mediterranean	Crop/wild	Cultivated and spontaneous
T. turgidum	Eastern Mediterranean, West Asia	Crop/wild	Cultivated and spontaneous
T. urartu	Caucasus, West Asia	Wild	–
T. zhukovskyi	Caucasus	Crop/wild	Cultivated and spontaneous
Aegilops bicornis	Southern Europe, West Asia, North Africa	Wild	Coastal grassland, shrubland and sand dunes
Ae. biuncialis	Southern Europe, West Asia, Caucasus, North Africa	Wild	Dry, disturbed areas, grassland and shrubland
Ae. caudata	Southeast Europe, West Asia	Wild	Fallow, roadside, field margin and grassland
Ae. columnaris	Southeast Europe, Caucasus, West Asia, Central Asia	Wild	Dry open fields, road and hillsides
Ae. comosa	Southeast Europe	Wild	Grassland, road and hillsides
Ae. crassa	Caucasus, West Asia, Central Asia	Wild	Dry steppe, fallow, roadside and grassland
Ae. cylindrica	Southern Europe, Caucasus, West Asia, Central Asia	Wild	Disturbed areas, grassland, road and hillsides
Ae. geniculata	Southern Europe, West Asia, North Africa	Wild	Dry, disturbed areas, grassland and shrubland
Ae. juvenalis	West Asia, Central Asia	Wild	Dry steppe, fallow, roadside, field margin and grassland
Ae. kotschyi	Caucasus, West Asia, Central Asia, North Africa	Wild	Dry riverbeds and sand dunes

Taxon	Geographic distribution	Status	Ecological preferences
Ae. longissima	West Asia, North Africa	Wild	Sandy fields
Ae. neglecta	Southern Europe, Caucasus, West Asia, Central Asia, North Africa	Wild	Dry, disturbed areas, grassland and shrubland
Ae. peregrina	Southeast Europe, Caucasus, West Asia, Central Asia, North Africa	Wild	Dry disturbed, coast, hill and mountainsides
Ae. searsii	West Asia	Wild	Dry open fields, road and hillsides
Ae. sharonensis	West Asia	Wild	Coastal grassland, shrubland and sand dunes
Ae. speltoides	Southeast Europe, Caucasus, West Asia, Central Asia	Wild	Grassland and moderately disturbed sites
Ae. tauschii	Southern Europe, Caucasus, West Asia, Central Asia, Southern Asia	Wild	Wide ecological amplitude
Ae. triuncialis	Southern Europe, Caucasus, West Asia, Central Asia, North Africa	Wild	Dry, disturbed areas, fallow grassland and roadsides
Ae. umbellulata	Southeast Europe, Caucasus, West Asia	Wild	Fallow, grassland, roadside, field margins and forest
Ae. uniaristata	Southeast Europe, West Asia	Wild	Dry, disturbed areas, grassland and shrubland
Ae. vavilovia	Caucasus, West Asia, Central Asia	Wild	Disturbed areas, grassland, road and hillsides
Ae. ventricosa	Southern Europe, Caucasus, Central Asia, North Africa	Wild	Disturbed areas, grassland, road, edges and within cultivation
Amblyopyrum muticum	Caucasus, West Asia	Wild	Open places, road and hillsides, mountain slopes



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) found Northwest Jordan, Israel, Lebanon, western Syria, Iraq and Turkey as areas containing more than nine *Aegilops* species, but two particular hotspots containing between 12 and 14 *Aegilops* species were identified—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 by 100 km grid cells required to capture all 22 species in the *Aegilops* genus (Figure 22), 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 23), 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 22

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

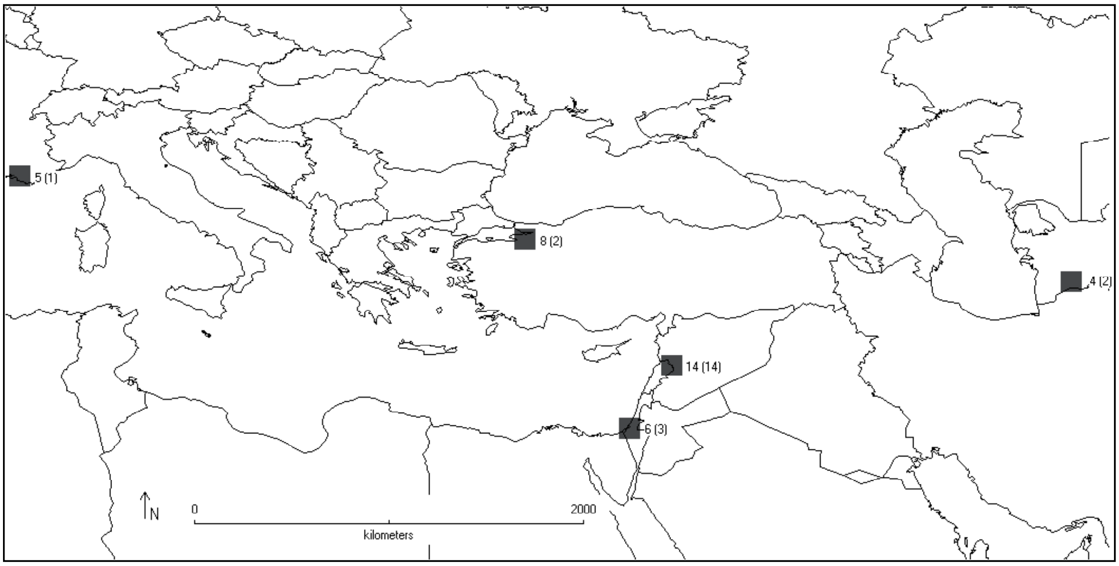
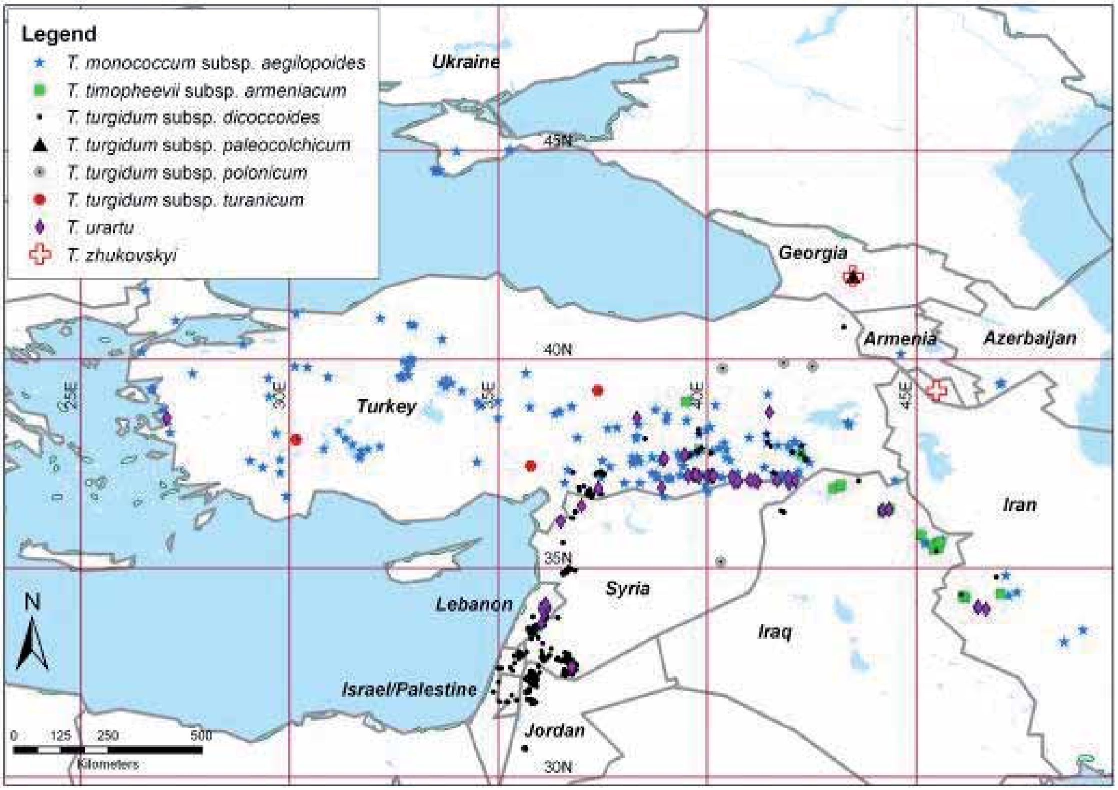


FIGURE 23

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)



Based on the data presented in Figures 22 and 23, the following sites/locations are important for the *in situ* conservation of wheat wild relatives (see Figure 24):

- Qal'at Al Hosn, 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. This would also present a good second choice for a single wheat diversity genetic reserve and the fact that it is mountainous and on the Syrian–Lebanese border means it is less likely to be threatened by future human-induced genetic erosion. 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 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.

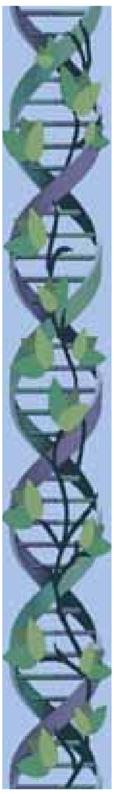
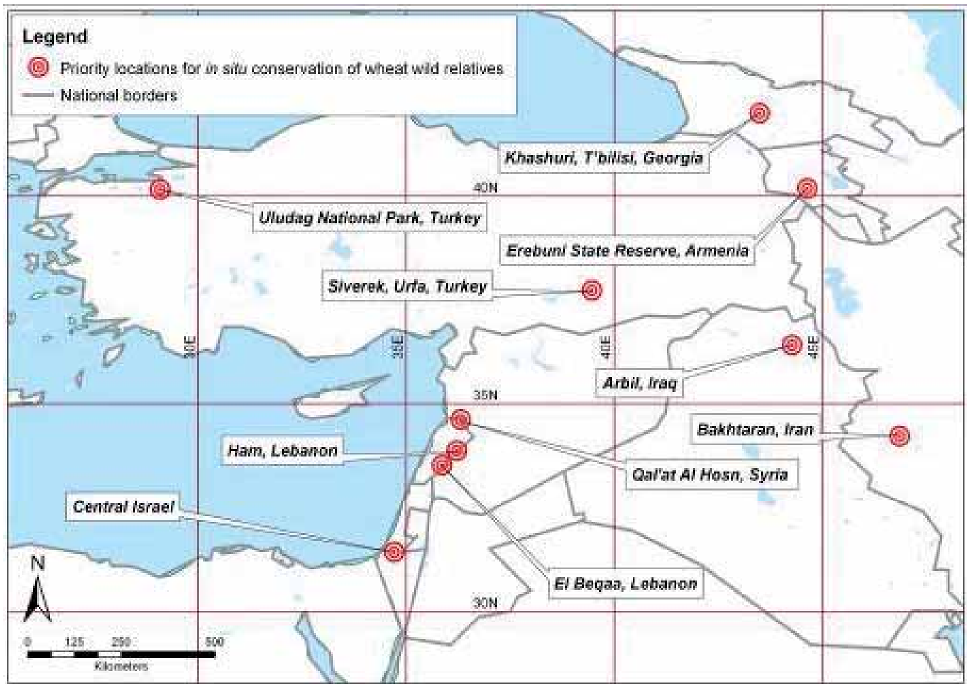


FIGURE 24

Priority locations for wheat wild relative genetic reserve conservation



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. The sites/locations identified in this study (Figure 22) should be considered. 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.

2.12 Faba bean

Scientific name

Vicia faba L. (*Fabaceae*)

Principle synonyms

Faba vulgaris Tragus, Strip., *Pisum sativus* Dodoens, *Faba vulgaris* Bernhardi, *Faba sativa* Bernhardi, *V. vulgaris* Gray, *V. pliniana* (Trabut) Murat.

Global, regional and local importance

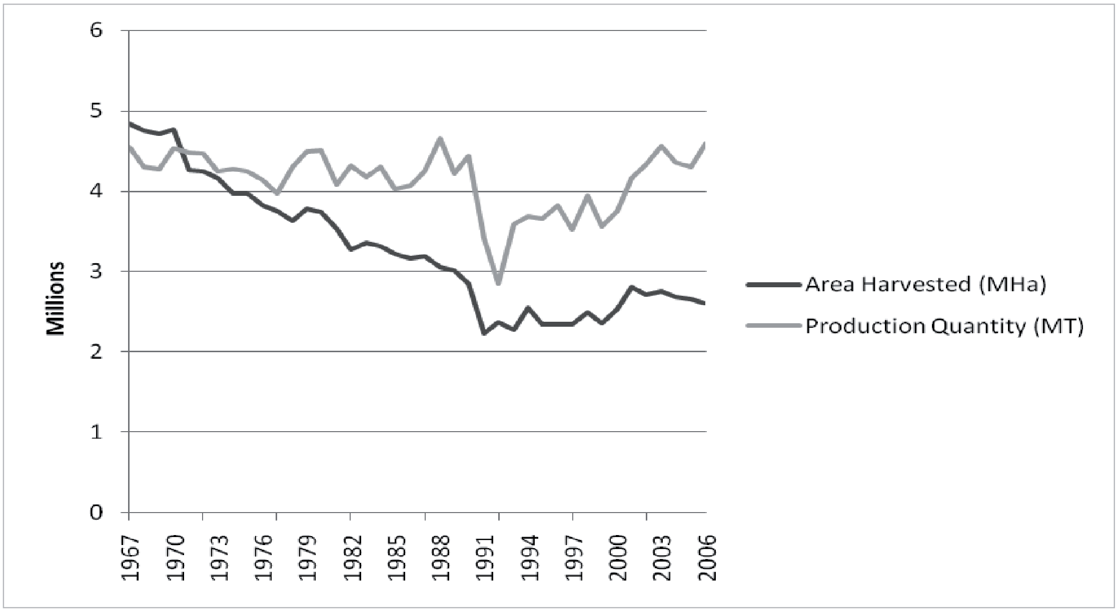
The faba bean or broad bean (*Vicia faba* L.) is an important global pulse, fodder crop and vegetable throughout the temperate world and at higher altitudes in some sub-tropical regions (Bond, 1995). It has been referred to as the 'poor man's meat' due to the fact that it may be harvested early for green pods and beans and later harvested for dry seed (De

Wouw *et al*., 2001). The distribution of the faba bean is entirely controlled by humans, as it is not known in the wild. It is cultivated throughout Europe and was introduced to South America during European colonization but is mostly grown at higher elevations where *Phaseolus* beans cannot be grown. Its usefulness is associated with its erect habit and easily threshed pods with large seed of high protein content. It is a common breakfast food in the Middle East, Mediterranean region, China and Ethiopia (Bond, 1995). As well as a staple human food, faba beans are also used to feed animals in industrialized countries; such as pigs, horses, poultry and pigeons.

In 2006, 2.6 million ha were planted and 4.6 million tonnes were harvested of this crop (FAO, 2008) (Figure 25). Approximately 1.05 million ha were planted with faba bean in China alone; with Ethiopia, Morocco and Australia cultivating 427 719, 169 000 and 153 000 ha, respectively (FAO, 2008). Compared to the other grain legumes, world trade in faba bean is significantly lower, with most produce consumed locally. However, there is an expectation that faba bean cultivation will expand in Australia, where it is likely to become a major export crop, as well as in China (De Wouw *et al*., 2001).

