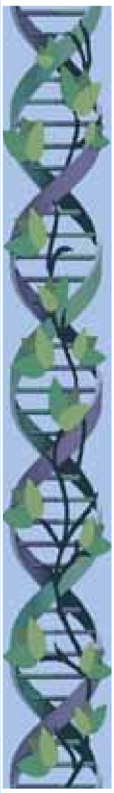
ANNEXE 4: IMPORTANT AREAS AND CONSERVATION GAPS FOR CWR

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).

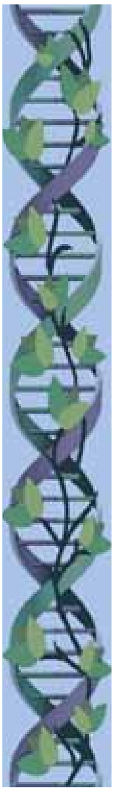
It has been argued that in the light of recent biotechnological advances, all wild species are potential gene donors to crops (Maxted *et al*., 1995). However, this kind of advanced breeding application remains relatively expensive and technically challenging and is currently mainly restricted to developed 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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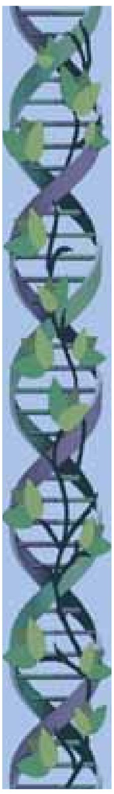
[16] For this background study, it has not been possible to obtain all available occurrence data for all the target taxa (i.e., by visiting herbaria and consulting the full range of Floras). However, we have consulted the primary references for each of the target taxa and also obtained occurrence data 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).

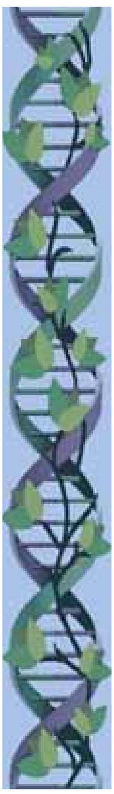
Taxonomic classification

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

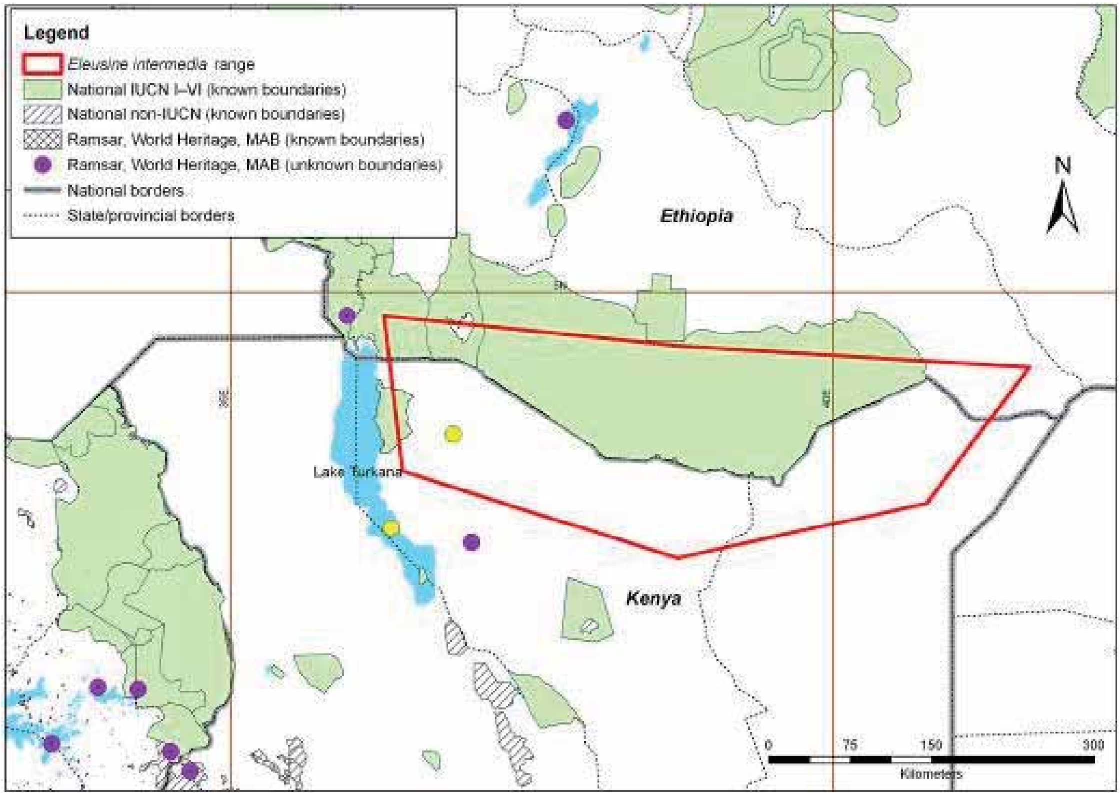
- *E. intermedia*, which is confined to the uplands of northern Kenya and adjacent parts of southern Ethiopia (Bisht and Mukai, 2002).
- *E. kigeziensis*, which was reported by Phillips (1972) to be localized in mountainous regions extending from Kigezi Province, Uganda and adjacent parts of the Congo 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

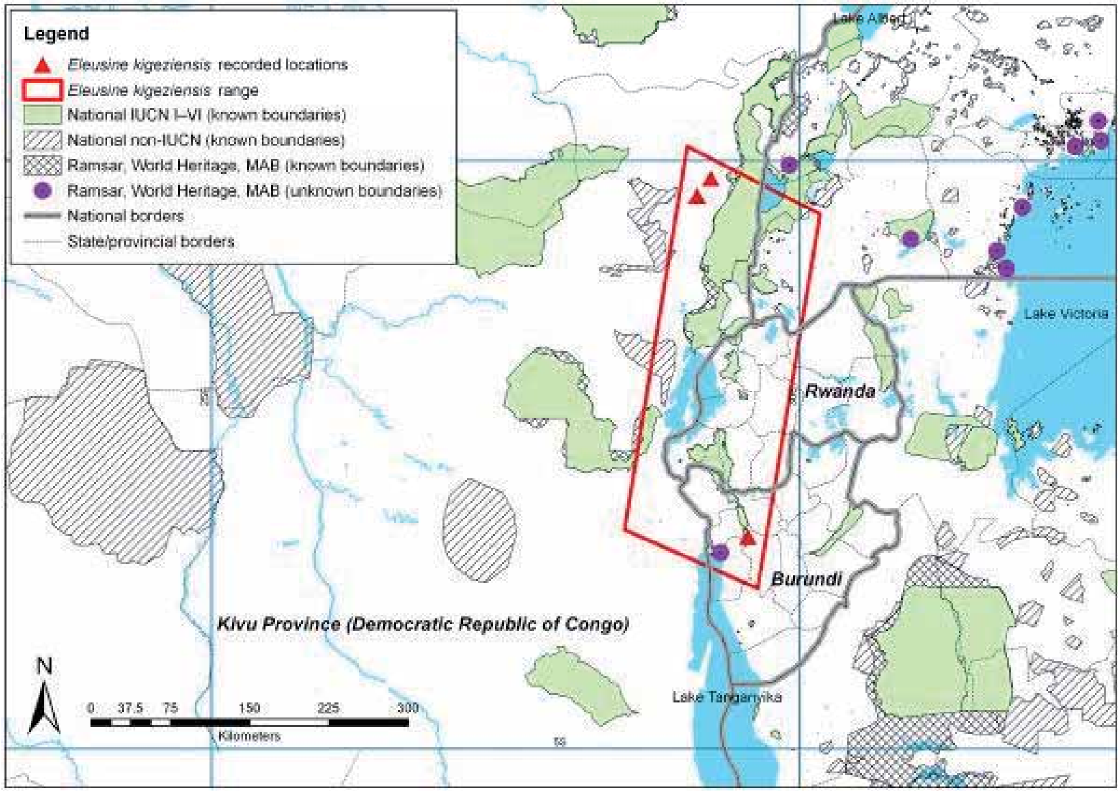
- Chelbi Wildlife Reserve (IUCN category IV)
- Borana Controlled Hunting Area (IUCN category VI)
- Murle Controlled Hunting Area (IUCN category VI)

