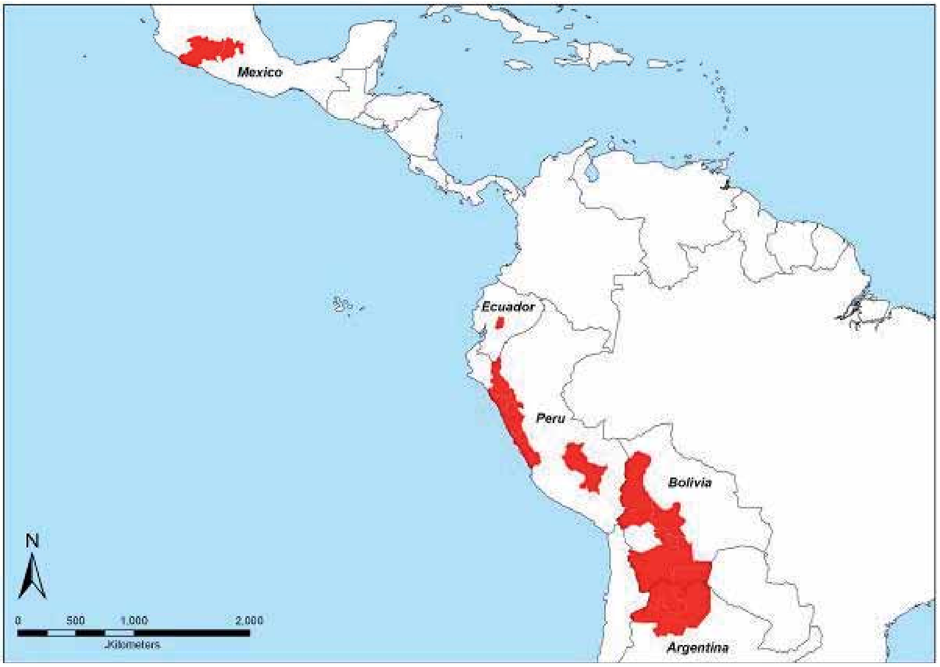
FIGURE 19

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



Recommendations

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

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

2.10 Sorghum

Scientific name

Sorghum bicolor (L.) Moench

Principle synonyms

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

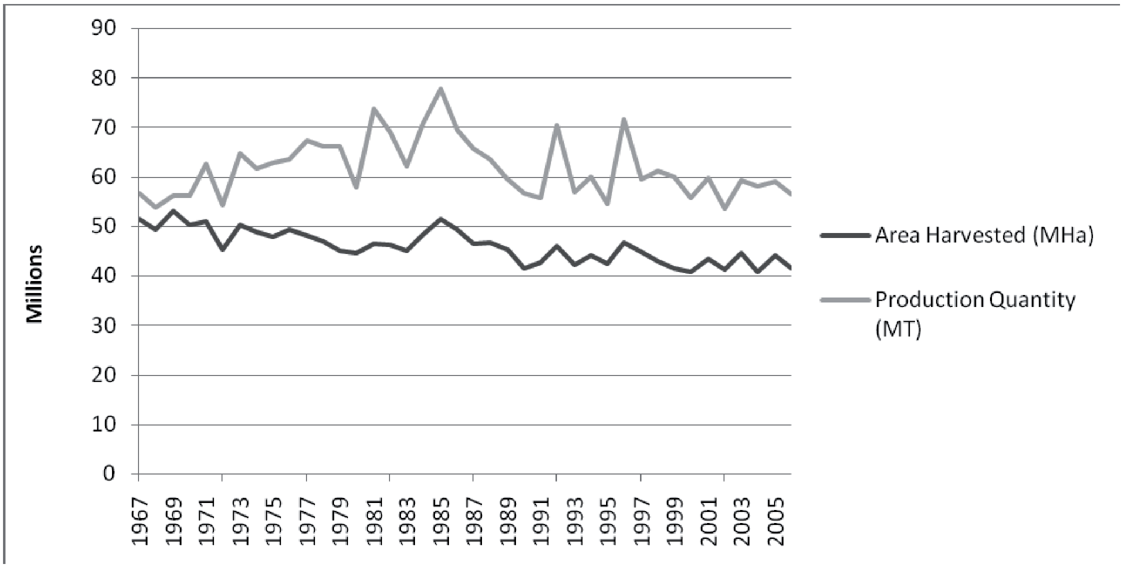
Global, regional and local importance

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

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

FIGURE 20

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



Taxonomic classification

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

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

TABLE 7

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

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

Wild relatives

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

Primary wild relatives