FIGURE 25

World area harvested and production quantity for faba beans (FAO, 2008)



Taxonomic classification

The faba bean is a peripheral member of the genus *Vicia* L. (legume tribe *Vicieae* of the *Papilionoideae*). The precise generic boundaries of *Vicia* remain a focus of debate, with 20 major classifications of the genus since Linnaeus (Maxted, 1993). Much of the debate has focused around *V. faba* and its appropriate position and rank within the genus and the search for its wild progenitor. Following an extensive review of morphology, cytology and hybridization studies, Maxted (1993) concluded that *V. faba* is clearly genetically distinct from all other *Vicia* species, but argued that although reinstatement of faba bean's generic rank as *Faba bona* Medik. may be warranted, the resultant inconvenience of nomenclatural changes for a major crop would be unjustified. Therefore, the author proposed that *V. faba* should be retained as the monospecific distinct section *Faba* within *Vicia*. Even though in recent years there has been systematic collecting throughout the eastern Mediterranean, no close ally of the faba bean has been discovered (Maxted *et al*., 1991) and the species remains peripheral to the genus as a whole. Schäfer (1973) hypothesized that *V. faba* originated from an extinct ancestor, though De Wouw *et al*. (2001) suggested that a progenitor may appear in areas not yet thoroughly surveyed (e.g., Southeast Turkey, Iran or Afghanistan). V. *faba* is composed of four infra-specific groups (Muratova, 1931) based on leaflet and flower number and flower and seed length characteristics, as indicated in Table 9. Although all four are cultivated, the large seeded form, *V. faba* subsp. *faba* var. *faba*, is the true faba bean.

TABLE 9

Intra-specific classification of Vicia faba (Muratova, 1931)

Taxon	Description
V. faba subsp. *faba*	2–2.5 leaflets/leaf, flowers 2.5–2.7 cm, 2–3 per inflorescence
var. *faba* (faba bean)	seed length 1.88–3.05 cm
var. *equina* (horse bean)	seed length 1.25–1.65 cm
var. *minor* (tick bean)	seed length 0.65–1.25 cm
V. faba subsp. *paucijuga*	3–4 leaflets/leaf, flowers 2.8–3.5 cm, 4–11 per inflorescence

Wild relatives

The faba bean is unusual among pulse crops in that there is still no clear picture of the species ancestry or even its close taxonomic allegiances (Smartt, 1984; Maxted *et al*., 1991). Significant effort has been made to hybridize the faba bean with other *Vicia* species, though with very limited success. Morphologically, *V. narbonensis* L. is considered by many authors (Davis and Plitmann, 1970; Hanelt, 1972; Schäfer, 1973; Kupicha, 1976; Maxted, 1993) to be the closest wild relative of the faba bean and has received the greatest attention as its putative ancestor. However, *V. narbonensis* (2n=14), with a different karyotype and different chromosome number (*V. faba* has 2n=12), has never been successfully crossed with *V. faba*, and therefore cannot be regarded as a direct ancestor of faba bean. *V. narbonensis* is a common wild and minor cultivated forage species of southern Europe, the Mediterranean and western Asia in its own right. It is one species of a morphologically closely related group of less common species in *Vicia* section *Narbonensis* (Maxted, 1993). The gene pool grouping for faba bean can be derived from the discussion of the classification and relatedness in Maxted *et al*. (1991) and Maxted (1993).

Primary wild relatives

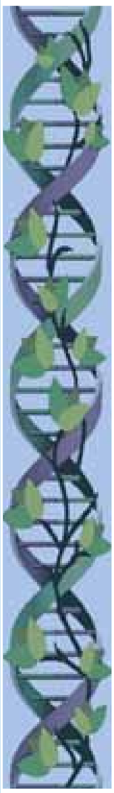
- *Vicia faba* L.
    - subsp. *paucijuga* Murat.
    - subsp. *faba*
        a. var. *minor* Beck
        b. var. *equina* Pers.
        c. var. *faba*

Secondary wild relatives

There is no secondary gene pool for *V. faba*.

Tertiary wild relatives

- *V. kalakhensis* Khattab, Maxted & Bisby
- *V. johannis* Tamamschjan in Karyagin
    - var. *ecirrhosa* (Popov) H. Schäfer
    - var. *procumbens* H. Schäfer
    - var. *johannis*
- *V. galilaea* Plitm. & Zoh. in Plitm.
    - var. *galilaea*
    - var. *faboidea* (Plitm. & Zoh. in Plitm.) H. Schäfer
- *V. serratifolia* Jacq.
- *V. narbonensis* L.
    - var. *salmonea* (Mout.) H. Schäfer
    - var. *jordanica* H. Schäfer
    - var. *affinis* Kornhuber ex Asch. & Schweinf.
    - var. *aegyptiaca* Kornhuber ex Asch. & Schweinf.
    - var. *narbonensis*
- *V. hyaeniscyamus* Mout.
- More distantly, *V. bithynica* (L.) L. and *V. eristalioides* Maxted are also related (Maxted, 1993).



Distribution and centre of diversity

The Mediterranean Basin is the most important centre of diversity for *Vicia*, although secondary centres exist in South America, North America and southern Siberia (Kupicha, 1981; Hanelt and Mettin, 1989; Maxted, 1995). The genus as a whole is adapted to temperate regions but can also be found at high altitudes in tropical Africa. Endemic species are present on all continents, except for Australia and Antarctica.

V. faba is one of the earliest domesticated plants of the world and it is believed to have been domesticated during the Neolithic period (Hopf, 1970, 1986: Zohary, 1989; Zohary and Hopf, 2000) in western Asia—probably in the region between Afghanistan and the eastern Mediterranean during the period 7 000–4 000 BC (Hanelt, 1972). Cubero (1972) concluded that the cultivation of faba bean spread in four directions from its centre of origin—north to Central Europe, northwest to western Europe, west to the Mediterranean, and east to the Far East (India, China and Japan). The var. *minor* faba bean was introduced to China in 100 BC (Tao, 1981) and the major type in 1 200 AD (Hanelt, 1972). *V. faba* is divided into two subspecies: *faba* and *paucijuga*; the most primitive of these and less adapted as a crop, is the relatively small seeded subsp. *paucijuga*. This small plant has a more restricted distribution, being confined to Afghanistan, Pakistan and India (Muratova, 1931) and the Terai region of Nepal. Subspecies *faba* is divided into varieties according to the size of its seeds. The large seeded faba bean (*V. faba* subsp. *faba* var. *major*), which has a seed weight of more than 1 g, was developed in the southern Mediterranean and China. The small seeded types (var. *minor*), with a seed weight of less than 0.5 g, which are found in the Ethiopian highlands and Sudan, have become important in North European agriculture. The varieties with an intermediate seed size (var. *equina*), developed in the Middle East and North Africa, are the main type grown and eaten in Egypt (Maxted, 1995; Duc, 1997).

V. narbonensis is a common wild and minor cultivated forage species of southern Europe, the Mediterranean and western Asia, in its own right. It was formerly cultivated more widely on limestone and volcanic soils, often inter-cropped with faba beans, but *V. narbonensis* cultivation is now restricted to Syria, Turkey and Iraq (Enneking and Maxted, 1995). The other species of *Vicia* section *Narbonensis* are less common, more geographically restricted and mostly found in field margins, grasslands, as well as weeds of cultivated fields. They generally prefer calcareous soils, except for *V. narbonensis var. jordanica* and *V. hyaeniscyamus*, which have only been found on basaltic soils. *V. serratifolia* was also historically cultivated as a forage crop in central Europe and parts of France (Clos, 1898). *V. johannis* is a species with a more northerly distribution than *V. narbonensis*; it has better cold adaptation and could offer potential as a forage crop (De Wouw *et al*., 2001). Generally, the species of *Vicia* section *Narbonensis* are found in the countries surrounding the Mediterranean, Europe and Southwest Asia, with the largest number found in Turkey, Syria and Greece (Bennett and Maxted, 1997).

Known uses of wild relatives in crop improvement

As a pulse crop, there has been significant phenotypic characterization of the genetic diversity within *V. faba* and landraces have been widely used in crop improvement (Robertson, 1985). Because there are no species in the secondary gene pool of *V. faba*, there remain few examples of the use of CWR in faba bean improvement; however, the work that has taken place has focused on *V. narbonensis* and other members of sect. *Narbonensis* and therefore these are priority CWR taxa.

Priority taxa

High priority taxa

- *V. eristalioides*
- *V. faba* subsp. *paucijuga*
- *V. galilaea*[32]
- *V. hyaeniscyamus*
- *V. kalakhensis*

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[32] There is some dispute over whether *V. galileae* exists as a specific entity from *V. johannis* and it seems likely the former should be reduced to a synonym of the latter.

Other priority taxa

- *V. johannis*
- *V. narbonensis* var. *narbonensis*
  - var. *aegyptiaca*
  - var. *affinis*
  - var. *jordanica*
  - var. *salmonea*
- *V. serratifolia*

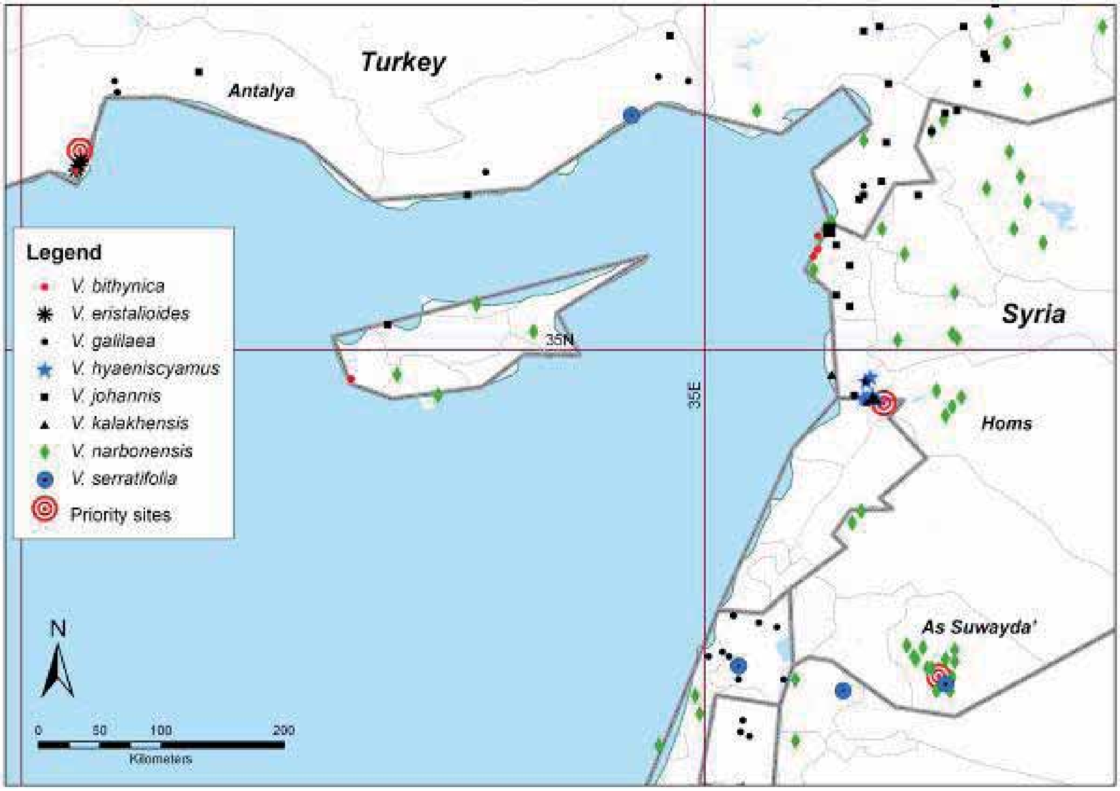
Priority sites

Maxted (1995) identified five priority sites for the establishment of genetic reserves to conserve *Vicia* genetic diversity *in situ* in Syria and Turkey. Of these five, three are particularly relevant for the *in situ* conservation of taxa in *Vicia* sect. *Narbonensis*—the closest wild relatives of *V. faba* (Figure 26):

- Qal'at Al Hasn, Homs province, Syria (34 46 29N, 36 18 57E). This would be the best option for a single reserve as there are two local endemic species present—*V. kalakhensis* and *V. hyaeniscyamus*—as well as significant populations of *V. narbonensis* and *V. johannis*. However, a recent study (Keisa *et al*., 2007) has shown that this area is being developed for tourism very rapidly and is highly threatened, so designation and site protection is a priority.
- Mimas, As Suwayda province, Syria (32 36 25N, 36 43 02E). This is a good general site to conserve *Vicia* diversity that also contains populations of *V. narbonensis* and *V. johannis*.
- Between Belin and Cavus, Antalya province Turkey (36 27 24N, 30 25 40E). This is the type location of *V. eristalioides* within the Olimpos Beydaglari National Park, Belin and so the site already has a level of protection. However, there has been extensive planting of conifers within the reserve and these plantations are likely to threaten the relatively small endemic population of *V. eristalioides*; therefore, reserve management policy needs to be reconsidered.

FIGURE 26

Priority sites for genetic reserve establishment identified by Maxted (1995), showing the distribution of priority *Vicia* wild relatives in the region



Recommendations

- Although existing genetic reserves (e.g., Ammiad in eastern Galilee, Israel; Kaz Dag, Aegean Region; Ceylanpinar of southeastern Turkey; and Amanos, Mersin in Turkey) and other protected areas throughout the range of sect. *Narbonensis* contain the target species, in these locations the conservation is 'passive' (species and genetic diversity is not being monitored and managed), therefore the taxa are susceptible to further unobserved genetic erosion. As such, we recommend that genetic reserves are established at the three priority sites listed above in Syria and Turkey for the closest CWR wild species of faba bean in *Vicia* sect. *Narbonensis* (Maxted, 1995).
- Relatively large *ex situ* seed collections exist of cultivated and wild *Vicia* species (De Wouw *et al*., 2001), but there remain numerous gaps in conserved materials. Even for those species of sect. *Narbonensis* which are of most immediate utilization potential, their germplasm has not been systematically conserved *ex situ*. Therefore, there is a need to systematically conserve Vicia genetic diversity *ex situ* as a back-up for active *in situ* activities (Maxted, 1995).
- The relatively recent discoveries of new species closely related to faba bean (Khattab *et al*., 1988; Maxted, 1988) suggest that a wild progenitor of faba bean may still be found. This progenitor species would be very interesting to plant breeders, bearing in mind the current lack of secondary wild relatives; therefore, the search should be continued in those areas of the Middle East and West Asia that are still under-explored, specifically Southeast Turkey, Iran and Afghanistan.
- In terms of safe-guarding the gene pool of faba bean, there is a need to systematically conserve the diversity within *V. faba* itself. Further, as the taxa are dependent on cultivation (i.e., not being found in the wild), there is a need to establish on-farm projects to conserve the ancient landraces of cultivated *V. faba*, particularly in areas with less developed agriculture, such as Spain, southern Italy, Sicily, Albania, the former Yugoslavia, Turkey, Lebanon, Iran, Afghanistan and many of the Mediterranean islands.
- It is interesting to note that the conservation of the primitive *V. faba* subsp. *paucijuga* has been largely ignored, there are very few *ex situ* conserved accessions and none held within the System-wide Information Network for Genetic Resources (SINGER - http://singer.grinfo.net/). Muratova (1931) records the taxon as being cultivated in Afghanistan, Pakistan and India and if still extant it could provide useful traits for a crop that lacks close CWR diversity, so there is a need to re-locate and conserve this diversity.

2.13 Cowpea

Scientific name

Vigna unguiculata (L.) Walp.

Principle synonyms

Dolichos unguiculatus L., *Phaseolus cylindricus* L., *Dolichos sinensis* L., *Dolichos catjang* Burm.f., *Vigna catjang* (Burm.f.) Walp., *Vigna sinensis* (L.) Hassk.