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

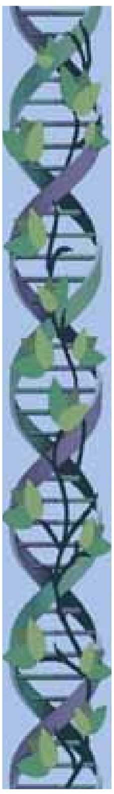
- Kibira National Park (IUCN category IV)
- Rusizi National Park (IUCN category IV)
- Democratic Republic of Congo:
- Virunga National Park (IUCN category II, World Heritage in Danger List (World Heritage Convention) and Ramsar)
- Rutshuru Hunting Reserve (IUCN Category VI)
- Sud Masisi/Quest Lac Kivu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

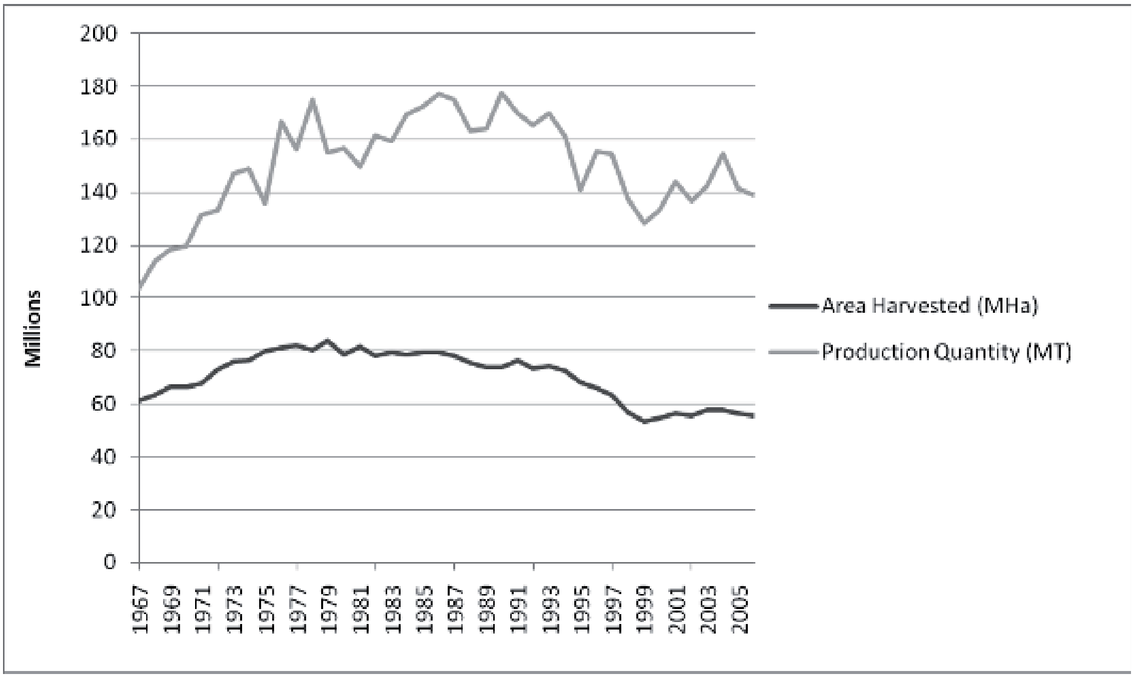
Global, regional and local importance

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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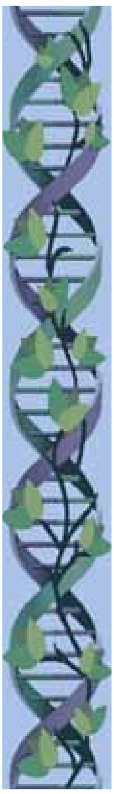
[17] von Bothmer et al. (1995)

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*

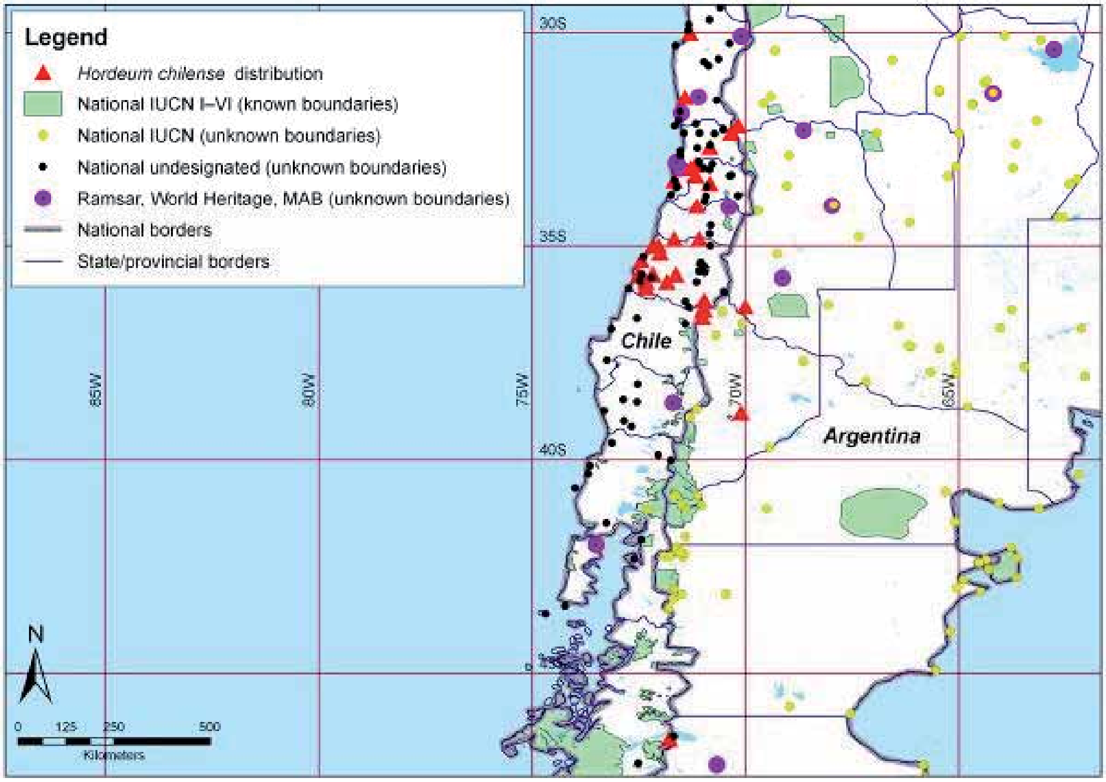
Priority sites (high priority taxa)

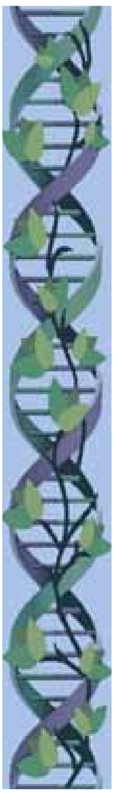
Data analysis indicates that few, if any of the recorded populations of *H. chilense* fall within existing protected areas (Figure 4); however, proximity indicates that the following sites may contain populations of the taxon:

- 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

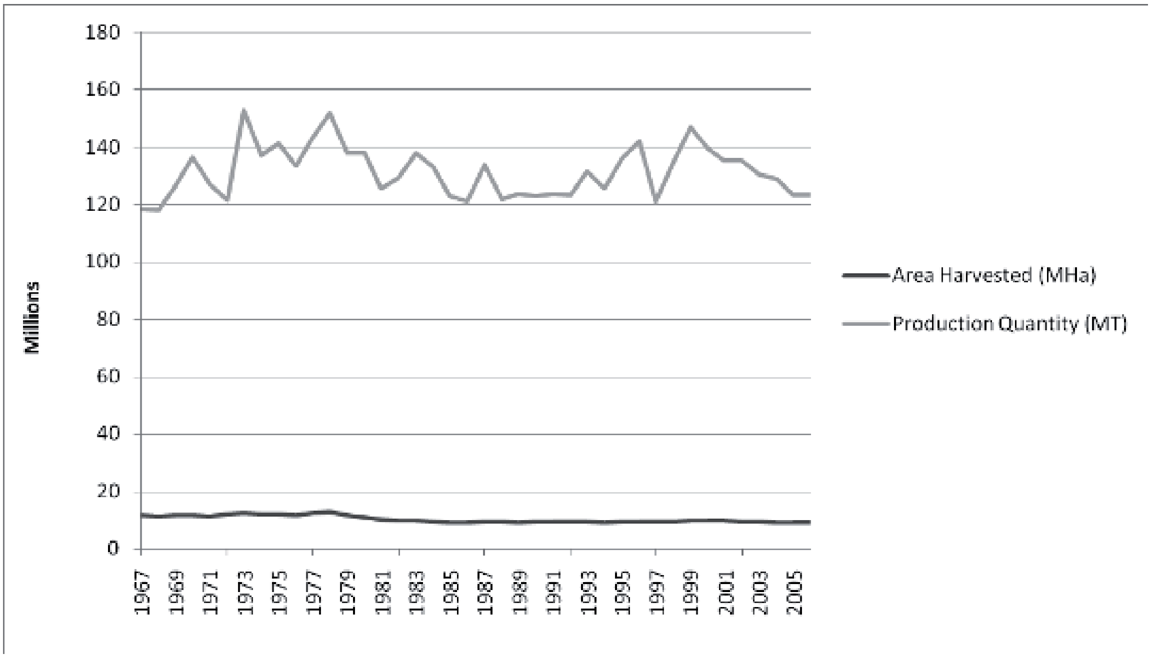
Convolvulus batatas L.

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

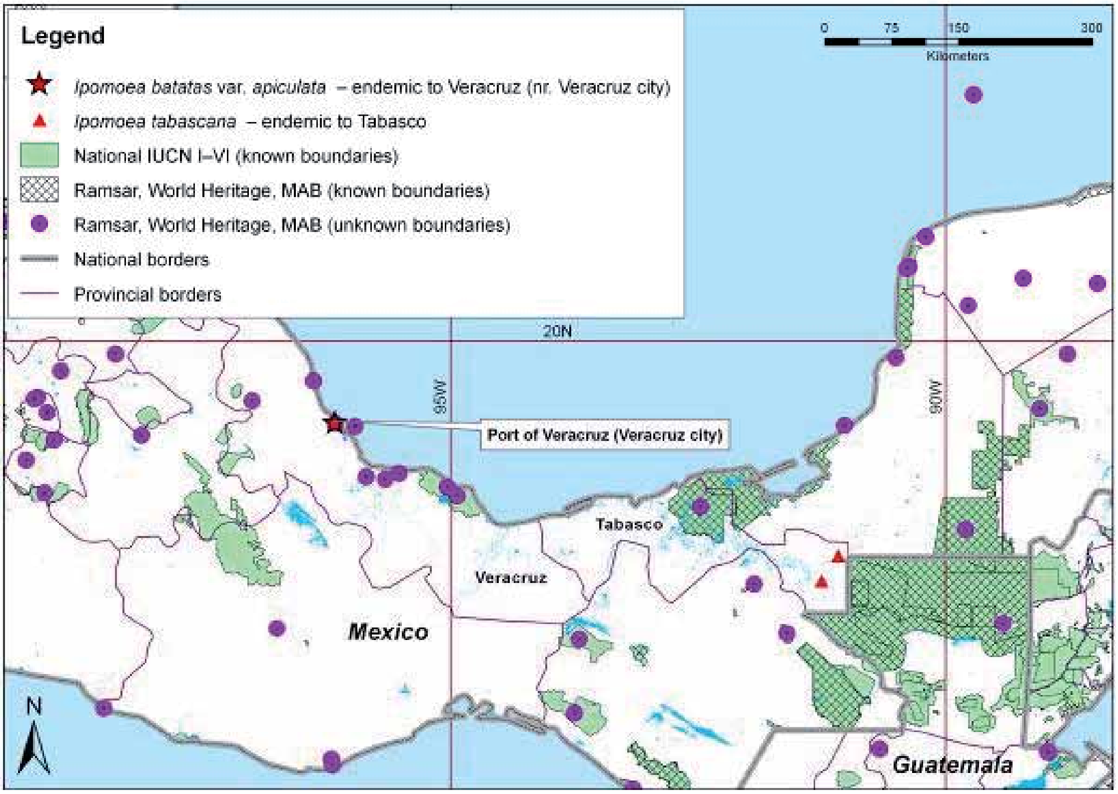
- *I. batatas* var. *apiculata*: endemic to Veracruz, Mexico (MacDonald and Austin, 1990). MacDonald and Austin only found this ecotype near the Port of Veracruz, where it is a littoral plant growing in dunes.
- *I. tabascana*: endemic to Tabasco, Mexico, where it is endangered (Austin *et al*., 1991).

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

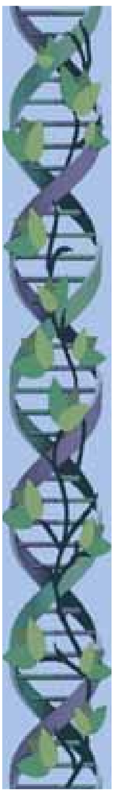


Recommendations

- 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

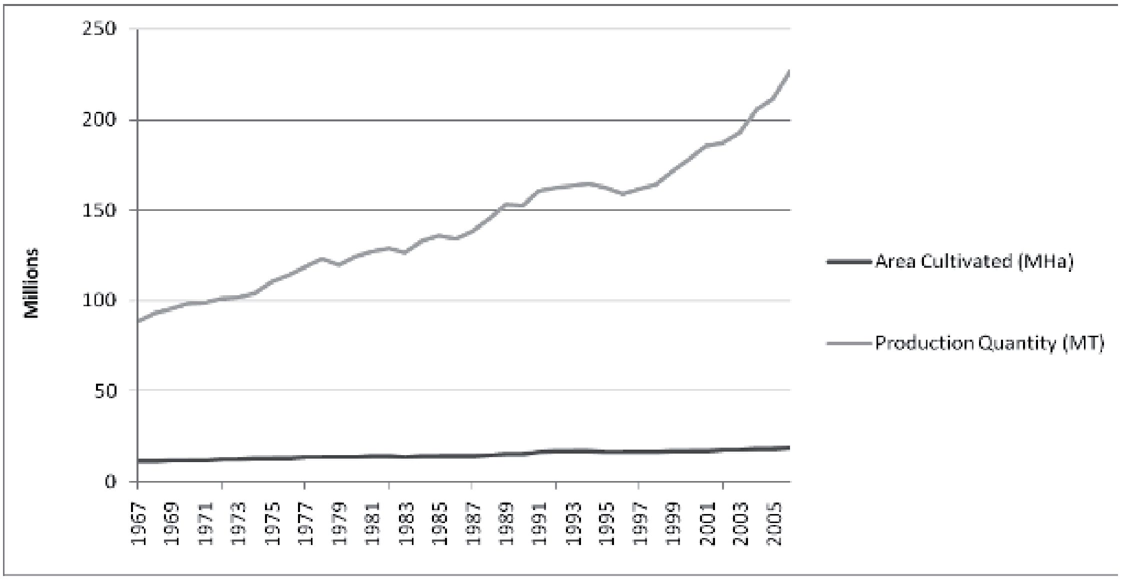
Cassava is grown for its enlarged starch-filled roots, which contain nearly the maximum theoretical concentration of starch on a dry weight basis among food crops (O'Hair, 1995). It is an important food crop for more than 900 million people in the tropics and subtropics (Nassar, 2006) and one of the 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)