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

Secondary wild relatives

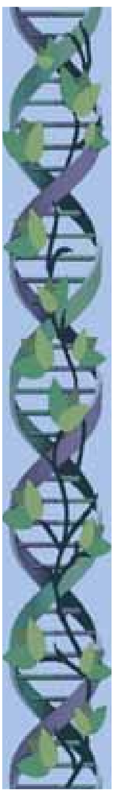
- *S.* × *almum* Parodi
- *S. halepense* (L.) Pers

Tertiary wild relatives

All non-section *Sorghum* species

Distribution and centre of diversity

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



Known uses of wild relatives in crop improvement

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

Priority taxa

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

Priority sites

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

Recommendations

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

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

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

2.11 Wheat

Scientific name

Triticum aestivum L.

Principle synonyms

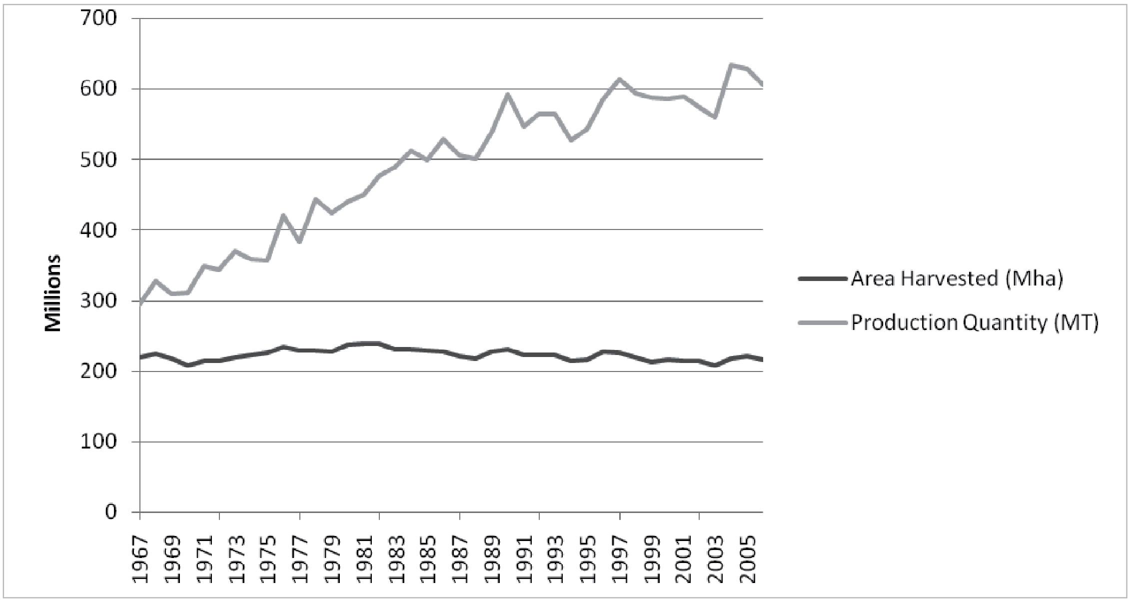
T. hybernum L., *T. macha* Dekap. & Menab., *T. sativum* Lam., *T. sphaerococcum* Percival, *T. vulgare* Vill.