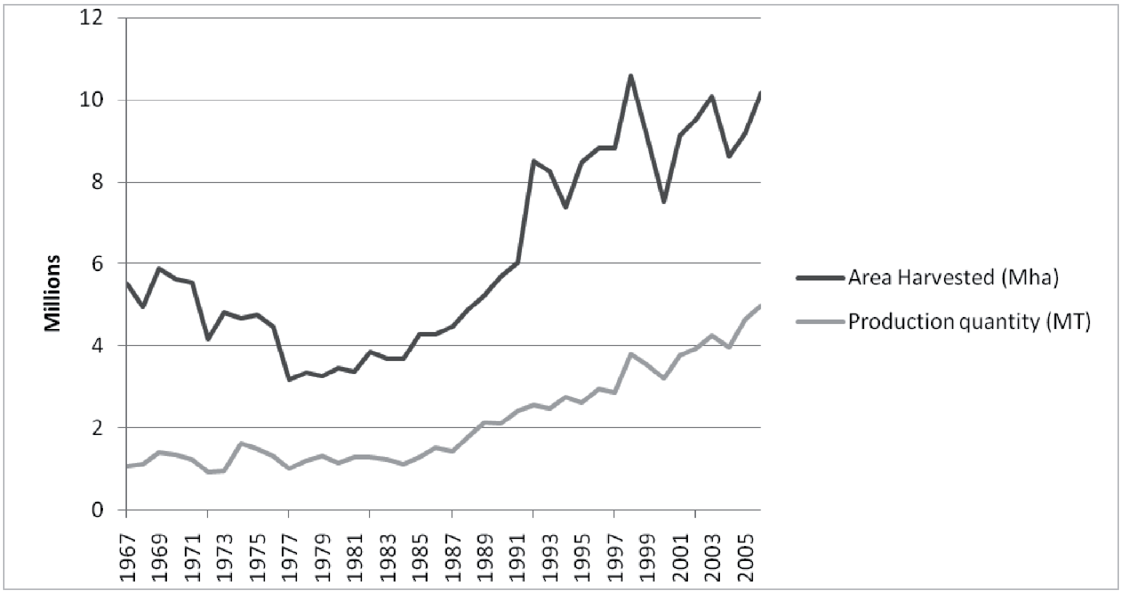
Global, regional and local importance

Cowpea (*Vigna unguiculata* (L.) Walp.) is the third most important global pulse crop (FAO, 2008), domesticated in Northeast Africa (Pasquet, 1999) with a secondary centre of domestication in West Africa (Pasquet, 1996b; Garba and Pasquet, 1998) and the Indian sub-continent (Steele *et al*., 1985). The crop is now cultivated in all tropical and some temperate areas, but is a major subsistence crop in sub-Saharan Africa. Cowpea does best in the savannah regions of the tropics and subtropics, where the climate is characterized by wet summer seasons and dry winter seasons and where droughts and poor soils restrict other crops. It is widely adapted and noted for its stress tolerance as a grain legume, vegetable and fodder crop of warm to hot regions of Africa, Asia and Americas (Ehlers and Hall, 1997).

The crop's value lies in the high protein content of the seeds, the vitamins and minerals in young plants and its ability to tolerate droughts and to fix atmospheric nitrogen, which allows it to improve poor soils (IITA, 2004). As shown in Figure 27, the area harvested and production has increased markedly in recent years (Ehlers and Hall, 1997), with cowpea now cultivated on approximately ten million hectares and with an annual production of five million tonnes of cowpea dry grain worldwide in 2006 (FAO, 2008). Nigeria produced 3.04 MT making it the world's largest producer, followed by Niger (0.69 MT) and Mali (0.45 MT). The total area grown to cowpea was 10.1 million hectares—about 9.3 million hectares of these in West Africa. World average yield was 1400 kg /ha, although average yield in Nigeria was 690 kg /ha, and in Niger was 170 kg /ha (FAO, 2008).

FIGURE 27

World area harvested and production quantity for cowpea (FAO, 2008)



Although plant breeders have striven to enhance and improve production (IITA, 2004), exploitation has been hampered by a lack of:

- Taxonomic, genetic and ecogeographic knowledge,
- *In situ* and *ex situ* conserved material that is easily exploitable by breeders,
- Characterization and evaluation of existing conserved germplasm,
- Coordination of national, regional or international coordinated conservation strategies for *Phaseolus* and *Vigna* diversity.

Production is characterized by limited use of purchased inputs and the crop is traditionally inter-cropped with cereals such as maize, millets, sorghum and cassava (Singh *et al*., 1997; Rao and Mathuva, 2000). It has been suggested that intercropping has the advantage of minimizing the destructive effects of insect pests; however, a recent study reported that mixed cropping with pearl millet had no effect on major pests (Bottenburg and Singh, 1997).

Cowpea is mainly used for human and livestock consumption. A wide range of nutritional value exists between cultivars of cowpea (Breassani, 1985). Cowpea grain contains 24–28% protein (Eneobong, 1995), which is significantly higher than values reported for African Yam beans (*Sphenostylis stenocarpa*) and pigeon pea (*Cajanus cajun*) in the same study, making it extremely valuable where people cannot afford protein foods such as meat and fish. A recent study on six Brazilian cultivars reports protein, carbohydrate and oil content ranging from 195–261, 678–761 and 12–36 g/kg of dry matter respectively, as well as significant differences in amino acid content between varieties (Maia *et al*., 2000). When fresh, the young cowpea leaves, immature pods and peas are used as vegetables, while snacks and main meal dishes are prepared from the dried grain. Cowpea haulms after harvest are used for feeding cattle, goats, pigs, sheep and other farm animals (IITA, 2004); while the decaying root residues provide manure for cultivated fields (Singh *et al*., 1997). In many regions cowpea is inter-cropped with cereals, where the indeterminate or semi-determinate growth has the added advantage of preventing soil erosion and suppressing growth of weeds (Singh *et al*., 1997). The major limitation to the production of cowpea in many parts of Africa is attack by insect pests (Jackai and Adalla, 1997); notably, storage weevil (*Callosobruchus maculatus*). Other pests of cowpea include: thrips (*Megalurothrips sjostedti*), pod borers (*Maruca vitrata*), aphids (*Aphis craccivora*) and pod-sucking bugs (*Clavigralla tomentosicollis*). Therefore, for subsistence farmers, on-farm storage often involves the mixing of infested cowpea grain with wood ash from cooking fires to discourage insects. Parasitic weeds, such as *Striga gesneroides* are also an important limitation to cowpea production (Toure *et al*., 1997). In a recent experiment, Karungi *et al*. (2000) found that insect damage alone accounts for 24–69 % of the total variation in grain yield.

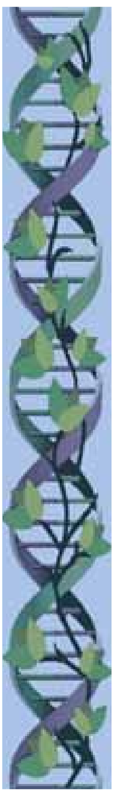
Taxonomic classification

Cowpea is morphologically and genetically variable, including wild perennial, wild annual and annual cultivated forms (Pasquet, 1999). Linnaeus (1753, 1763) did not recognize *Vigna* as a distinct entity, but recognized three of the cultivated forms of *V. unguiculata* as distinct species within *Dolichos*; namely, *Dolichos unguiculatus, D. biflorus* and *D. sinensis. Vigna* was erected by Savi (1824) to contain cowpea (*V. unguiculata* (L.) Walp.) and related species. Pasquet (1998) noted that several approaches have been taken to the taxonomy of the cultivated forms and although the number of taxa has been generally agreed, their rank has been much debated. Piper (1912) took the three groups recognized on the basis of seed and pod characters by Linnaeus (1763) and raised them to specific rank, while Westphal (1974) developed the concept of cultivar-group rank that is now accepted. However Pasquet (1998) noted that it is not easy to distinguish cv. gr. *Unguiculata* from *Biflora* and following a phenetic analysis, introduced a fourth cultivar-group, cv. gr. *Melanophthalmus*, as follows:

- Cultivar-group *Unguiculata* (Westphal, 1974) – Cowpea, black-eye bean. The most widespread and economically most important group of the species, cultivated in many (sub)-tropical and warmer temperate countries. Main production regions are in the Sahel belt in Africa, Brazil and Venezuela, but it is also frequently grown in other African, Asian, Australasian and American countries. It is mostly used as a pulse (especially in Africa) and consumed in various preparations (cooked, ground and made into fried or steamed cakes etc.). Less often, young pods and leaves are used as a vegetable. In the United States of America it is often cultivated as forage or a green manure crop. Cultivar-group *Unguiculata* was originally domesticated in Africa in Neolithic times and remains the dominant African grain legume.
- Cultivar-group *Melanophthalmus* (Pasquet, 1998) – The most recently recognized cultivar-group, based on the taxonomy proposed by Chevalier (1944), with a thin testa and often wrinkled. It is mainly cultivated in West Africa.
- Cultivar-group *Biflora* (Westphal, 1974) – Catjang (bean). Mainly cultivated in South Asia (India, Sri Lanka) and less often in Southeast or East Asia, rarely in Africa or elsewhere in (sub) tropical regions. It is grown as a pulse, as a vegetable for the green pods, as a forage crop, especially for hay and silage and as a green manure crop. The Catjang bean is much less variable than the true cowpea.
- Cultivar-group *Sesquipedalis* (Westphal, 1974) – Yard-long bean, asparagus bean. Cultivated mainly in South and Southeast Asia, from India to Indonesia and the Pacific islands—also in East Asia and as a minor garden crop widely grown in many (sub)tropical countries of Africa (especially West Africa) and America (e.g., the Caribbean). The very long young pods (to 90 cm) are used as a vegetable (sometimes also the leaves or seedlings). Dry seeds are less often consumed and also more infrequently the yard-long bean is grown as a forage or green manure plant. Breeding programmes have produced many cultivars in India, Nigeria, the United States of America, Cuba and the Philippines; some of them originating from hybridizations between cowpea and yard-long bean.

In their revision of the taxonomy of *V. unguiculata*, Mithen and Kibblewhite (1993) placed heavy emphasis on separating the wild and cultivated forms, placing them in separate subspecies, with all wild taxa being assigned varietal rank. While Padulosi (1993) recognized 4 wild subspecies of *V. unguiculata*, namely, subsp. *dekindtiana* (with varieties *dekindtiana*, *ciliolata, congolensis* and *grandiflora*), *pubescens*, *protracta* (with varieties *protracta*, *kgalagadiensis* and *rhomboidea*), *tenuis* (with varieties *tenuis* and *parviflora*) and *stenophylla*. However, the most widely accepted classification of *V. unguiculata* infra-specific diversity is that presented by Pasquet (1993a, 1993b, 1996a), where the wild taxa are subdivided into 10 subspecies and 1 variety, and can be broadly subdivided into three groups. The first group consists of perennial out-breeders, which can be distinguished from each other on the basis of floral characters. These include subspecies *baoulensis*, *burundiensis*, *letouzey* and *pawekiae*. The second groups are the perennial out/inbreeds associated with mostly drier, coastal environments, this group includes subspecies *alba*, *pubescens*, *tenuis*, *stenophylla* and *dekindtiana*. The last group consists of wild or weedy annuals, which are all classified under subspecies *spontanea*. To these subsequently, Pasquet (1997) described an additional subspecies *aduensis*, an Ethiopian endemic. The perennial out-breeders appear primitive and are somewhat separated from each other and from the perennial out/inbreeds. Although distinct morphologically, two subspecies of *V. unguiculata*, subsp. *pubescens* and subsp. *unguiculata*, appeared most closely related (Pasquet, 1999).

For the genus *Vigna* as a whole, the accepted classification is that proposed by Verdcourt (1971) and amended by Maréchal *et al*. (1978). When subsequently described taxa are included, the genus contains 61 species and 63 infra-specific *Vigna* taxa (Maxted *et al*., 2004).



Wild relatives

The majority of *Vigna* species have been described and classified using a combination of morphological characteristics and information on the genetic relationships among the taxa; as a consequence, the make-up of the gene pool is only relatively well understood for the cowpea (Ng and Padulosi, 1991). The cowpea primary gene pool is unusually large, with eleven subspecies plus several varieties recognized by Pasquet (1993a, 1993b, 1997) (i.e., ten perennial and one annual subspecies (*unguiculata*)). Subsp. unguiculata is split into var. *unguiculata*—which is the cultivated cowpea and contains four cultivar groups—and var. *spontanea*, which is the annual wild cowpea found from Senegal to Eritrea and south to Namibia and South Africa. *V. unguiculata* is placed in section Catiang (DC.) Verdc. with *V. schlechteri Harms, V. keraudrenii* Du Puy & Labat and *V. monantha*, so these species are the closest wild relatives of cowpea and have as yet untapped potential for exploitation. Vaillancourt and Weeden (1996) reviewed existing data sets for intra- and inter-specific relationships of *V. unguiculata* and suggested the closest genetic relatives to cowpea outside of section *Catiang* is subgenus *Plectotropis* (=*V. vexillata*), a finding later corroborated by Jaaska (1999), who also suggested subgenus *Vigna* section *Reticulatae* (*V. reticulata*).

Primary wild relatives

Group A

- *Vigna unguiculata* subsp. *unguiculata* var. *unguiculata* cultivar group *Sesquipedalis*
- *V. unguiculata* subsp. *unguiculata* var. *unguiculata* cultivar group *Melanophthalmus*
- *V. unguiculata* subsp. *unguiculata* var. *unguiculata* cultivar group *Unguiculata*
- *V. unguiculata* subsp. *unguiculata* var. *unguiculata* cultivar group *Biflora*

Group B

- *V. unguiculata* subsp. *unguiculata* var. *spontanea*
- *V. unguiculata* subsp. *baoulensis*
- *V. unguiculata* subsp. *letouzeyi*
- *V. unguiculata* subsp. *burundiensis*
- *V. unguiculata* subsp. *pubescens*
- *V. unguiculata* subsp. *dekindtiana*
- *V. unguiculata* subsp. *tenuis*
- *V. unguiculata* subsp. *stenophylla*
- *V. unguiculata* subsp. *alba*
- *V. unguiculata* subsp. *pawekiae*
- *V. unguiculata* subsp. *aduensis*

Secondary wild relatives

- *V. schlechteri* Harms (Syn. *V. nervosa* Markötter)
- *V. keraudrenii* Du Puy & Labat
- *V. monantha* Thulin

Tertiary wild relatives

Other *Vigna* subgenus *Vigna* species

Distribution and centre of diversity

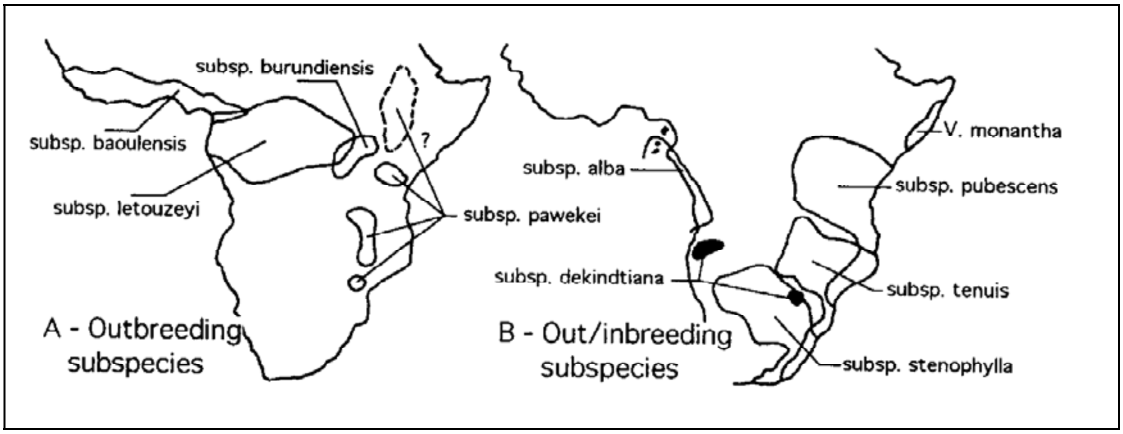
Cultivated cowpea originated in Africa—the only continent where wild relatives are encountered (Maréchal *et al*., 1978). Wild and cultivated forms cross readily. Sauer (1952) argues a solely Ethiopian centre of origin, followed by subsequent evolution predominantly in the ancient farming systems of the African savannah. There are two centres of diversity for this variable crop species: Tropical Africa (*Unguiculata* group and wild forms) and India/Southeast Asia (the other cultivar-groups). Domestication took place in Africa in Neolithic times (Hanelt, 2001). The crop spread in the second millennium BC via the Near East to India and in the first millennium BC to the Mediterranean countries and to Southeast and East Asia. Here, the cultivar-groups *Biflora* and *Sesquipedalis* were developed as a result of selection for grain. Where exactly the crop was domesticated in Africa is still a matter of debate; Ethiopia, West Africa or a diffuse origin in the sub-Saharan belt having been proposed. The crop was subsequently taken to the Americas in the 17th century.