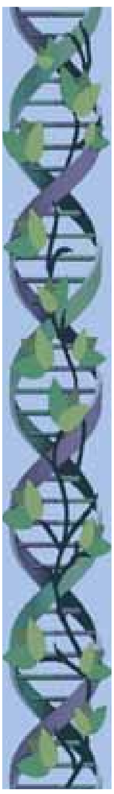
- *Manihot esculenta* Crantz subsp. flabellifolia (Pohl) Cif.
- *M. esculenta* Crantz subsp. *peruviana* (Müll. Arg.) Allem
- *M. pruinosa* Pohl

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)

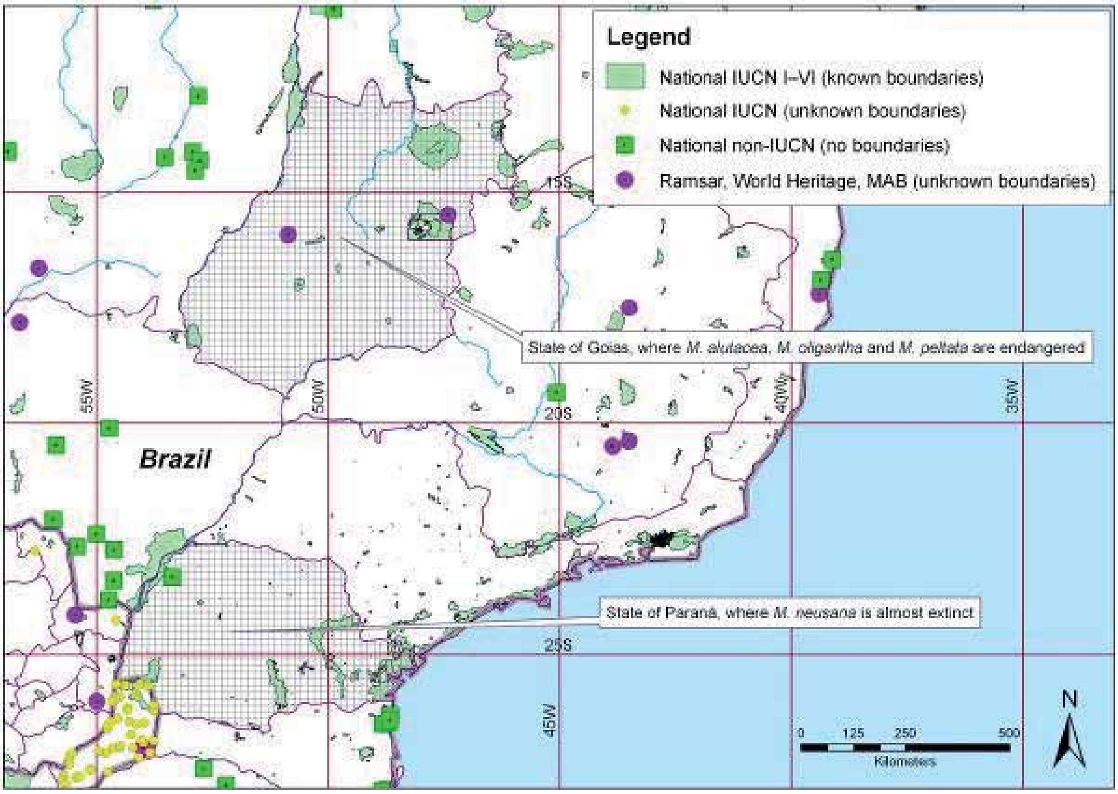
Distribution data for most of the high priority taxa are not readily available via online sources; therefore, before priority sites can be identified, comprehensive ecogeographic surveys of these taxa are needed. Although all the taxa listed have been classified as endangered by Nassar *et al*. (2008), 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'I banana).

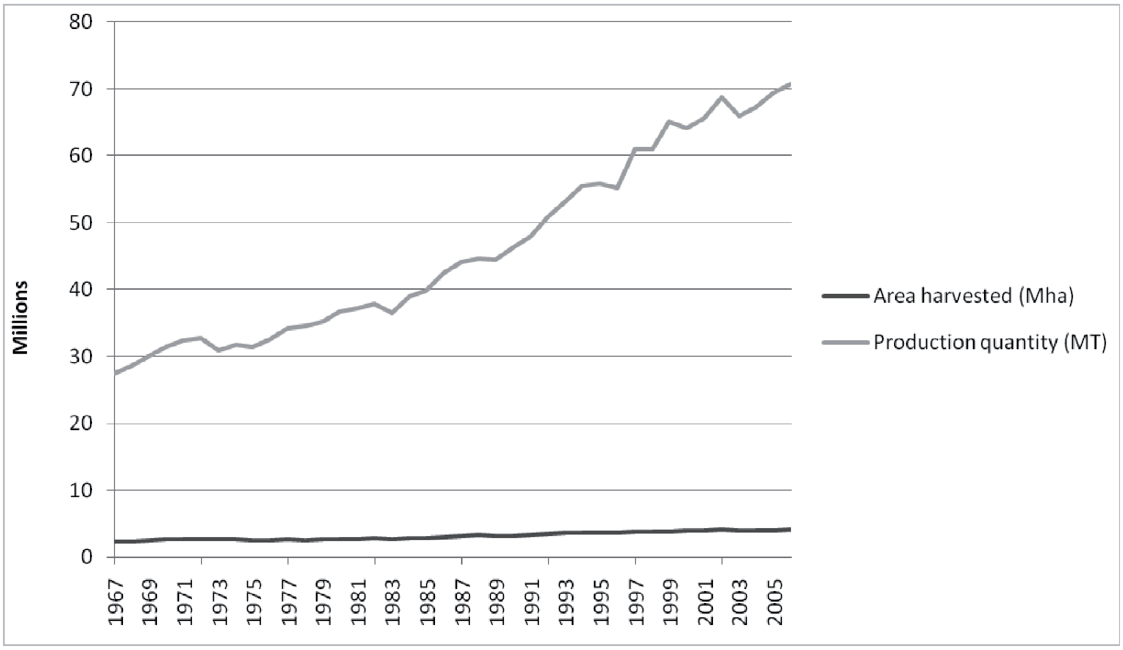
Global, regional and local importance

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

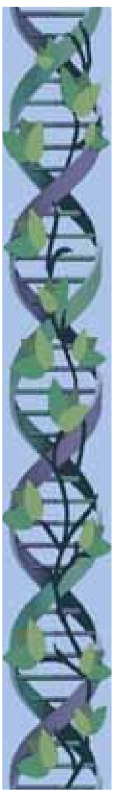
World area harvested and production quantity for banana and plantain (FAO, 2008)