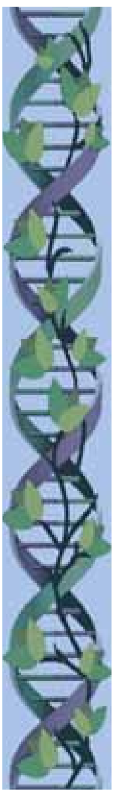
Global, regional and local importance

Wheat is grown in almost all areas that are cropped, except the humid lowland tropics. Rain-fed winter wheat dominates the agricultural production in Europe, the USA, Ukraine and southern Russia, while spring sown wheat predominates in semi-arid conditions of Canada, Kazakhstan and Siberia. Bread wheat (*Triticum aestivum* subsp. *aestivum*) forms the most widely cultivated taxon of a group of closely related cultivated wheat species, including: durum or macaroni wheat (*T. turgidum* subsp. *durum*), grown primarily in the drier areas of the Mediterranean Basin, Australia, India, the former USSR, Argentina and the central plains of the USA and Canada; the less widely cultivated emmer (*T. turgidum* subsp. *dicoccon*) which is currently cultivated in Morocco, Spain (Asturias), the Carpathian mountains on the border of the Czech and Slovak republics, Albania, Turkey, Switzerland and Italy; einkorn (*T. monococcum* subsp. *monococcum*) whose cultivation is primarily in Ethiopia, but is also grown as a minor crop in India, Italy and the north-eastern parts of the eastern Mediterranean; and *T. timopheevii* which is cultivated in restricted areas of the Transcaucasia (Feldman *et al*., 1995; Dubin *et al*., 1997). Today, bread wheat is cultivated in a wide range of environments from 67° N in Canada, Scandinavia and Russia to 45° S in Argentina, but in the tropics its cultivation is restricted to higher altitudes. The largest wheat-producing countries in 2006 were China (104.5 MT), India (69.4 MT), United States of America (57.3 MT), Russian Federation (45.0 MT), France (35.4 MT) and Canada (27.3 MT) (FAO, 2008). As is shown in Figure 21, the area harvested has remained relatively constant over recent years, but the production has increased markedly, with wheat now cultivated on approximately 200 million hectares and with an annual production of 600 million tonnes worldwide in 2006 (FAO, 2008).

FIGURE 22

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





Taxonomic classification

The tribe *Triticeae* of the family *Poaceae* is economically the most important of the grass family, as it contains numerous important crop and forage species (wheats, barleys, ryes and others) (Feldman *et al*., 1995). The wheat genus, *Triticum* L., comprises a series of diploid, tetraploid and hexaploid forms that have arisen by hybridization and introgression between various closely related *Triticum* and *Aegilops* L. species. For example, bread wheat is thought to have originated as a natural hybrid between the amphidiploid emmer *Triticum turgidum* (AABB genome) with *Aegilops tauschii* (syn. *Ae. squarrosa*) (DD genome) (McFadden and Sears, 1946). Linnaeus (1753) recognized both *Triticum* and *Aegilops*, which comprise the core gene pool of the wheats, as two distinct genera. However, subsequent taxonomists have failed to agree on the precise distinction between the two genera, leading to an abundant and complex synonymy, with some suggesting merging the genera (Stebbins, 1956) and at the other extreme, Löve (1984) arguing for the establishment of 37 genera on the basis of genomically homogeneous taxa. Following a detailed review, van Slageren (1994) argued for the retention of the two options, with the cultivated taxa and their closest wild relatives in *Triticum* and the wild forms in *Aegilops*, though there are those who many consider this strict division rather over-simplistic. The genus *Triticum* is composed of six species—two diploids, two tetraploids and two hexaploids (van Slageren, 1994), while *Aegilops* comprises 22 species, inclusive of ten diploids, ten tetraploids and two hexaploids (Manners and van Slageren, 1998).

Wild relatives

The gene pool of wheat has been defined; however, there remains disagreement between taxonomists over the precise delimitation of GP1, GP2 and GP3. One interpretation of the bread wheat gene pool is that proposed by van Slageren (1994):

Primary wild relatives

- *Triticum aestivum* subsp. *compactum*
    - subsp. *macha*
    - subsp. *spelta*
    - subsp. *sphaerococcum*
- *T. monococcum* subsp. *aegilopoides* (wild einkorn)
    - subsp. *monococcum* (cultivated einkorn)
- *T. timopheevii* subsp. *armeniacum*
    - subsp. *durum*
    - subsp. *timopheevii*
- *T. turgidum* subsp. *carthlicum*
    - subsp. *dicoccoides* (wild emmer)
    - subsp. *dicoccon* (cultivated emmer)
    - subsp. *durum*
    - subsp. *paleocolchicum*
    - subsp. *polonicum*
    - subsp. *turanicum*
    - subsp. *turgidum*
- *T. urartu*
- *T. zhukovskyi*