The most widely accepted concept of *V. unguiculata* infra-specific diversity is that presented by Pasquet (1993a, 1993b, 1996a, 1998), where the wild taxa are subdivided into 11 subspecies and 2 varieties. The infra-specific diversity within

V. unguiculata and its close allies is summarized in Table 10 and shown in Figure 28. The highest taxon richness (five subspecies) is found at the southern tip of Mozambique, close to the border with South Africa, with additional potentially interesting areas for *V. unguiculata* diversity in eastern Tanzania (with five subspecies) and central Angola (with four subspecies.

FIGURE 28

Distribution of *V. unguiculata* infra-specific diversity with its close allies (Pasquet, 1996a)



For the whole genus, the highest concentration of *Vigna* species occurs in the Zambezian centre of endemism (White, 1983), with 80 % of all African *Vigna* species present. The Guineo–Congolian and Sudanian centres of endemism have the next highest level with 59 % of all species of *Vigna* in both, while the Guinea-Congolian/Sudanian transition region contains 55 % of all species. Other regions of high species richness include the Lake Victoria Mosaic, the Guinea-Congolian/ Zambezian regional transition zone, each with 45 % of all *Vigna* species, as well as the Somalia–Masai centre of endemism, with 43 % of all species. Conversely, the Sahara regional transition zone, the Cape regional centre of endemism, Karoo-Namib and the Tongaland–Pondoland regional mosaics are the most species poor, with 3.5 %–12.5 % of *Vigna* species. The highest concentration of *Vigna* species (i.e., the hotspots for *Vigna* diversity), occurs between 10°N and 20°N in the Zambezi River basin and Central African regions; mainly within the Democratic Republic of the Congo (Maxted *et al*., 2004). There are three particular hotspots at the southern tip of Lake Tanganyika (24 species), around the Great Lakes (23 species), and in the Cameroon Highlands (19 species). Members of the genus are predominantly herbaceous plants which occur in a wide range of habitats, but particularly grasslands, open woodlands, bush-lands and thickets. Perennial species generally possess large, woody rootstocks, which usually die back in the colder months, growing again from the rootstocks in warm weather or following burning.

TABLE 10

Geographic distribution of priority *Vigna* taxa (Maxted *et al*., 2004)

Taxon	Geographic distribution	Status	Ecological preferences
V. unguiculata subsp. *unguiculata* var. *unguiculata* cv. *Sesquipedalis*	–	Crop	Cultivated
V. unguiculata subsp. *unguiculata* var. *unguiculata* cv. *Melanophthalmus*	–	Crop	Cultivated
V. unguiculata subsp. *unguiculata* var. *unguiculata* cv. *Unguiculata*	–	Crop	Cultivated
V. unguiculata subsp. *unguiculata* var. *unguiculata* cv. *Biflora*	–	Crop	Cultivated
V. unguiculata subsp. *unguiculata* var. *spontanea*	Central, East, Northeast and southern Africa	Wild	Savannah, especially disturbed areas, often as a weed, 0–1 850 m.
V. unguiculata subsp. *baoulensis*	West Africa and Zambia	Wild	Disturbed areas, 80–1 250 m.
V. unguiculata subsp. *letouzeyi*	Central Africa and Cameroon	Wild	Disturbed areas, 320–800 m.
V. unguiculata subsp. *burundiensis*	Central and East Africa	Wild	Disturbed areas, 1 800–1 900 m.

Taxon	Geographic distribution	Status	Ecological preferences
V. unguiculata subsp. *pubescens*	Central, East, Northeast, southern, West and Zambesiacan Africa	Wild	Widespread, grasslands, coastal thickets, rocky outcrops, roadsides, savannas and fallow fields, usually near water, 0–1 550 m.
V. unguiculata subsp. *dekindtiana*	Central, East, Northeast, southern, West and Zambesiacan Africa	Wild (though utilized as a wild harvested resource)	Very widespread, roadsides, woodlands, grasslands (especially if burnt seasonally), various savannas, swamps, cultivated fields, riversides, riverine forests, littoral zones, 1–2800m
V. unguiculata subsp. *tenuis*	East, southern and Zambesiacan Africa	Wild	Miombo woodland, grassland, and sandy places near coast, 1– 1 550 m.
V. unguiculata subsp. *stenophylla*	Central, southern and Zambesiacan Africa	Wild	Kalahari sands in FZ region, 1–2 350 m.
V. unguiculata subsp. *alba*	Central, East and Zambesiacan Africa	Wild	Disturbed grassland and forest margin, 1–1 700 m.
V. unguiculata subsp. *pawekiae*	Central, East, Northeast, southern, West and Zambesiacan Africa	Wild	Tree and palm savannas, swampy areas, roadsides, gallery forests, grasslands and fallow fields, 1–2 700 m (–3 650 m in Kenya).
V. unguiculata subsp. *aduensis*	Ethiopia	Wild	Disturbed areas, 1 200–2 900 m.
V. schlechteri	Southern and Zambesiacan Africa	Wild	Montane grasslands, Ngongoni veld, amongst rocks and disturbed areas; loams, 650–2 290 m.
V. keraudrenii	Madagascar and Mozambique	Wild	Rocky hillsides and high altitude woodland with mosses and lichens, 1 420–1 940 m.
V. monantha	Somalia	Wild	Sandy plains of ancient dunes, 20–230 m

Known uses of wild relatives in crop improvement

Since no adequate levels of resistance to major pests and diseases have been identified in accessions of any *V. unguiculata* taxa (Barone and Ng, 1990), it is necessary to identify genotypes and species which can be used as bridge parents in wide crosses. The only species with which concerted efforts have been made to hybridize *V. unguiculata* is *V. vexillata*, due to its resistance to major insect pests. Studies have shown that these two species cannot easily hybridize, as any pods obtained from crosses have been observed to shrivel within a few days (Barone and Ng, 1990; Fatokun, 1991; Fatokun *et al*., 1993; Barone *et al*., 1992). However, it has been confirmed that pollen tube germination and subsequent fertilization occur normally (Fatokun, 1991), which implies that embryo rescue remains a possibility. Gomathinayagam *et al*. (1998) have recently reported success in growing immature embryos (10–12 days old) resulting from a cross between *V. unguiculata* and *V. vexillata* in Murashige and Skoog (MS) medium supplemented with BAP to produce callus. Cytological studies of the resulting plantlets showed a high rate of univalent formation in hybrids, suggesting genetic differentiation between the two parental species.

V. marina and *V. luteola* have also been hybridized with *V. unguiculata* (Smartt, 1979), but both attempts have been unsuccessful. In a hybridization experiment involving *V. schlechteri* (syn. *V. nervosa*) and *V. unguiculata*, it has been reported that developing pods aborted within five days of pollination (Mithen, 1987), which seems to indicate that these two species cannot hybridize successfully. Although *V. unguiculata* is morphologically similar to species in sections *Macrodontae* and *Liebrechtsia*, it is unlikely that hybridization with these species would be successful because of the different chromosome numbers—2n = 20, as opposed to 2n = 22 in *V. unguiculata* (Baudoin and Maréchal, 1991).

It appears that the full range of genetic diversity within *V. unguiculata* has yet to be fully characterized and evaluated for useful traits that might be bred into cowpea. Coulibaly *et al*. (2002) found that the wild annual cowpea was more diverse than the domesticated cowpea for AFLP markers, based on 117 accessions with a mixture of wild and weedy annuals, domesticated types and perennial subspecies. This study corroborates an earlier study using allozymes on the cultivar groups that showed low levels of genetic diversity in cultivated cowpea, but higher diversity in wild cowpea taxa (Vaillancourt and Weeden, 1996). Mithen (2000) suggests that while domestication of cowpea occurred in West Africa, considerable genetic and biochemical diversity of *V. unguiculata* is also found in southern Africa, providing a potentially valuable, but so far relatively unexploited resource for cowpea breeding programmes. The wild conspecific forms of *V. unguiculata* have all been reported to hybridize easily with the cultigen and have thus been placed in the primary gene pool (Smartt, 1979; Smartt, 1981; Mithen, 1987), although reduction in seed weight has been reported in F1 progeny of crosses between the wild forms and cultivated forms (Rawal *et al*., 1976). Fatokun and Singh (1987) report that in a cross between IT84S-2246-4, an improved cowpea variety, and *V. unguiculata* subsp. *dekindtiana* var. *pubescens* (= subsp. *pubescens*), pods collapsed within 12 days and embryo rescue was required. Similarly, F1 hybrids of a cross between cultivated cowpea and *V. unguiculata* subsp. *rhomboidea* (= subsp. *stenophylla*) were only partially fertile (Fatokun *et al*., 1997).

Priority taxa

High priority taxa

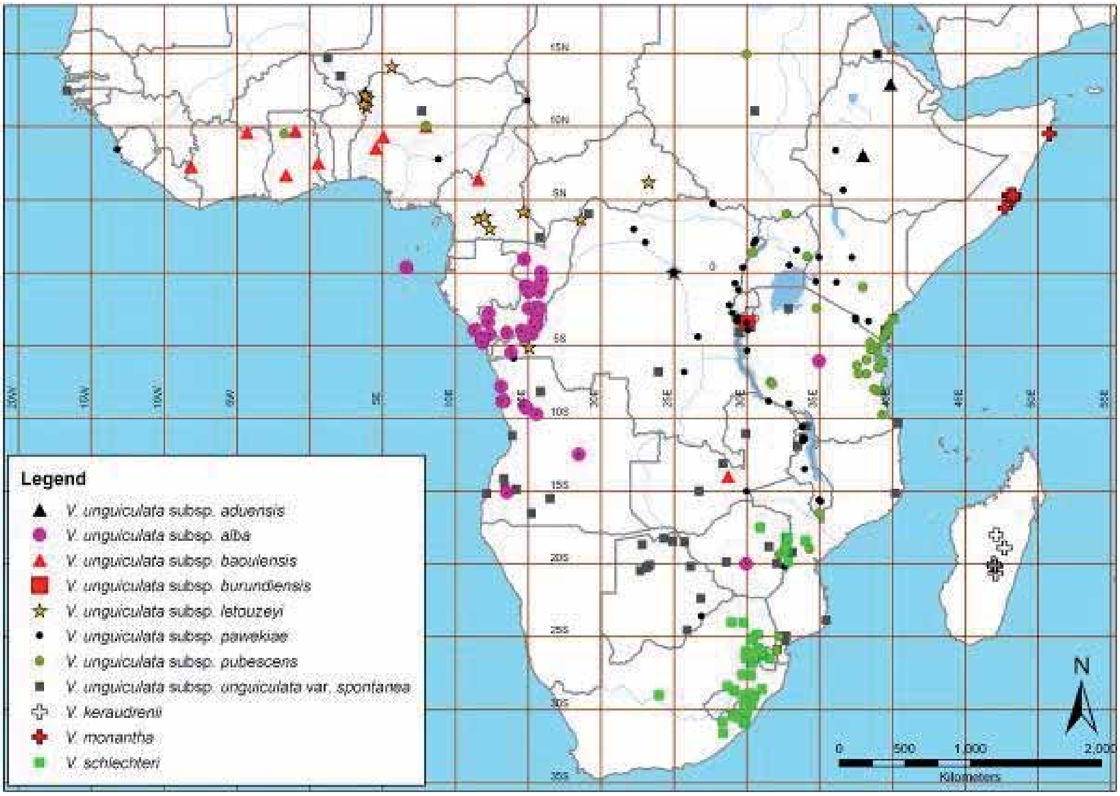
- *V. unguiculata* subsp. *aduensis*
    - subsp. *alba*
    - subsp. *baoulensis*
    - subsp. *burundiensis*
    - subsp. *letouzeyi*
    - subsp. *pawekiae*
    - subsp. *pubescens*
    - subsp. *unguiculata* var. *spontanea*

Other priority taxa

- *V. keraudrenii*
- *V. monantha*
- *V. schlechteri*

FIGURE 29

Distribution of priority cowpea (*Vigna*) wild relatives. Data source: Maxted *et al.* (2004)



Priority sites

Based on the analysis presented in Figure 29, the following locations should be investigated further as potential sites for *in situ* conservation of cowpea (*Vigna*) wild relatives:

- Amhara (Tigray) and Shewa, Ethiopia. Only two locations of *V. unguiculata* subsp. *aduensis* have been recorded in these two provinces of Ethiopia—neither location is currently protected. The record from Tigray (Lat: 12.94, Long 39.87), east of Adi Keyih dates back to 1909. This location is some 40 km directly east of Gumburda-Grakaso National Forest Priority Area, but there are no other protected areas in the near vicinity. The record from Shewa

(Lat: 8, Long: 38) dates back to 1832. This location is in the vicinity of Boyo Swamp Controlled Hunting Area (IUCN category VI), Abijatta-Shalla Lakes National Park (IUCN category II) and Butajira National Forest Priority Area, but does not lie within a protected area itself. *V. unguiculata* subsp. *pawekiae* has also been recorded at this location.