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

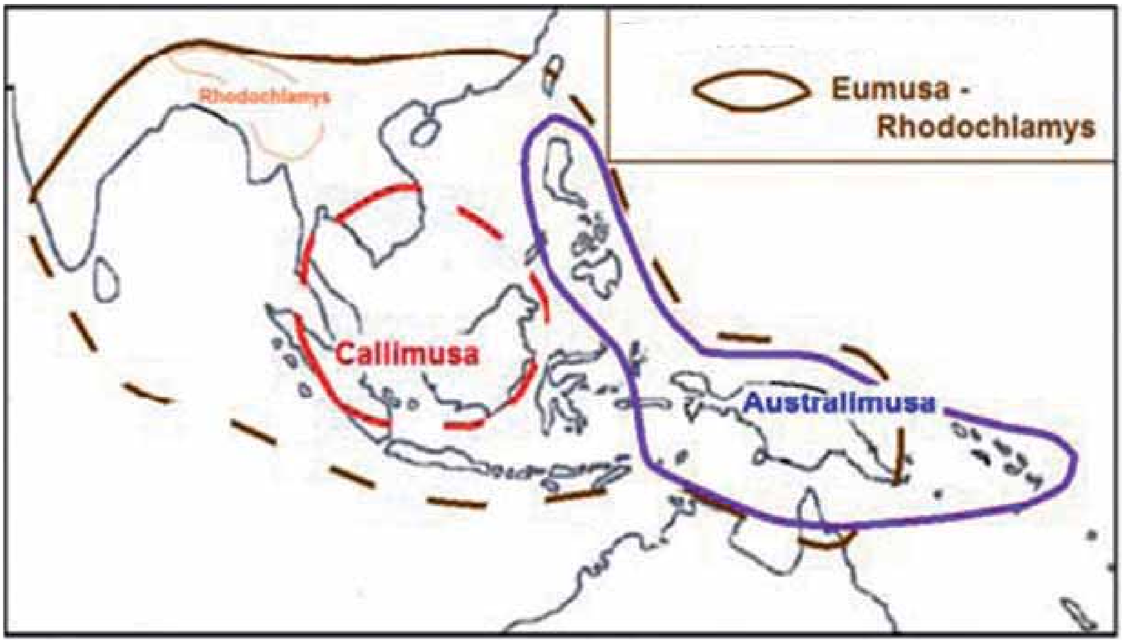
- *Ensete* species (including *E. ventricosum* which is cultivated in Ethiopia).

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

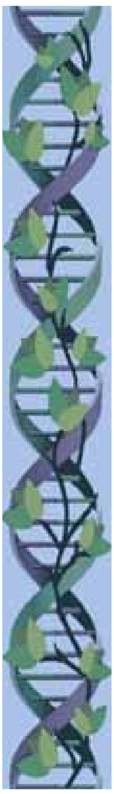
- *M. basjoo* – distribution: China (Fujian, Gansu, Guandong, Guangxi, Guizhou, Hubei, Hunan, Jiangsu, Jiangxi, Sichuan, Yunnan and Zhejiang), Japan (introduced).
- *M. cheesmani* – distribution: India (Assam)
- *M. flaviflora* – distribution: Bhutan
- *M. halabanensis* – distribution: Sumatra
- *M. 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

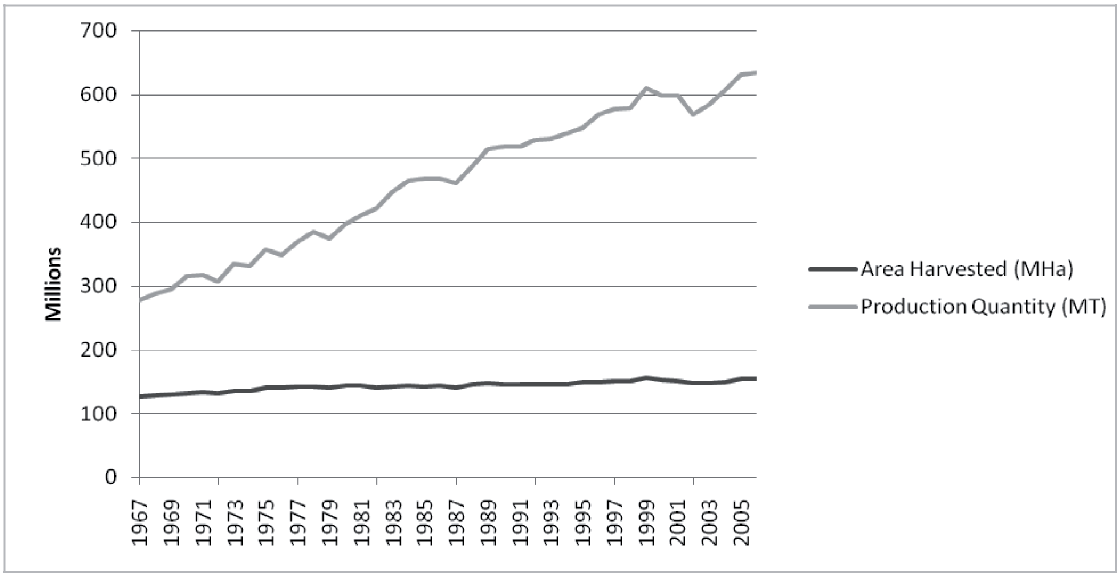
Padia meyeriana Zoll. & Moritzi, *Oryza formosana* Masamune & Suzuki

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.

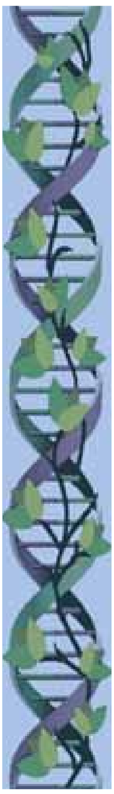
TABLE 2

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)

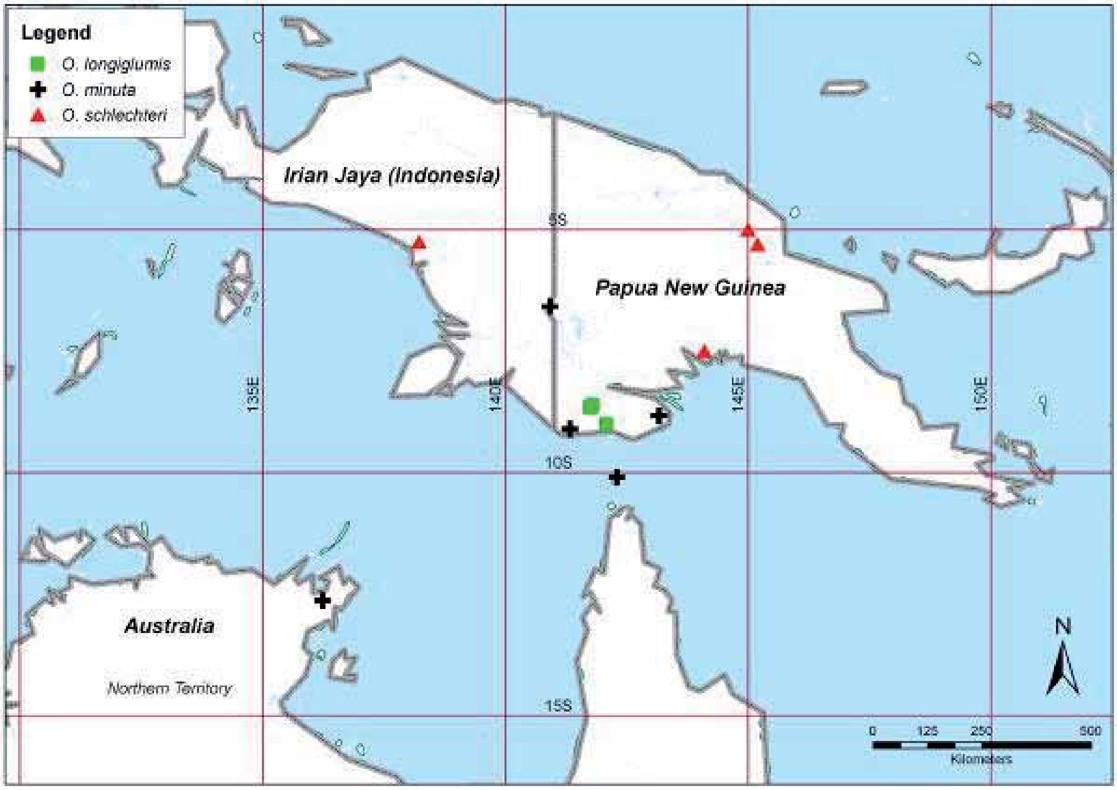
Based on the analysis presented in Figures 12 and 13, the following locations should be investigated further as potential sites for *in situ* conservation of the highest priority rice wild relatives:

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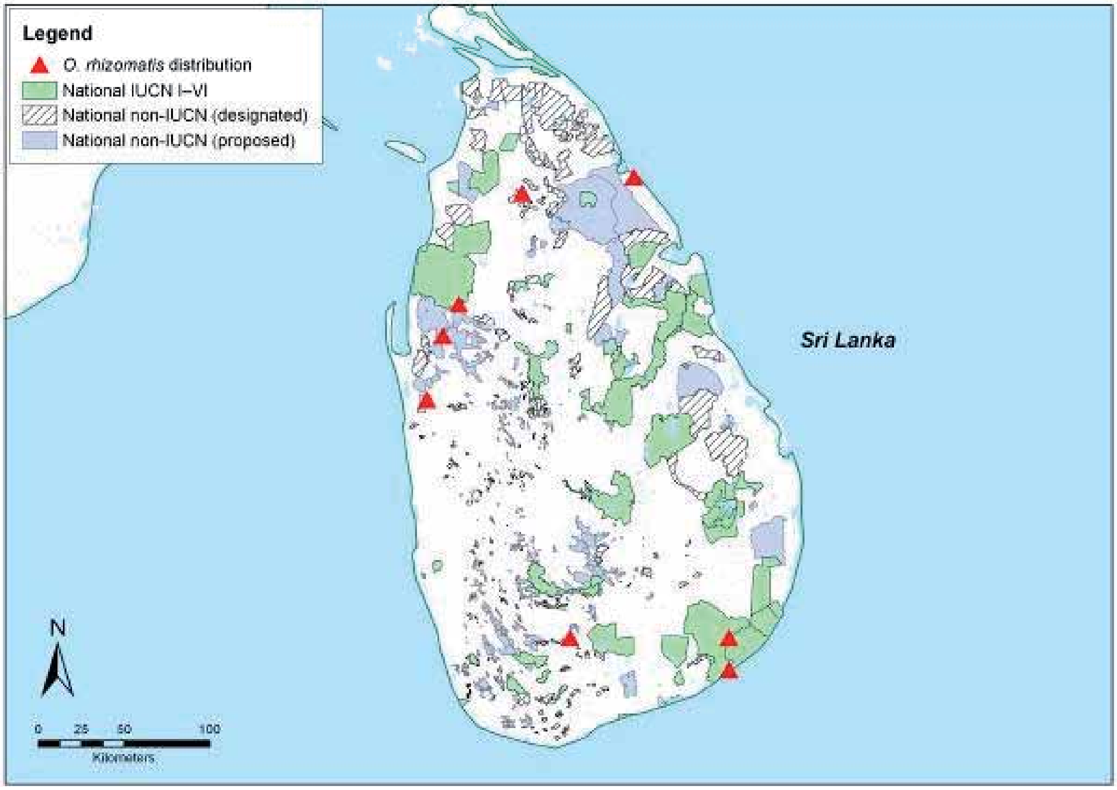
[20] *O. minuta* is also distributed in the Philippines, but coordinate data were not available for this study.

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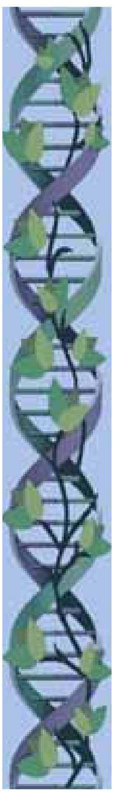
[21] *O. eichingeri* has also been recorded within this protected area (coordinates not available) [Data source: Australian National Herbarium (CANB) (accessed through GBIF data portal, http://data.gbif.org/datasets/resource/47 05/08/2008)].

[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.

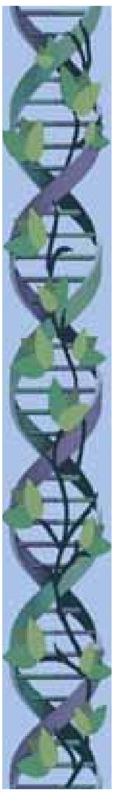
Priority taxa

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)

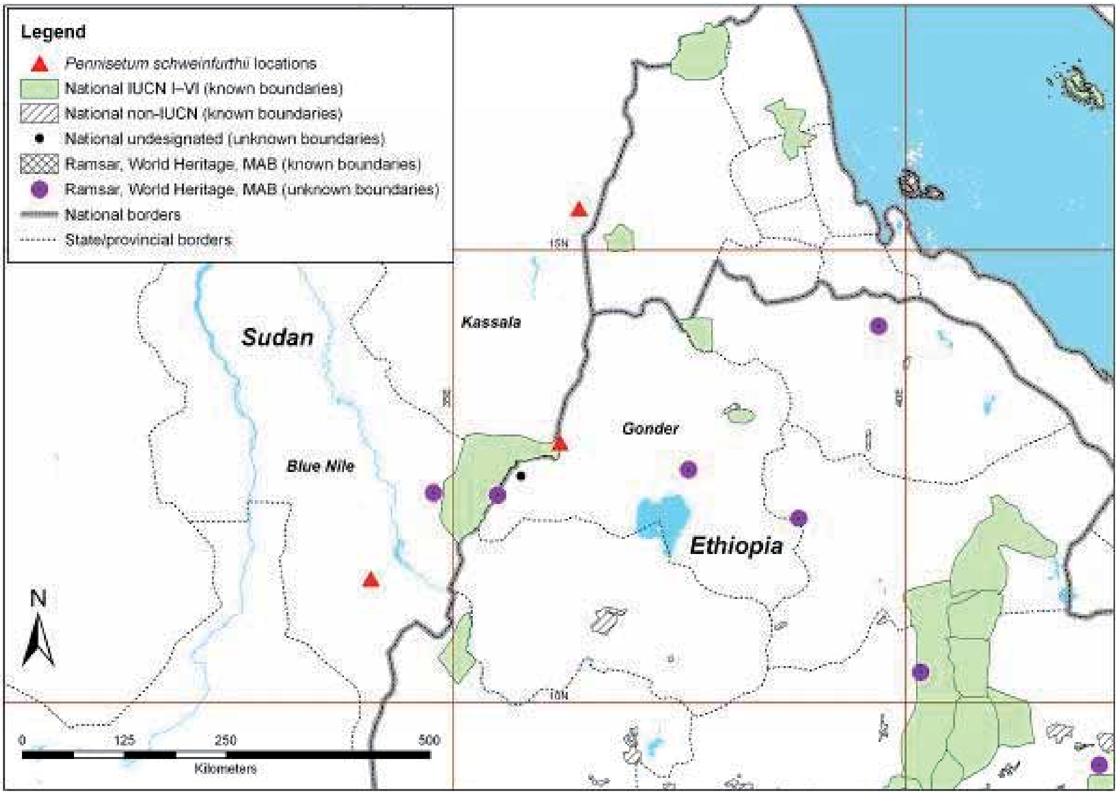
Pennisetum schweinfurthii is recorded as occurring in Sudan and Ethiopia. Ethiopian records are on the Sudan–Ethiopia border only (see Figure 14).