Secondary wild relatives

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

Tertiary wild relatives

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

Distribution and centre of diversity

The primary centre of natural distribution of *Triticum* and *Aegilops* is Transcaucasia, the Fertile Crescent and the eastern Mediterranean regions, where the species still cross freely amongst themselves and with *Secale*. The cultivated wheats spread from this region in Neolithic times (Zeven, 1979) and established secondary centres of variation in the Hindu Kush, China and Japan; and probably the African Sahara. The distribution of the cultivated *Triticum* species is heavily influenced by man—the hexaploid species are found worldwide in drier and cooler regions, the tetraploid species are found throughout the Mediterranean Basin, Transcaucasia and Ethiopia, and the diploid species are more restricted to the north-eastern Mediterranean (Kimber and Feldman, 1987). *Aegilops* species have a much wider distribution, extending circum-Mediterranean and into Central Asia, as well as Transcaucasia and the Fertile Crescent (van Slageren, 1994) (see Table 8).

Wild *Triticum* species tend to grow in medium to large sized, relatively compact populations, while the diploid *Aegilops* species are usually found in smaller, more dispersed populations (*Ae. speltoides* being the exception) (van Slageren, 1994). The tetraploid species of *Triticum* often occur in massive, dense stands, reflecting their invasive, weedy habit. They are essentially pasture species that tend to occupy poor, thin and rocky, dry soils, but they respond well to better soils. They prefer open steppe-like communities, degraded deciduous forests (e.g., of oaks and pistachio), garrigue and maquis vegetation, wadi beds, roadsides, edges of cultivation and recently disturbed land. Climatically, *Triticum* and *Aegilops* species are limited to areas with hot, dry summers and winter rainfall, while away from the sea they can also be found in dry continental areas with colder winters. The entire altitudinal range of the taxa is from -400 (near the Dead Sea) to 2 700 m, but most species are much more specific and are most commonly found from 500–1 200 m (van Slageren, 1994).

Known uses of wild relatives in crop improvement

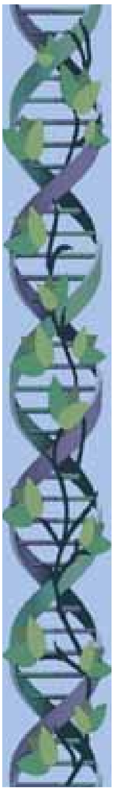
The hist ory and extent of the use of CWR for wheat improvement is unrivalled (Hodgkin and Hajjar, 2008); it is believed this may be partially due to the narrow genetic base of wheat following domestication (Feldman and Sears, 1981; Zohary, 1999). Millet *et al*. (2008) conclude that wheat wild relatives still hold additional potentially useful traits for resistance to biotic stress, abiotic stress resistance (particularly important in times of climate change), and technological and nutritional quality. McFadden (1930) was the first to transfer desirable traits via inter-specific hybridization to wheat when he introduced disease resistance from emmer wheat. The utilization of *Aegilops* species to broaden the genetic base of wheat has recently been reviewed by Schneider *et al*. (2008), who conclude that although many useful traits have been transferred from *Aegilops* species to wheat, there remains much that can be utilized, particularly in *Aegilops* species not previously evaluated and with the aid of advanced molecular characterization. Examples of beneficial traits introduced to wheat from related wild species include yellow rust resistance (McIntosh *et al*., 1966; Peng *et al*., 1999; Millet *et al*., 2008), leaf rust resistance (Kerber and Dyck, 1969; Gill *et al*., 1988; McIntosh *et al*., 2003), *Septoria*, stem rust, powdery mildew, eyespot and other disease resistances (Jahier *et al*., 1979; Miller *et al*., 1987; Lagudah and Appels, 1993; Mujeeb Kazi and Hettel, 1995; Mujeeb-Kazi *et al*., 2001), hessian fly-resistance (Cox and Hatchett, 1994), greenbug resistance (Wells *et al*., 1982), cyst nematode resistance (Delibes *et al*., 1993), root knot nematode resistance (Raupp *et al*., 1993), grain protein content (Avivi, 1978; Hoisington *et al*., 1999), water-logging tolerance (Villareal *et al*., 2001), sprouting suppression (Xiu-Jin *et al*., 1997) and quality-desirable glutenins improvement (William *et al*., 1993; Peňa *et al*., 1995).