- Lefini Faunal Reserve (IUCN category IV), Congo. Data analysis indicates that populations of *V. unguiculata* subsp. *alba* may occur within this existing protected area. Conkouati-Douli National Park (IUCN category II) and Dimonika UNESCO-MAB Biosphere Reserve (Congo) may also contain populations of this taxon. Populations of this taxon further south in Angola appear not to be protected.
- Comoé National Park, Côte d'Ivoire. *V. unguiculata* subsp. *baoulensis* has been recorded near (inside) the northwest boundary of this protected area, near Cercle de Boule-Nord. This taxon has also been recorded in the vicinity of Owabi Wildlife Sanctuary (IUCN category IV) and Ramsar site and Mole National Park (IUCN category II), Ghana, Deux Rivières Bena Forest Reserve, Togo, and Kainji Lake and Old Oyo National Parks (IUCN category II), Nigeria.
- Burundi, c. 15 km northeast of Gitega (Lat: -3.5, Long: 30). This location is the only recorded site of *V. unguiculata* subsp. *burundiensis*. Subsp. *pawekiae* has also been recorded at the same location. The site is not protected but is in the vicinity of Ruvubu National Park (IUCN category IV) (c. 25 km to the northeast).
- Dja Wildlife Reserve (IUCN category IV), UNESCO-MAB Biosphere Reserve and World Heritage Convention Faunal Reserve, Cameroon. Occurrences of *V. unguiculata* subsp. *letouzeyi* have been recorded c. 15 km to the west and c. 80 km to the northwest of this protected area. The taxon may also occur within Libenge Hunting Zone, Democratic Republic of the Congo. Populations recorded in western Nigeria are probably not currently protected.
- Virunga National Park (IUCN category II, World Heritage in Danger List (World Heritage Convention) and Ramsar), Democratic Republic of Congo. *V. unguiculata* subsp. *pawekiae* has been recorded within the boundaries of, and in the vicinity of this protected area and the neighbouring Rutshuru Hunting Reserve (IUCN category VI) (Democratic Republic of Congo) and Volcans National Park (IUCN category II and UNESCO–MAB Biosphere Reserve), Rwanda.
- Kibira and Rusizi National Parks (IUCN category IV), Burundi. V, unguiculata subsp. pawekiae and subsp. *pubescens* have been recorded in the near vicinity of these two protected areas.
- Haut-Zaire, Democratic Republic of Congo, c. 25 km northwest of Mombala (Lat: 0, Long: 25). *V. unguiculata* subsp. *letouzeyi*, subsp. *pawekiae* and subsp. *unguiculata* var. *spontanea* have been recorded at this location, which is not protected.
- Nyika National Park (IUCN category II), Malawi. *V. unguiculata* subsp. *pawekiae* has been recorded inside this protected area. *V. unguiculata* subsp. *unguiculata* var. *spontanea* has also been recorded close to (outside) the eastern boundary.
- Rufunsa Game Management Area (IUCN category VI), Zambia. *V. unguiculata* subsp. *pawekiae* has been recorded within this protected area. *V. unguiculata* subsp. *baoulensis* has also been recorded c. 60 km to the northwest of the adjacent Luano Game Management Area (IUCN category VI).
- Serengeti National Park (IUCN category II) and Uwanda Game reserve (IUCN category IV), Tanzania. *V. unguiculata* subsp. *pubescens* has been recorded within these protected areas.
- Zanzibar Central/South, Tanzania. *V. unguiculata* subsp. *pubescens* and subsp. *unguiculata* var. *spontanea* have been collected on this island. The collection sites are some 12 km north of Menai Bay Conservation Area (IUCN category VI).
- Antananarivo and Fianarantsoa provinces, Madagascar. *V. keraudrenii* is probably endemic to Madagascar, with records from Mozambique indicating introductions. None of the known locations in Madagascar are protected.
- Mudug and Bari, Somalia. *V. monantha* is endemic to Somalia and has only been collected in these regions, which are not protected.
- Rhodes Nyanga National Park (IUCN category II), *Zimbabwe*. *V. schlechteri* has been recorded within and just outside the boundaries of this protected area.
- Manicaland, Zimbabwe, between Mutare and Umtali. *V. schlechteri* and *V. unguiculata* subsp. *pawekiae* have been collected at this location, which is not protected.
- Bewaarkloof, Mount Sheba and Motlatse Nature Reserves (IUCN category IV), South Africa. *V. schlechteri* has been recorded in the near vicinity of these protected areas.
- QwaQwa National Park (IUCN category IV), South Africa. *V. schlechteri* has been recorded near the northern boundary of this protected area.
- Malalotja Nature Reserve (IUCN category IV) and Mlilwane Game Sanctuary (IUCN category VI), Swaziland. *V. schlechteri* has been collected within and in the near vicinity of these two protected areas.

Recommendations

- Analysis of *Vigna* distribution data reveals that the priority taxa are rarely found at the same locations. This presents a particular challenge for *in situ* conservation because a number of genetic reserves will need to be established in multiple locations. The locations listed above should be investigated further; firstly, to verify that the taxa that have been recorded there in the past are still found there and secondly, to assess the possibility of genetic reserve establishment at the sites. Additional searches for the taxa should also be carried out in the locality, particularly in cases where a taxon has been recorded close to an existing protected area.
- Maxted *et al*. (2004) provided a conservation strategy for the genus *Vigna* as a whole but noted that although the cultivated forms of *V. unguiculata* subsp. *unguiculata* var. *unguiculata* are well conserved *ex situ*, with 11 500 accessions (76% of their global collection) held in trust by IITA's genebank (IITA, 2007), *ex situ* collection should continue in order to ensure full representation of all infra-specific taxa and ecological variants. In particular, efforts should be made to collect samples of the high priority taxa identified in this study; especially those of very limited distribution.
- Although there has been limited success with inter-specific crosses involving *V. unguiculata*, it is of paramount importance that the closest wild relatives are collected and evaluated in order to identify material that may be useful for cowpea improvement; then, if necessary, crossing can be attempted using bridging species.

2.14 Maize

Scientific name

Zea mays L.

Principle synonyms

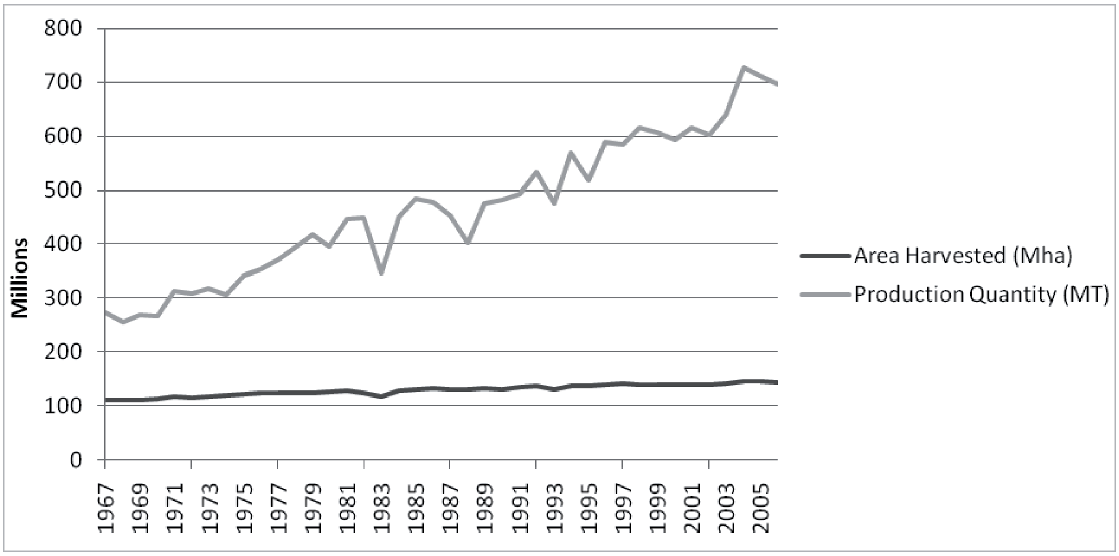
Zea curagua Molina, *Zea indentata* Sturtev., *Zea indurata* Sturtev., *Zea japonica* Van Houtte, *Zea saccharata* Sturtev.

Global, regional and local importance

Maize is the world's third most important crop, providing about 7% of global food energy supply after wheat and rice (FAO, 1998), and is the crop with highest production in terms of total production (695.2M Mt in 2006) (FAO, 2008). It is the most important human food energy source in Central America and southern Africa (FAO, 1998), but is also used widely as feed for livestock, with average yields of 4.8t/ha (FAO, 2008). Maize is widely cultivated between 55°N and S and from sea level to 3600m in the cool tropical highlands of the Andes. Maize is produced under a wide variety of climatic conditions ranging from tropical lowlands, tropical and subtropical mid-altitudes, temperate and cool tropical highland climates (Taba, 1997). The six countries with highest maize areas cultivated and production are USA (28.5MHa or 19.8%/267.6MT or 38.5%), China (27.1MHa or 18.8%/145.6MT or 20.9%), Brazil (12.6MHa or 8.7%/42.6MT or 6,1%), Mexico (7.3MHa or 5.1%/21.8MT or 3.1%), India (7.6MHa or 5.2%/14.7MT or 2.1%) and Argentina (2.4MHa or 1.7%/14.4MT or 2,1%) (FAO, 2008). Figure 30 indicates an impressive global increase in production of maize based on a slight increase in the area cultivated, indicating yields have increased from 2426 kg/Ha in 1967 to 4815 kg/Ha in 2006 (FAO, 2008).

FIGURE 30

World area harvested and production quantity for maize (FAO, 2008)



It is believed that maize was domesticated well before 4000 BC in Tehuscán, Puebla Tstae, Mexico (MacNeish, 1985). There is pollen of maize, teosinte (*Zea luxurians* (Durieu and Ascherson) Bird) and their common ancestor from 60,000–80,000 years ago from around Mexico City (Goodman, 1988), and maize had became a dietary staple in Mesoamerica by 1500 BC (Goodman, 1988). There are basically two hypotheses of the origin of maize; first, that maize, teosinte and *Tripsacum* all evolved from an unknown common ancestor (Weatherwax, 1954), and second, the more widely accepted thesis is that maize was derived from teosinte (Goodman, 1988). The early maize had very small, fragile, eight-rowed ears and it was thought to readily introgress with teosinte (Bird, 1980), although as modern maize evolved, so genetic barriers were establish to limit hybridization (Kato, 1984). It is thought that Central American maize was first taken to South America in about 2000 BC (Grobman *et al*., 1961) and to southwest North America in around 1000 BC (Adams, 1994), soon following to New England (Bendremer and Dewar, 1994). It is believed that Columbus found maize in Cuba and introduced it to Europe (Magelsdorf, 1974); then, via Europe, maize spread to Asia and Africa in the 16th century.

Taxonomic classification

The genus *Zea* L. of family *Poaceae* is made up of four species native to Mexico and Central America (Doebley and Iltis, 1980) with a base chromosome number of x=10. The genus includes the crop maize or Indian corn, as well as the closest wild relatives of maize known collectively as teosintes. Doebley and Iltis (1980) divide the genus into two sections, four species and four subspecies.

Section *Luxuriantes* is the more 'primitive' section and shows a close resemblance to the sister genus *Tripsacum*, while section *Zea* is mono-specific, containing *Z. mays* with its four subspecies. All four subspecies are annual, have more slender tassel branches (although secondarily thickened in cultivated maize) and longer pedicels in the male spikelets as compared to plants of section *Luxuriantes*. Iltis and Doebley (1980) classified the annual teosintes as subspecies of *Z. mays* to emphasize their close biological relationship to maize with which they hybridize freely to produce fertile descendents. The genus *Tripsacum* is the most closely related genus to *Zea*. It is a New World native with 13 perennial species that range from Massachusetts to Paraguay; the base chromosome number is x=18 and there are diploid, triploid, tetraploid and higher ploidy forms. Inter-generic crosses are possible, as evidenced by *T. andersonii* which is actually a sterile *Zea*–*Tripsacum* hybrid (Doebley, 2003).

Wild relatives

Primary wild relatives

- *Zea mays* L. subsp. *huehuetenangensis* (Iltis and Doebley) Doebley
- *Z. mays* L. subsp. *mexicana* (Schrader) Iltis
- *Z. mays* L. subsp. *parviglumis* Iltis and Doebley

Secondary wild relatives

- *Z. diploperennis* Iltis, Doebley and Guzman
- *Z. perennis* (Hitchcock) Reeves and Mangelsdorf
- *Z. luxurians* (Durieu and Ascherson) Bird

Tertiary wild relatives

Tripsacum species

Distribution and centre of diversity

The four wild *Zea* species have a relatively restricted distribution. Doebley (2003) summarized the ecogeographic distribution and cultivation status for *Zea* taxa (see Table 11) and showed the centre of diversity to be western and southern Mexico, with peripheral populations found in Guatemala, Honduras and Nicaragua. The range of the crop has been modified significantly by human activities during the millennia it has been cultivated, but Mexico and/ or lowland Central America is the centre of diversity of the important dent grain types of maize, with the flint grain types being found along the northern edge of South America, the Caribbean and along the coast to Argentina (Goodman, 1988).

TABLE 11

Classification and summary information for *Zea* (from Doebley, 2003)

Taxon	Cytology	Habit	Distribution	Altitudinal range (m)
Sect. *Luxuriantes* Doebley and Iltis				
Zea diploperennis Iltis, Doebley and Guzman	n=10	perennial	Sierra de Manantlán, south-western Jalisco state, Mexico	1 400–2 400
Zea perennis (Hitchcock) Reeves and Mangelsdorf	n=2x=20	perennial	Northern slopes of Volcán de Colima, Jalisco state, Mexico	1 500–2 000
Zea luxurians (Durieu and Ascherson) Bird	N=10	annual	Southeastern Guatemala, Honduras and Nicaragua (Mexico?)	0–1 100
Sect. *Zea*				
Zea mays Linnaeus	N=10	annual		
Zea mays L. subsp. *huehuetenangensis* (Iltis and Doebley) Doebley			Western Guatemala	900–1 650
Zea mays L. subsp. *mexicana* (Schrader) Iltis			Central and northern Mexico	1 700–2 600
Zea mays L. subsp. *parviglumis* Iltis and Doebley			Western Mexico from Nayarit to Oaxaca	400–1 800
Zea mays L. subsp. *mays*			Crop	

Known uses of wild relatives in crop improvement

Maize is an outbreeding crop from which inbreeds and hybrids have been extensively created and which naturally introgress with related wild species. However, it is interesting to note that wild *Zea* germplasm has not been widely used for formal maize improvement or hybrid development (Goodman, 1988). Although viral resistances were reported in perennial teosintes (Nault *et al*., 1982), their use in maize improvement has been limited, possibly because existing maize lines were found that confer similar resistance (Louie *et al*., 1990) and differing levels of cross-incompatibility with inter-taxon crosses were found making intra-maize crosses more straightforward (Sanchez pers. comm., reported in Taba, 1997). However, teosintes have been used experimentally to increase yield in maize hybrid combinations (Cohen and Galinat, 1984). Taba (1997) notes that teosinte race Balsas from Guerrero state, Mexico has the greatest genetic diversity of any teosinte, making it a logical candidate for use in introgressive hybridization with maize.

Priority taxa

High priority taxa

- *Z. diploperennis* – of restricted distribution in south-western Jalisco and central Veracruz states, Mexico.
- *Z. luxurians* – of very limited distribution in southeastern Guatemala and western Nicaragua. Wilkes (1967) suggested that *Z. luxurians* was extinct in Honduras and Taba (1997) concludes that if populations do remain extant they are likely to be highly threatened.
- *Z. mays* subsp. *huehuetenangensis* – only known from three locations in Huehuetenangensis department of Guatemala.