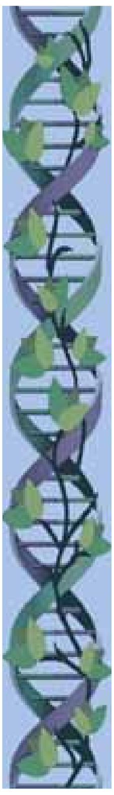
Recommendations

- 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.

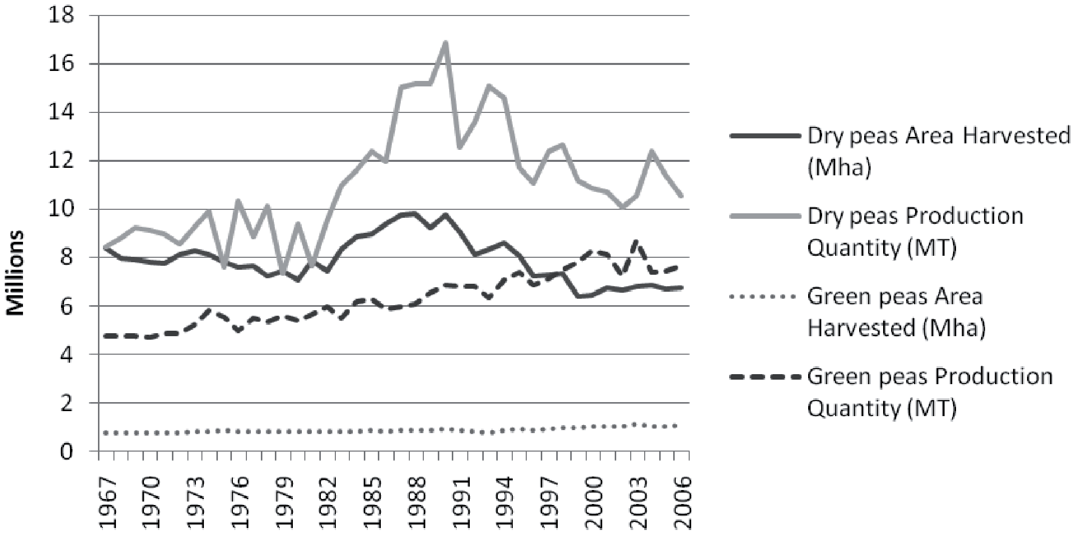
Global, regional and local importance

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.

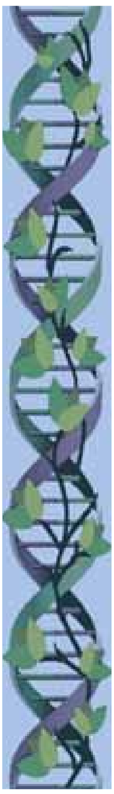
There has been some agreement in the literature over the number of taxa in the genus but much dispute over their rank. Boissier (1872) recognized four annual species: *P. elatius* Bieb., *P. humile* Boissier and Noë, *P. fulvum* and *P. formosanum* (Stev.) Alef. (syn. *V. formosa*). The former three 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

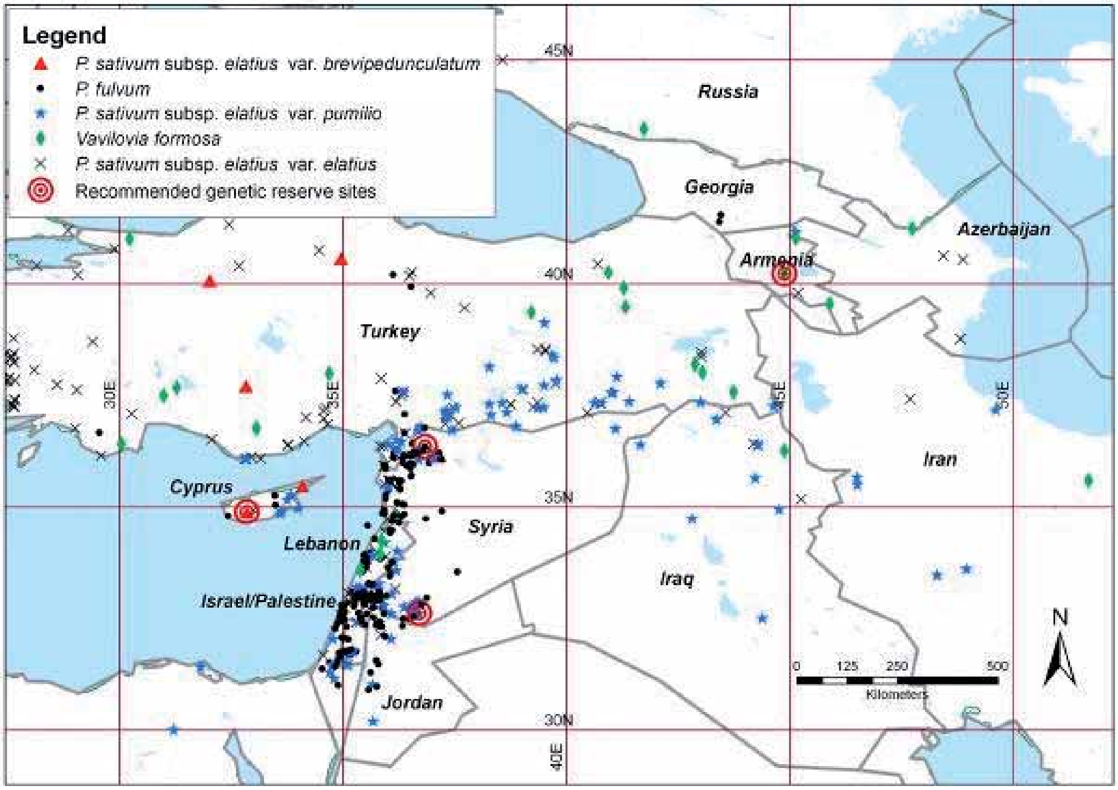
- *P. fulvum*
- *P. sativum* subsp. *elatius* var. *pumilio*
- *Vavilovia formosa*