Other priority taxa

- *Z. mays* subsp. *mexicana*
- *Z. mays* subsp. *parviglumis*
- *Z. perennis*

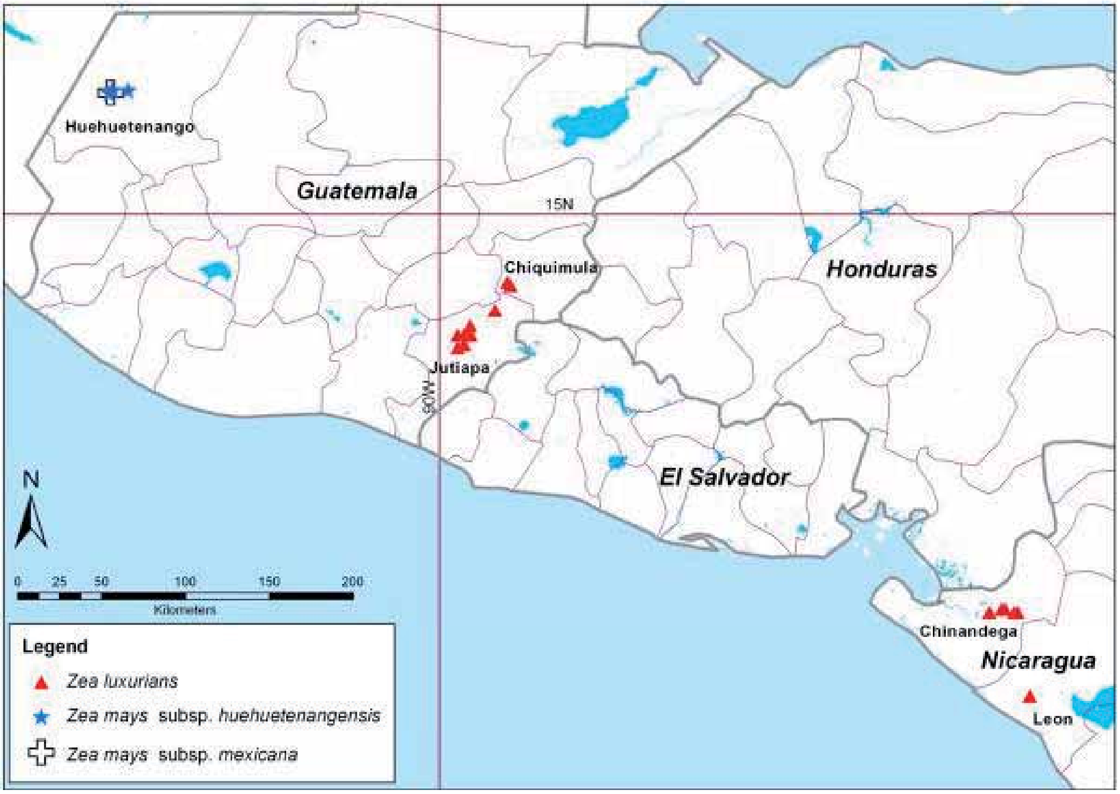
Priority sites

Zea luxurians

- None of the recorded locations of *Z. luxurians* in Guatemala appear to be protected (Figure 31), although one accession was collected in 1978 just outside the eastern boundary of the buffer zone (Zona de Amortiguamiento) of Volcán Culma Zona de Veda Definitiva (No Take (Hunting) Zone) (IUCN category III). Other recorded locations are in the vicinity (between c. 3–12 km) of Volcán Suchitán Regional Park (IUCN category VI) and Volcán Tahual and Volcán Ixtepeque Zonas de Veda Definitiva (IUCN category III).
- In Nicaragua, it may be found inside the boundaries of Estero Real Nature Reserve (IUCN category IV) and has been recorded close to (within c. 5 km) of the Ruins of León Viejo World Heritage Site.

FIGURE 31

Distribution of high priority maize wild relatives, *Zea luxurians* and *Z. mays* subsp. *huehuetenangensis*. *Z. mays* subsp. *mexicana* is also shown at the same site as one of the *Z. mays* subsp. *huehuetenangensis* populations[33]



Zea mays subsp. *huehuetenangensis*

The three recorded locations of *Z. mays* subsp. *huehuetenangensis* are not currently protected. However, one location (a canyon near San Antonio Hiusta, Lat: 15.66, Long: -91.66) appears to be only about 5 km to the west of the western boundary of the Sierra de los Cuchumatanes protected area (IUCN management category unknown).

Zea diploperennis

All but two of the recorded locations of *Z. diploperennis* are found within the Sierra de Manantlán Biosphere Reserve (IUCN category VI) (Figure 32). *Z. mays* subsp. *parviglumis* and *Z. perennis* have also been recorded within the boundaries of this reserve.

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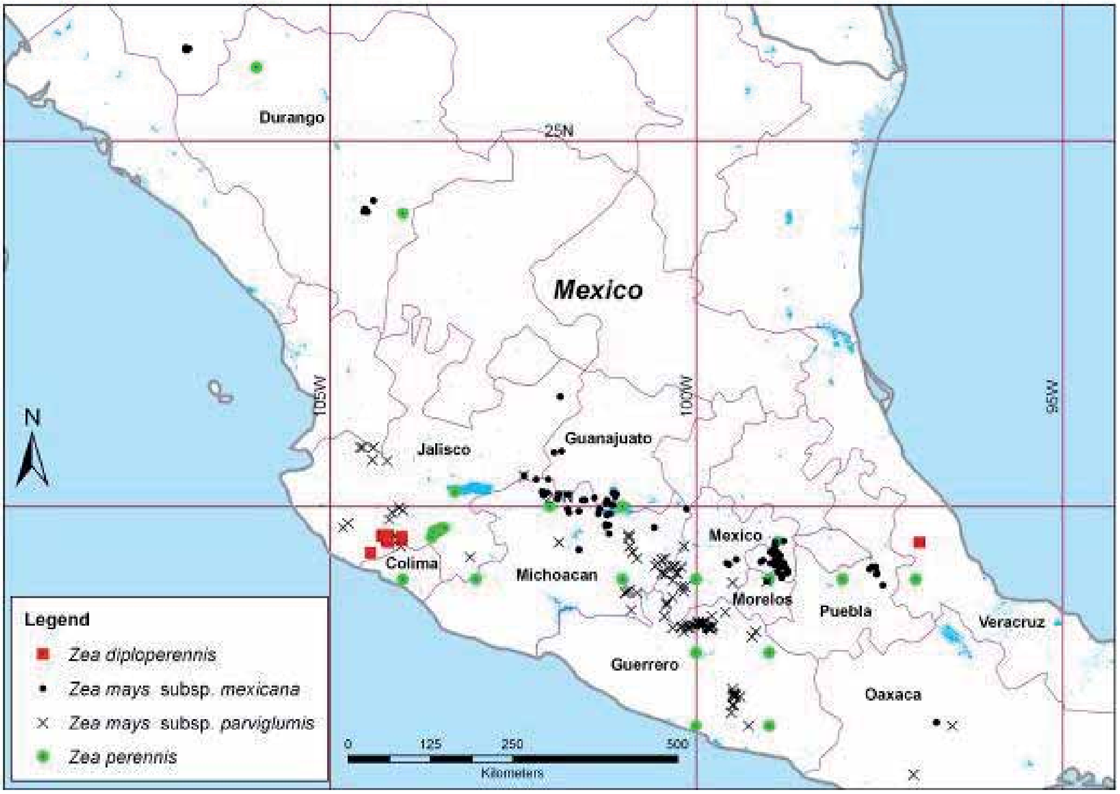
[33] Data sources: J.F. Doebley, Wisconsin, pers. comm., 2008; USDA, ARS, National Genetic Resources Program. pcGRIN. National Germplasm Resources Laboratory, Beltsville, Maryland; Missouri Botanical Garden (accessed through GBIF data portal, http://data.gbif.org/datasets/resource/621 09/08/2008); The AAU Herbarium Database (http://data.gbif.org/datasets/resource/224 09/08/2008); USU-UTC Specimen Database (http://data.gbif.org/datasets/resource/1508 09/08/2008)

FIGURE 32

Distribution of maize wild relatives, *Zea diploperennis, Z. mays* subsp. mexicana, *Z. mays* subsp. *parviglumis* and *Z. perennis* in Mexico[34,35]



Zea mays subsp. *mexicana*

Z. mays subsp. *mexicana* has been recorded within the boundaries of Altamirano Biosphere Reserve (IUCN category 1a), Michoacan state, and within Z.N.I. Chalchihuites Flora and Fauna Protection Area (IUCN category 1a) and Cobio Chichinautzin Flora and Fauna Protection Area (IUCN category VI), Morelos state. *Z. mays* subsp. *parviglumis* has also been recorded within Z.N.I. Chalchihuites Flora and Fauna Protection Area and *Z. perennis* has been recorded within Cobio Chichinautzin Flora and Fauna Protection Area. Our analysis indicates that the main clusters of populations of *Z. mays* subsp. *mexicana* (southern Mexico State, Distrito Federal, northern Michoacan, southern Guanajuato and eastern Jalisco) are not found within the boundaries of existing protected areas.

Zea mays subsp. *parviglumis*

One recorded location of *Z. mays* subsp. *parviglumis* is within the boundaries of Bosencheve National Park (IUCN category II), eastern Michoacan state. The taxon has also been recorded within Z.N.I. Chalchihuites Flora and Fauna Protection Area, at the same site as *Z. mays* subsp. *mexicana*. *Z. mays* subsp. *parviglumis* may also be found within the Sierra de

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[34] *Z. mays* subsp. *mexicana* is also known from Guatemala (see Figure 34).

[35] Data sources: J.F. Doebley, Wisconsin, pers. comm., 2008; USDA, ARS, National Genetic Resources Program. pcGRIN. National Germplasm Resources Laboratory, Beltsville, Maryland; Museo Nacional de Costa Rica (accessed through GBIF data portal, http://data.gbif.org/datasets/resource/566 09/08/2008); Repatriación de datos del Herbario de Arizona (ARIZ) (http://data.gbif.org/datasets/resource/2480 09/08/2008); Missouri Botanical Garden (http://data.gbif.org/datasets/resource/621 09/08/2008); USU-UTC Specimen Database (http://data.gbif.org/datasets/resource/1508 09/08/2008); NMNH Botany Collections (http://data.gbif.org/datasets/resource/1874 09/08/2008); Ejemplares tipo de plantas vasculares del Herbario de la Escuela Nacional de Ciencias Biológicas, México (ENCB, IPN) (http://data.gbif.org/datasets/resource/2498 09/08/2008); Herbario del Instituto de Ecología, A.C., México (IE-BAJIO) (http://data.gbif.org/datasets/resource/1595 09/08/2008); Instituto de Ciencias Naturales (http://data.gbif.org/datasets/resource/2559 09/08/2008); Vascular Plant Type Specimens (accessed through GBIF data portal, http://data.gbif.org/datasets/resource/731 09/08/2008); SINGER (http://data.gbif.org/datasets/resource/1430 09/08/2008)

Manantlán Biosphere Reserve, where *Z. diploperennis* and *Z. perennis* are also found. Another population is very close to (c. 2 km outside) the eastern boundary of Insurgente Jose Maria Morelos National Park (IUCN category II), Northeast Michoacan.

Zea perennis

Our analysis indicates that *Z. perennis* is found within the boundaries of Sierra de Manantlán Biosphere Reserve (IUCN category VI) (where *Z. diploperennis* and *Z. mays* subsp. *parviglumis* have also been recorded), Nevado de Colima National Park (IUCN category II), Jalisco state, and Cobio Chichinautzin Flora and Fauna Protection Area (IUCN category VI), Morelos state (where Z. mays subsp. *mexicana* has also been recorded).

Recommendations

- Wilkes (1993) suggested the establishment of a genetic reserve for *Z. mays* subsp. *huehuetenangensis* in Guatemala. Our analysis indicates that the three recorded locations of this rare taxon in Huehuetenango province of Guatemala are not currently protected; all three locations should be earmarked for protection. Potentially *Z. mays* subsp. *mexicana* distribution overlaps with *Z. mays* subsp. *huehuetenangensis* and therefore a site with a healthy population of both could provide the best option for genetic reserve conservation.
- Further searches for *Z. mays* subsp. *huehuetenangensis* should be undertaken to ascertain whether populations may be found at other sites in the same area and possibly within the existing Sierra de los Cuchumatanes protected area.
- Data collected at one of locations reveal that *Z. mays* subsp. *huehuetenangensis* was found in "maize fields and abandoned old maize fields with large populations of *Z. mays* subsp. *mexicana* and many (about 5% or more) F1 hybrids, on steep slopes" (H. Iltis collection 21880 – PI number 441934). If this taxon is particularly associated with cultivated and abandoned maize fields, it could be under threat from shifting or changing agriculture. This requires further investigation.
- *Zea* is one of the few crop genera where there is already active *in situ* conservation at the Sierra de Manantlán Biosphere Reserve (IUCN category VI) in south-western Jalisco state, Mexico. The reserve was established in 1987 to conserve the close wild relative, *Zea diploperennis* and other endemic species (Sanchez-Velasquez, 1991). *Z. diploperennis* is found only in Jalisco and Veracruz states, but the main cluster of locations are found in Jalisco, with only one record from central Veracruz, which is not protected. The Jalisco population has a very narrow range of around 50 km and all but one of the recorded locations in this state are found within the Sierra de Manantlán reserve; therefore, it is critical that active genetic conservation is implemented for this taxon at this site. Therefore it is a matter of some concern that (Wilkes, 2007) reported that populations of wild teosinte (the closest wild relative of maize) in Mexico and Central America have shrunk by over 50% in the last 40 years – obviously urgent remedial action is required to ensure the populations are secure. *Z. mays* subsp. *parviglumis* and *Z. perennis* have also been recorded within the boundaries of this reserve, so all three taxa could be actively conserved within one genetic reserve at this site.
- In addition to the Sierra de Manantlán Biosphere Reserve, our analysis shows the following protected areas to be potential sites for the establishment of further genetic reserves for *Zea* wild relatives:
    - Altamirano Biosphere Reserve (IUCN category 1a), Michoacan state (*Z. mays* subsp. *mexicana*);
    - Z.N.I. Chalchihuites Flora and Fauna Protection Area (IUCN category 1a), Morelos state (*Z. mays* subsp. *mexicana* and *Z. mays* subsp. *parviglumis*);
    - Cobio Chichinautzin Flora and Fauna Protection Area (IUCN category VI), Morelos state (*Z. mays* subsp. *mexicana* and *Z. perennis*);
    - Bosencheve National Park (IUCN category II), eastern Michoacan state (*Z. mays* subsp. *parviglumis*);
    - Jose Maria Morelos National Park (IUCN category II), Northeast Michoacan (*Z. mays* subsp. *parviglumis*).
- Given that Wilkes (1967) considered *Z. luxurians* to be extinct in Honduras (although Taba (1997) concluded it was present but endangered), and combined with the fact that maize is such an important global crop, there is a need for a systematic review of teosinte populations south of the Mexican border. Also, there does seem to be an obvious distributional gap in teosinte populations in El Salvador which warrants further study.
- In terms of *ex situ* conservation, Sanchez pers. comm. (reported in Taba, 1997) estimates that about 100 populations of teosinte have been collected from Mexico and transferred to *ex situ* storage, and approximately a further 20 remain uncollected, it would be wise to sample these remaining populations to provide full *ex situ* coverage.
- Doebley (1990) raised concern about the rate of natural introgression between wild and cultivated *Zea* that could potentially lead to the transfer of genetically engineered traits to the wild genepool. Subsequently this has been

shown to have occurred (Quist and Chapela, 2001), which suggests in terms of conservation that where possible wild Zea populations should be conserved in isolation from cultivated material and that as a precaution each population should be conserved *ex situ* as a back-up.

3. Important areas and conservation gaps: synthesis

3.1 Establishing the global network: first steps

In this study, we have identified immediate *in situ* CWR conservation priorities for 11 crops that are of major importance for food security in one or more sub-regions of the world and three further crops that are regionally important. As already noted, the 14 examples included are not a definitive list of globally, regionally, nationally or locally important crops; however, they are a first step in the critical process of establishing a global network of genetic reserves for some of the highest priority CWR based on their current and potential use as gene donors for crop improvement and relative degree of threat in the wild. In each crop case study, we have identified potential locations for the establishment of genetic reserves for the highest priority taxa (where access to the data needed for analysis is readily available[36]). The data used for each of the analyses are of varying quantity and quality and this is reflected in our recommendations for each of the crop complexes. In many cases, further research and ground-truthing is required in order to make final recommendations for genetic reserve sites, particularly as the presence of the taxa is largely based on historic occurrence records.

Table 12 shows the numbers of priority wild relative species in each of the 14 crop groups based on the analyses carried out in this study. The numbers of primary and secondary wild relative species are also shown. Based only on the degree of relationship of the wild relatives to their associated crop species, 6.45% of the species can be identified as a priority for conservation (see Annexe 1). However, taking into account a) tertiary wild relatives that have shown promise for crop improvement and b) relative threat, increases this percentage to 8.96. At least 6.81% of these are in urgent need of conservation action. The main reason for this significant increase in the percentage of priority species based on this sample of crop groups is that although we have identified 30 close wild relatives of potato based on taxonomic classification, almost any species in *Solanum* section *Petota* (196 species – Hijmans, 2001) can be used in potato improvement using ploidy manipulation and somatic fusion to overcome crossing barriers (Bradshaw *et al*., 2006). At least 110 of these are in urgent need of conservation action as there are five or fewer known observation records (Hijmans *et al*., 2002). On the other hand, of the four close wild relatives of sorghum, none of these are a high priority for conservation action, since they are all relatively widespread weedy species. Analysis of a larger sample of crop groups is needed to obtain a more reliable estimate of the overall percentage of priority CWR of all the major and minor food crops and of crops in general. However, this analysis does illustrate that the relative closeness of wild relatives to the crop cannot be used alone as a robust means of prioritizing CWR. A consolidated list of the priority taxa is shown in Annex 2.

As already noted, one of the commonly applied means of establishing conservation priorities is by applying the IUCN Red List criteria (IUCN, 2001); however, the current IUCN Red List of Threatened Species (IUCN, 2008) does not help in prioritization as so few CWR taxa have been assessed. Table 13 shows the taxa within the 14 crop gene pools included in this study that have been globally assessed. Only *Solanum* species have been systematically assessed and therefore can be prioritized using their Red List status. Provisional Red List assessments for all African *Vigna* species were undertaken by Maxted *et al*. (2004) and will be formally published in due course.

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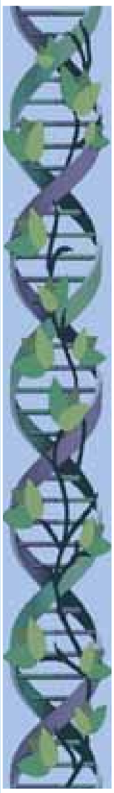
[36] In cases where data were not readily available for analysis, recommendations have been made for further study.

TABLE 12

Numbers and percentages of priority wild relative species of the 14 crops treated in this study

Crop	Crop taxon	Species in genus	Primary CWR species	Secondary CWR species	High priority CWR species	Other priority CWR species	Total priority CWR species	Notes
Finger millet	*Eleusine coracana*	9	3	3	2	4	6	
Barley	*Hordeum vulgare*	16	1	1	1	2	3	37
Sweet potato	*Ipomoea batatas*	600–700	3	11	2	–	2	
Cassava	*Manihot esculenta*	98	3	13	9	3	12	
Banana/plantain	*Musa acuminata*	30	10	15	10	–	10	
Rice	*Oryza sativa*	23	8	9	4	18	22	
Pearl millet	*Pennisetum glaucum*	80–140	1	2	1	3	4	
Garden pea	*Pisum sativum*	3	1	2	2	2	4	38
Potato	*Solanum tuberosum*	1000	6	24	110	–	110	39
Sorghum	*Sorghum bicolor*	25	2	2	0	0	0	40
Wheat	*Triticum aestivum*	6+22	6	12	5	9	14	41
Faba bean	*Vicia faba*	140	1	0	5	3	8	
Cowpea	*Vigna unguiculata*	61	1	3	1	3	4	
Maize	*Zea mays*	4	1	3	3	2	5	
	Totals	**2 117–2 277**	**47**	**100**	**155**	**49**	**204**	
	%	**100**	**2.06**	**4.39**	**6.81**	**2.15**	**8.96**	



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[37] The highest priority wild relative of *Hordeum vulgare* is the tertiary wild relative, *H. chilense,* which is known as a potential gene donor for wheat and triticale improvement (Martín and Cabrera, 2005).

[38] Includes two subspecies of *Pisum sativum* (one a high priority taxon and the other of lower priority) and one taxon in a related genus, *Vavilovia formosa*.[39] The highest priority wild relative of Hordeum vulgare is the tertiary wild relative, H. chilense, which is known as a potential gene donor for wheat and triticale improvement (Martín and Cabrera, 2005).

[39] The relative closeness of the wild species to *S. tuberosum* is of less significance in potato than for some other crops because a number of studies have shown that ploidy manipulation or somatic fusion can be used to overcome crossing barriers; therefore, virtually any potato species can be utilized in potato improvement (Bradshaw et al., 2006). By consulting the Wild Potato Species Atlas (http://www.cipotato.org/databases/) published online by the International Potato Centre (CIP), we identified 158 species (out of 196 in section Petota) that appeared to have 20 or fewer observations. Hijmans et al. (2002) identified 110 species that had five or fewer observation records; therefore, we have given these high priority status.

[40] Primary and secondary wild relatives of *Sorghum* are all relatively widespread species that are not a high priority for immediate conservation action.

[41] Species in the genus *Aegilops* are included as well as *Triticum* spp. (In total there are 6 *Triticum* spp. and 22 *Aegilops* spp.).

TABLE 13

Review of global Red List assessments of the 14 crop gene pools included in this study

Crop	Crop gene pool genera	Red List assessment			
		Assessed taxa[42]	Red List category and criteria applied	Version of Red List categories and criteria used	References
Finger millet	*Eleusine, Octhochloa*	–	–	–	–
Barley	*Hordeum*	–	–	–	–
Sweet potato	*Ipomoea*	*I. pulcherrima*	Vulnerable D2	IUCN (1994)	WCMC (1998)
Cassava	*Manihot*	–	–	–	–
Banana/ plantain	*Musa, Ensete*	–	–	–	–
Rice	*Oryza, Zizania, Porteresia, Leersia*	–	–	–	–
Pearl millet	*Pennisetum*	–	–	–	–
Garden pea	*Pisum, Vavilovia*	–	–	–	–
Potato	*Solanum*	*S. albornozii* *S. asteropilodes* *S. bellum* *S. betaceum* *S. bullatum* *S. burtonii* *S. cajanumense* *S. carchiense* *S. chilliasense* *S. chimborazense* *S. chrysasteroides* *S. chrysophyllum* *S. cinnamomeum* *S. cremastanthemum* *S. densepilosulum* *S. dolichorhachis* *S. drymophilum* *S. exiguum* *S. fallax* *S. fortunense* *S. granulosum-leprosum* *S. hypermegethes* *S. hypocalycosarcum* *S. imbaburense* *S. inaequale* *S. interandinum* *S. lanuginosum* *S. latiflorum* *S. leiophyllum* *S. leucodendron* *S. loxense* *S. melissarum* *S. minutifoliolum* *S. ovum-fringillae* *S. paralum* *S. paucijugum* *S. pinetorum* *S. regularifolium* *S. roseum* *S. semicoalitum* *S. sibundoyense* *S. sycocarpum* *S. ternifolium* *S. tobagense*	Endangered B1ab(iii) Vulnerable B1ab(iii) Near Threatened Data Deficient Lower Risk / Conservation Dependent Data Deficient Lower Risk/Near Threatened Endangered B1ab(iii) Vulnerable D2 Endangered B2ab(iii) Data Deficient Data Deficient Lower Risk/Conservation Dependent Data Deficient Data Deficient Critically Endangered A2c Critically Endangered C2b Vulnerable B1+2c Lower Risk/Near Threatened Vulnerable D2 Lower Risk/Conservation Dependent Vulnerable D2 Near Threatened Vulnerable D2 Lower Risk/Conservation Dependent Vulnerable B1ab(iii) Critically Endangered B1ab(iii) Lower Risk/Near Threatened Vulnerable D2 Lower Risk/Conservation Dependent Data Deficient Lower Risk/Near Threatened Least Concern Critically Endangered B1+2c Endangered A1c Least Concern Lower Risk/Near Threatened Vulnerable D2 Vulnerable B1+2c Critically Endangered A4; B1ab(iii) Vulnerable D2 Endangered A1c Data Deficient Lower Risk/Near Threatened	IUCN (2001) IUCN (2001) IUCN (2001) IUCN (1994) IUCN (1994) IUCN (2001) IUCN (1994) IUCN (2001) IUCN (2001) IUCN (2001) IUCN (2001) IUCN (2001) IUCN (1994) IUCN (2001) IUCN (2001) IUCN (2001) IUCN (1994) IUCN (1994) IUCN (1994) IUCN (1994) IUCN (1994) IUCN (2001) IUCN (2001) IUCN (2001) IUCN (1994) IUCN (2001) IUCN (2001) IUCN (1994) IUCN (2001) IUCN (1994) IUCN (2001) IUCN (1994) IUCN (2001) IUCN (1994) IUCN (1994) IUCN (2001) IUCN (1994) IUCN (2001) IUCN (1994) IUCN (2001) IUCN (1994) IUCN (1994) IUCN (2001) IUCN (1994)	Montúfar and Pitman (2004) Montúfar and Pitman (2004) Montúfar and Pitman (2004) WCMC (1998) Carvalho (1998) Montúfar and Pitman (2004) WCMC (1998) Montúfar and Pitman (2004) Montúfar and Pitman (2004) Montúfar and Pitman (2004) Montúfar and Pitman (2004) Montúfar and Pitman (2004) Carvalho (1998) Montúfar and Pitman (2004) Montúfar and Pitman (2004) Montúfar and Pitman (2004) WCMC (1998) WCMC (1998) WCMC (1998) WCMC (1998) Carvalho (1998) Montúfar and Pitman (2004) Montúfar and Pitman (2004) Montúfar and Pitman (2004) Carvalho (1998) Montúfar and Pitman (2004) Montúfar and Pitman (2004) WCMC (1998) Montúfar and Pitman (2004) Carvalho (1998) Montúfar and Pitman (2004) WCMC (1998) Montúfar and Pitman (2004) Bohs (1998) WCMC (1998) Montúfar and Pitman (2004) WCMC (1998) Montúfar and Pitman (2004) WCMC (1998) Montúfar and Pitman (2004) WCMC (1998) WCMC (1998) Montúfar and Pitman (2004) WCMC (1998)
Sorghum	*Sorghum*	–	–	–	–
Wheat	*Triticum, Aegilops, Amblyopyrum, Agropyron, Elymus*	–	–	–	–
Faba bean	*Vicia*	–	–	–	–
Cowpea	*Vigna*	–	–	–	–
Maize	*Zea, Tripsacum*	–	–	–	–

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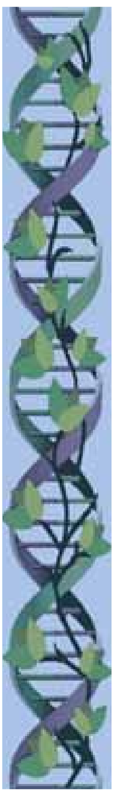
[42] – = no global Red List assessment published

Figures 33–36 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. These maps are provided to give an overview of priority sites for inclusion in the global network in terms of the individual crop case studies and regional priorities—for taxon and site details, the reader should refer to the individual crop case studies. In each case study, we have identified priority sites that are likely to be within the boundaries of existing protected areas, as indicated by data analysis. However, important sites that are probably outside of existing protected areas are also included where known taxon locations are very limited. Options for the complementary conservation of taxa outside of existing protected areas will have to be investigated on a case by case basis.

It is important to stress that the potential genetic reserve locations shown in Figures 33–36 are for a limited number of crop complexes (those included in this study) and within these, for the highest priority CWR taxa only. Within each crop complex, there are other taxa that could eventually be included in the global CWR genetic reserve network[43], once the complementary conservation of the highest priority taxa is secured. Further, the wild relatives of other crops will be included in the network over time, based on further global crop case studies and priorities arising from national CWR strategies. While the results of the 14 crop complex analyses (with the exception of the Middle East and Eastern Congo) show few obvious opportunities for multi-crop gene pool CWR genetic reserves, further research on other crop complexes is likely to identify additional potential multi-taxon CWR genetic reserves. Therefore, the results of this analysis should be considered as a first step in the process of establishing the 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, as has been initiated in this study). Therefore, it is vital that individual countries take steps to initiate national CWR conservation strategies (as shown in the methodology presented in Part 2 of this report), to ensure that the widest range of CWR taxa are actively conserved as quickly as possible; in particular, taking into account species rich areas and the establishment of multi-taxa genetic reserves where possible.



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[43] In each crop case study, taxa are categorized according to their level of conservation priority, as shown in the case study methodology.

FIGURE 33

Priority CWR genetic reserve network locations in Africa. For a detailed list of taxa and sites, refer to the crop case studies

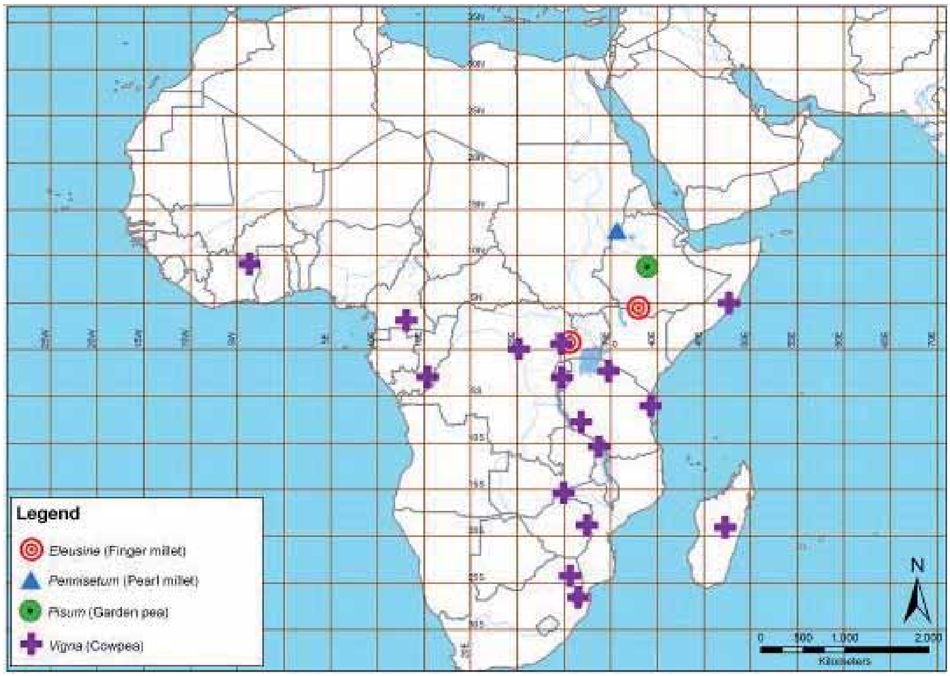


FIGURE 34

Priority CWR genetic reserve network locations in the Americas. For a detailed list of taxa and sites, refer to the crop case studies