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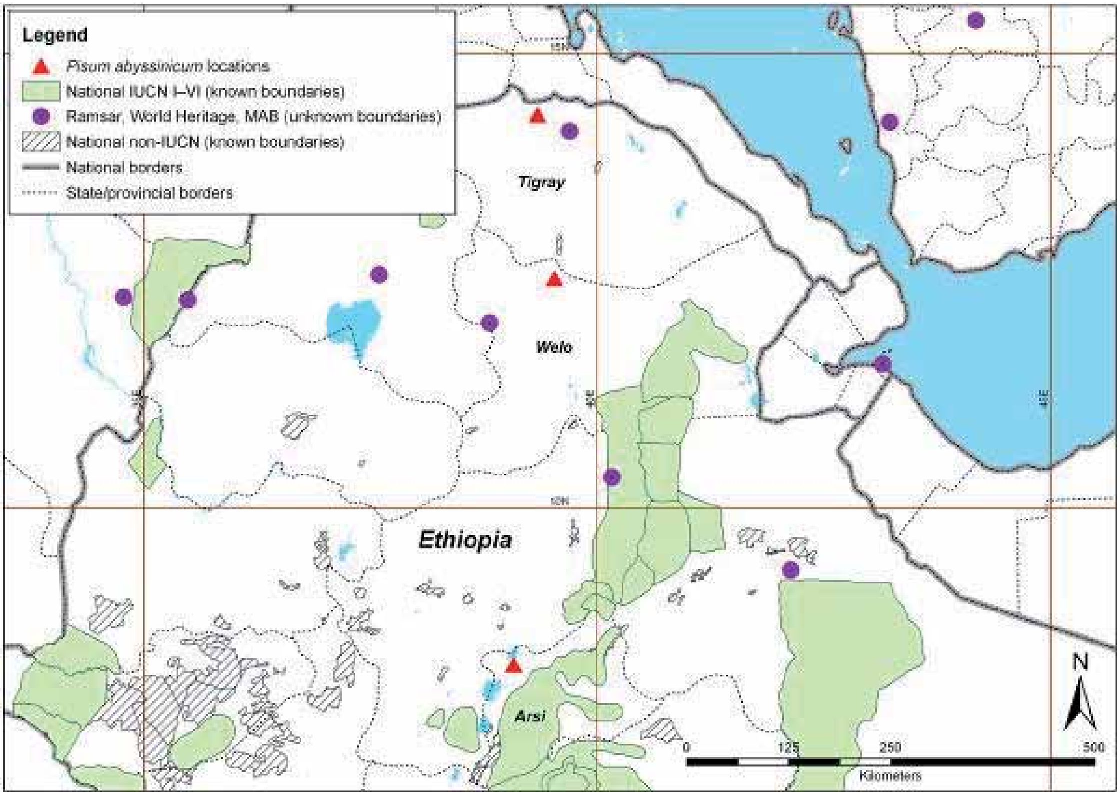
[28] From SINGER (accessed through GBIF data portal, http://data.gbif.org/datasets/resource/1430 18/07/2008), NPGS (http://data.gbif.org/datasets/resource/1429 18/07/2008), Israel Nature and Parks Authority (http://data.gbif.org/datasets/resource/1431 18/07/2008) and CIBIO, Alicante:ABH-GBIF (http://data.gbif.org/datasets/resource/251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



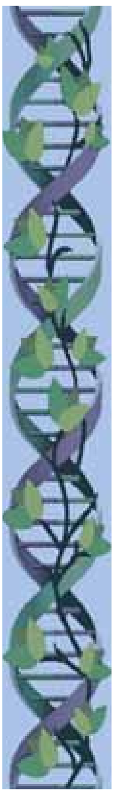
Based on this analysis, specific sites to conserve *Pisum* and *Vavilovia* should be located at:

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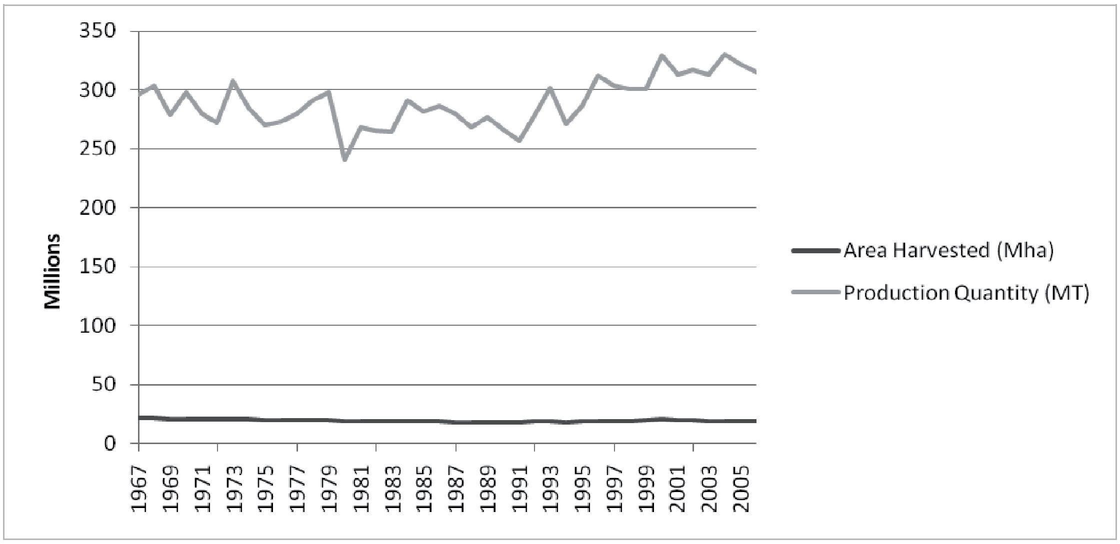
[29] Collections of cultivated material have also been made at other locations (mainly markets) in Ethiopia.

FIGURE 18

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

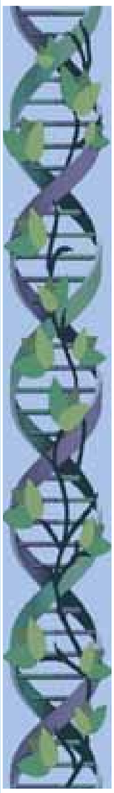


Hawkes (1999) noted that when we talk about the potato, there are in fact seven cultivated taxa known in the Andes (referred to either as species or cultivar groups), with diploid, triploid, tetraploid and pentaploid chromosome numbers, but the tetraploid *S. tuberosum* is the only one to have become 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. avilesii* Hawkes & Hjerting
- *S. brevicaule* Bitter
- *S. gandarillasii* Cárd.
- *S. hondelmannii* Hawkes & Hjerting
- *S. incamayoense* Okada & Clausen
- *S. leptophyes* Bitter
- *S. neocardenasii* Hawkes & Hjerting
- *S. okadae* Hawkes & Hjerting
- *S. sparsipilum* (Bitter) Juzepczuk & Bukasov, in Buk.
- *S. ugentii* Hawkes & Okada
- *S. vernei* Bitter & Wittrn.
- *S. alandiae* Cárd.
- *S. berthaultii* Hawkes
- *S. candolleanum* Berth.
- *S. gourlayi* Hawkes (syn. *S.* × *bruecheri*)
- *S. hoopesii* Hawkes & Okada
- *S. kurtzianum* Bitter & Wittrn.
- *S. microdontum* Bitter
- *S. neorossii* Hawkes & Hjerting
- *S. oplocense* Hawkes
- *S. spegazzinii* Bitter
- *S. venturii* Hawkes & Hjerting
- *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.

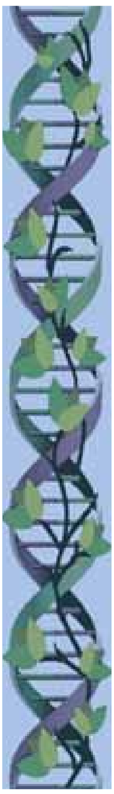
In their GIS analysis of wild potato, Hijmans *et al*. (2002) found that using 50 km2 grid cells, Bolivia, Peru and Argentina had the highest *Solanum* species richness (with 19, 17 and 17 species per grid cell), followed by Mexico (with cells containing 12 species) and Ecuador (with 9 species) (Table 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.