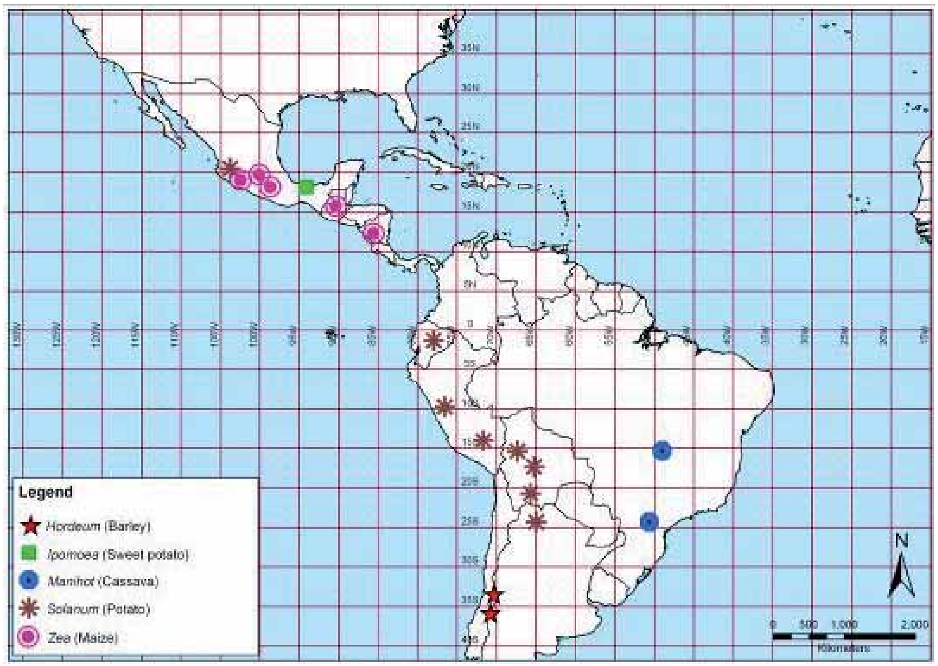


FIGURE 35

Priority CWR genetic reserve network locations in the Middle East. For a detailed list of taxa and sites, refer to the crop case studies

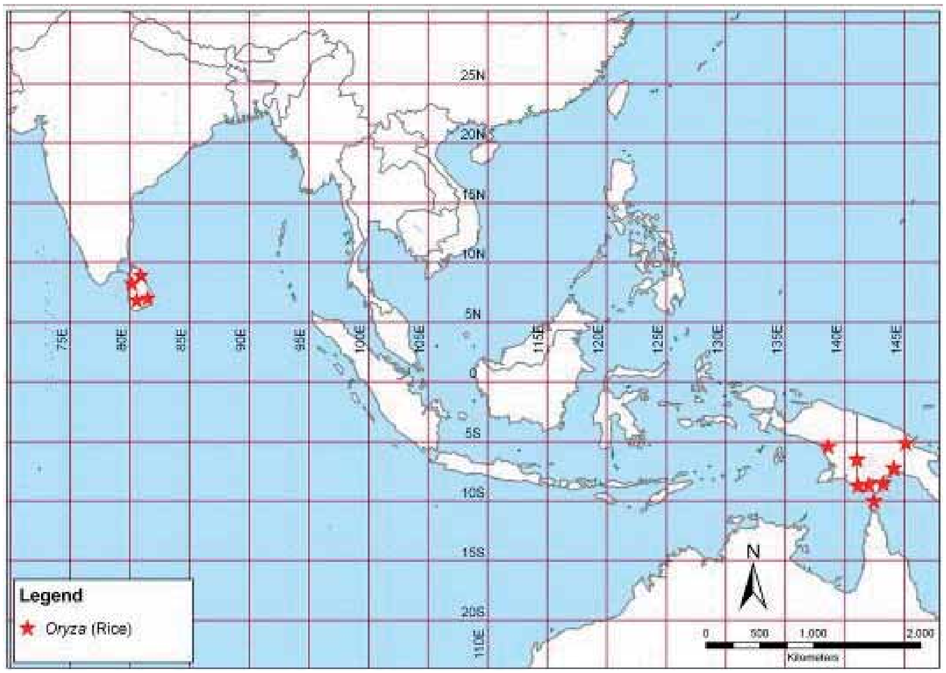
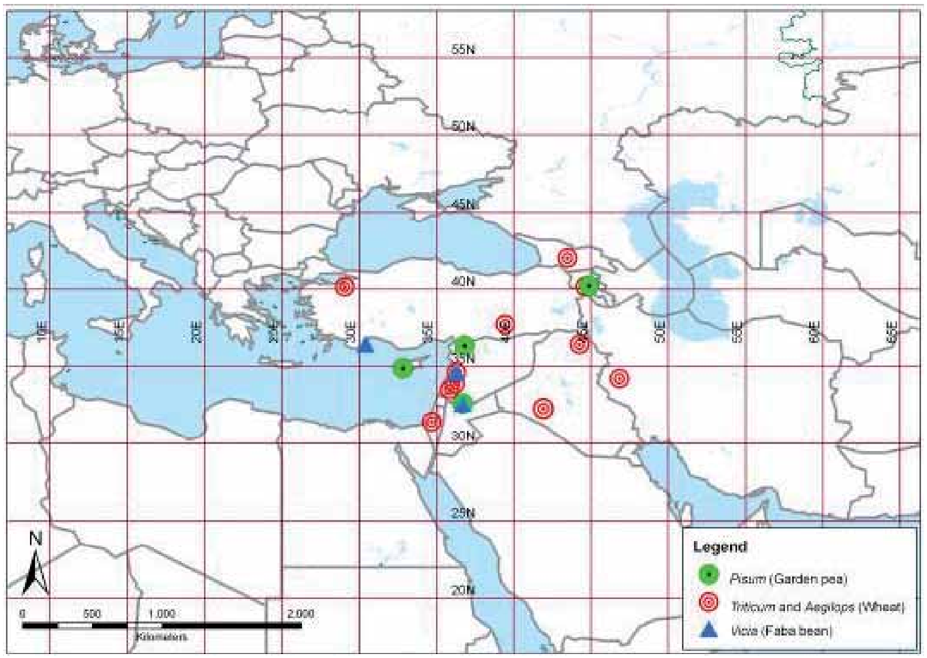


FIGURE 36

Priority CWR genetic reserve network locations in Asia and the Far East[44]. For a detailed list of taxa and sites, refer to the taxon data sheets



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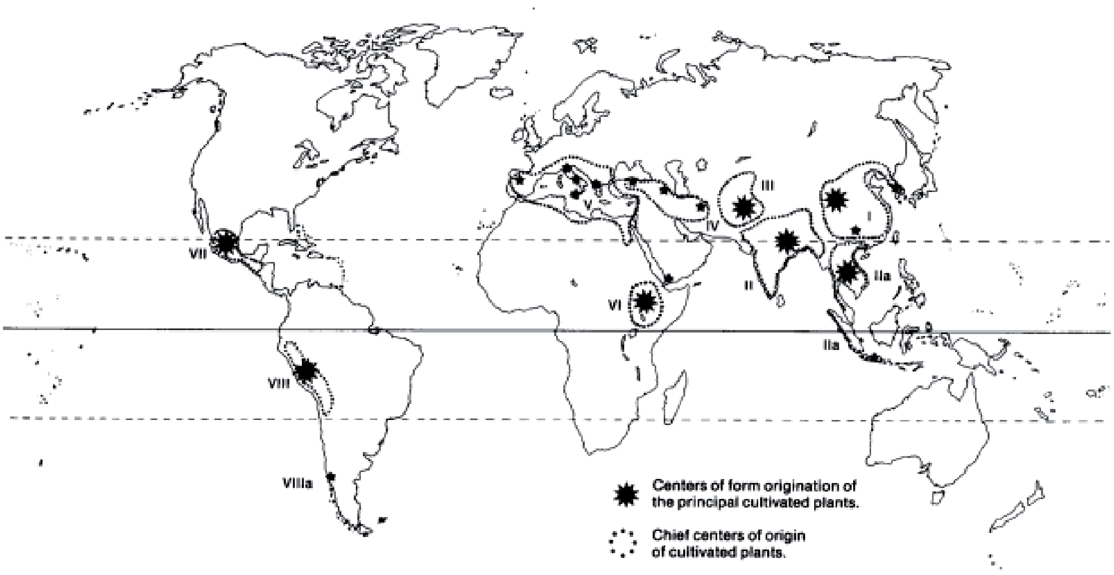
[44] The wild relatives of banana/plantain (*Musa* spp.) also have their centre of distribution in Asia (extending into Australasia). Priority sites for Musa species are not shown as data were not readily available for analysis.

It should not be surprising that even based on only 14 crops studied here the sites identified show a correlation with the Vavilov Centres of Origin (Vavilov, 1926, 1949 – see Figure 37) and it is likely that when more crop gene pools are analysed the correlation will grow even stronger. This point underscores the prescience of N.I. Vavilov in identifying the initial eight centres, but it will also provide an opportunity to objectively test the boundaries of the Vavilov Centres. It also highlights the fact that the Vavilov Centres are almost exclusively located in developing countries, many of which may have limited technical and financial resources to take responsibility for maintaining the global network of CWR genetic reserves. Further, it could be argued that some of these developing countries have limited technical and financial resources to take advantage of the CWR diversity contained within the global network. As acknowledged in the ITPGRFA (FAO, 2001), the onus is on developed countries to work with developing countries to help conserve CWR diversity by providing financial and technical support and assisting with capacity building.

FIGURE 37

The Vavilov Centres of Crop Diversity (Vavilov, 1949; modified by Hawkes, 1993)



3.2 Overview of crop gene pool priorities by region

As already noted, the potential genetic reserve locations presented in Figures 33–36 are based only on 14 crop case studies and the highest priority CWR within each group. Options for the establishment of genetic reserves, both within and outside existing protected areas will have to be investigated on a case by case basis. It is evident from this study that there are relatively few options for the establishment of multi-crop complex genetic reserves for the highest priority taxa, 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, see the individual crop case studies). 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 to 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 33 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 34 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–Southwest 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 due to the large number of taxa in the genus and the fact that nearly all of them can be crossed relatively easily with the crop in breeding programmes. As shown in the *Solanum* case study, several species rich areas have been identified in Mexico, Ecuador, Peru, Bolivia and Argentina. 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 analysis of distribution data overlaid with protected area shapefiles is needed to begin to formulate an appropriate *in situ* conservation strategy for this group.

The Middle East

Figure 35 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 & 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 East Syria, close to the Lebanese border.

Asia and the Far East

Figure 36 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 36 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.

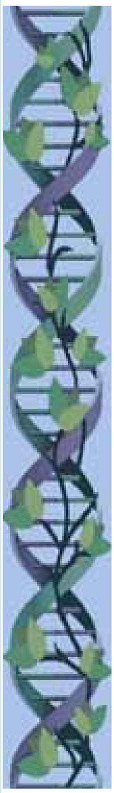
3.3 Coordinating the establishment of the CWR genetic reserve network

For each of the 14 crop gene pools treated in this study, priority locations or areas for the *in situ* conservation of the highest priority CWR taxa have been identified. In some cases, further research is required to obtain additional data to carry out a more detailed analysis and in all cases, verification of the locations of taxa is needed *in situ* before genetic reserves can be formally proposed and established. However, the results of the analyses presented in this report are a significant first step in the process of establishing the necessary *Global Network of CWR Genetic Reserves*.

The Global Network could build in a largely uncoordinated ad hoc manner but it would be more effective if an agency with an international remit led the systematic establishment of such a network—the FAO Commission on Genetic Resources for Food and Agriculture would be ideally placed to lead such an initiative. This Global Network could be seen as the counterpart to the network of *ex situ* gene banks within the CGIAR, which have responsibility for global *ex situ* conservation of the world's CWR diversity.

Having argued for the establishment of a Global Network of CWR Genetic Reserves there are a few generic recommendations that need to be considered before the sites are formally designated:

- **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 CGRFA could use the crop case studies provided in this study as a template for each of the ITPGRFA Annex I list of Crops Covered Under the Multilateral System, so that over time the 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, the 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. Therefore, a dialogue between the coordinating body of the Global Network of CWR Genetic Reserves and National PGRFA



Coordinators will be essential for the success of the Network. The publication of the current study and subsequent inclusion of *in situ* CWR conservation priorities 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 the Network, 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 the 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*. (2008) 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 the Global Network is likely to be located.

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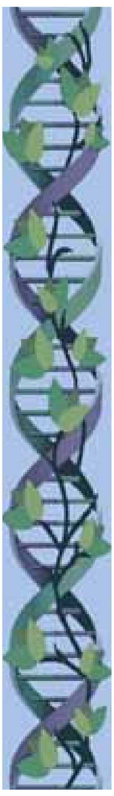

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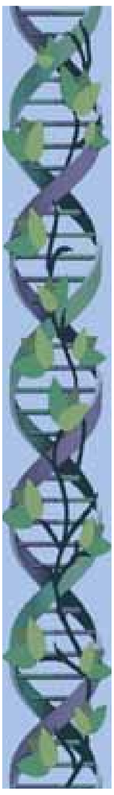

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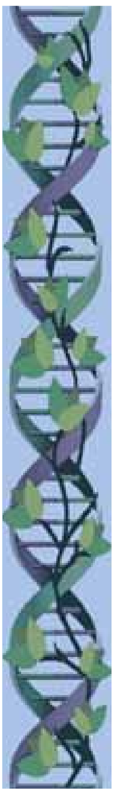

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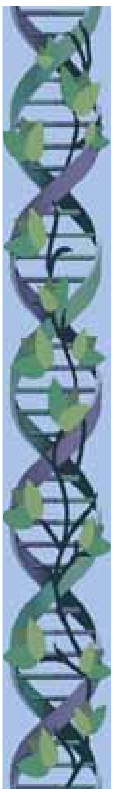

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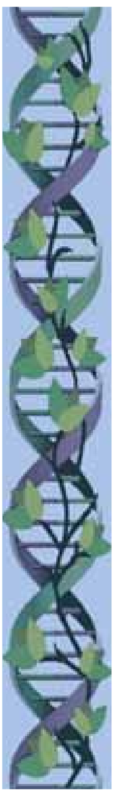

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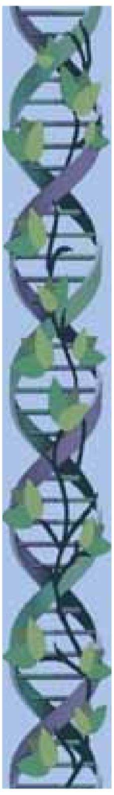

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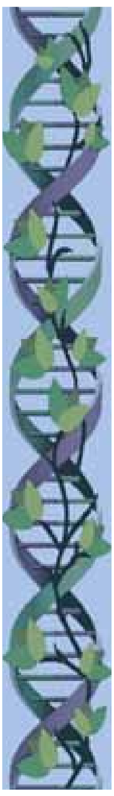

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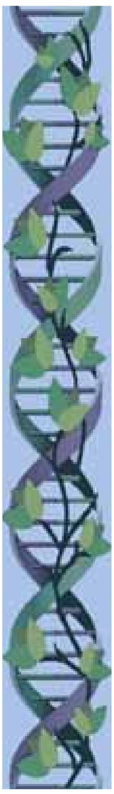

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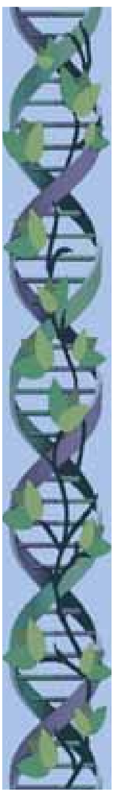

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