TABLE 8

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

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

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



Priority taxa

High priority taxa

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

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

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

Priority sites

A recent study of *Aegilops* taxa diversity (Maxted *et al*., 2008c) found Northwest Jordan, Israel, Lebanon, western Syria, Iraq and Turkey as areas containing more than nine *Aegilops* species, but two particular hotspots containing between 12 and 14 *Aegilops* species were identified—the first in western Syria (covering Damascus, Homs, Hama, Idlib and Halab provinces) and Northeast Lebanon (North, Central and East Bekaa Valley), and the second in northern Iraq (Ninawa and Arbil provinces). The same study undertook complementarity analysis on an *Aegilops* dataset of 9 866 records and identified the five 100 by 100 km grid cells required to capture all 22 species in the *Aegilops* genus (Figure 22), giving the most suitable sites to implement complementary genetic reserve conservation for the *Aegilops* gene pool.

In the current study, distribution data for high priority *Triticum* species obtained from NPGS and GBIF were plotted (see Figure 23), showing Turkey as the main centre of diversity of the taxa, with Iraq, Iran, Georgia, Azerbaijan, Syria, Lebanon, Israel and Palestine also containing populations of high priority taxa. A more complete data set obtained through a detailed ecogeographic survey would most likely reveal further locations of high priority taxa; for example, Armenia and central Israel are known centres of wild wheat diversity, but this is not reflected in these data sets.

FIGURE 22

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

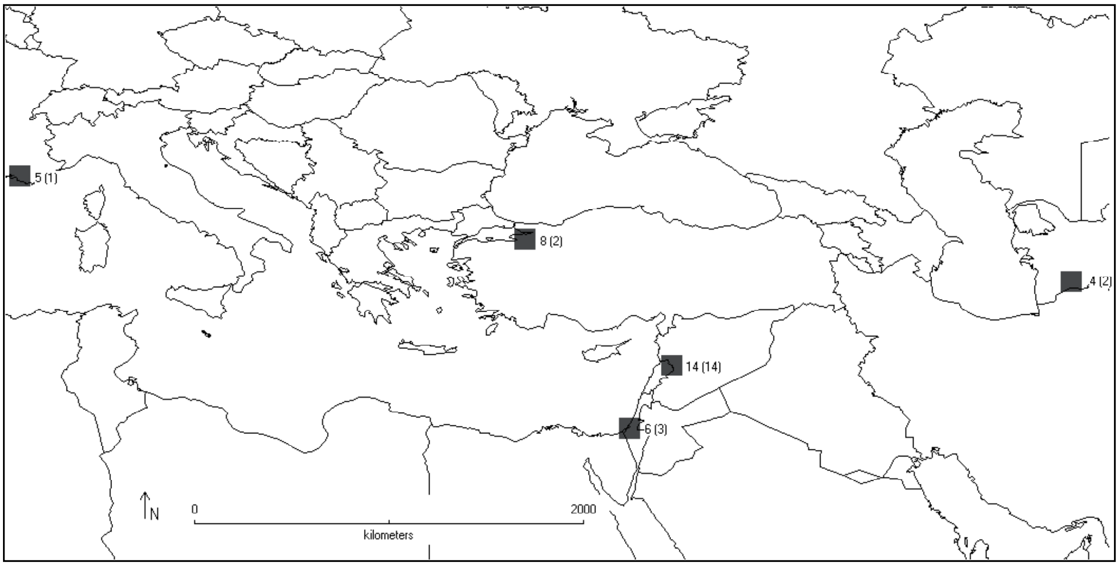
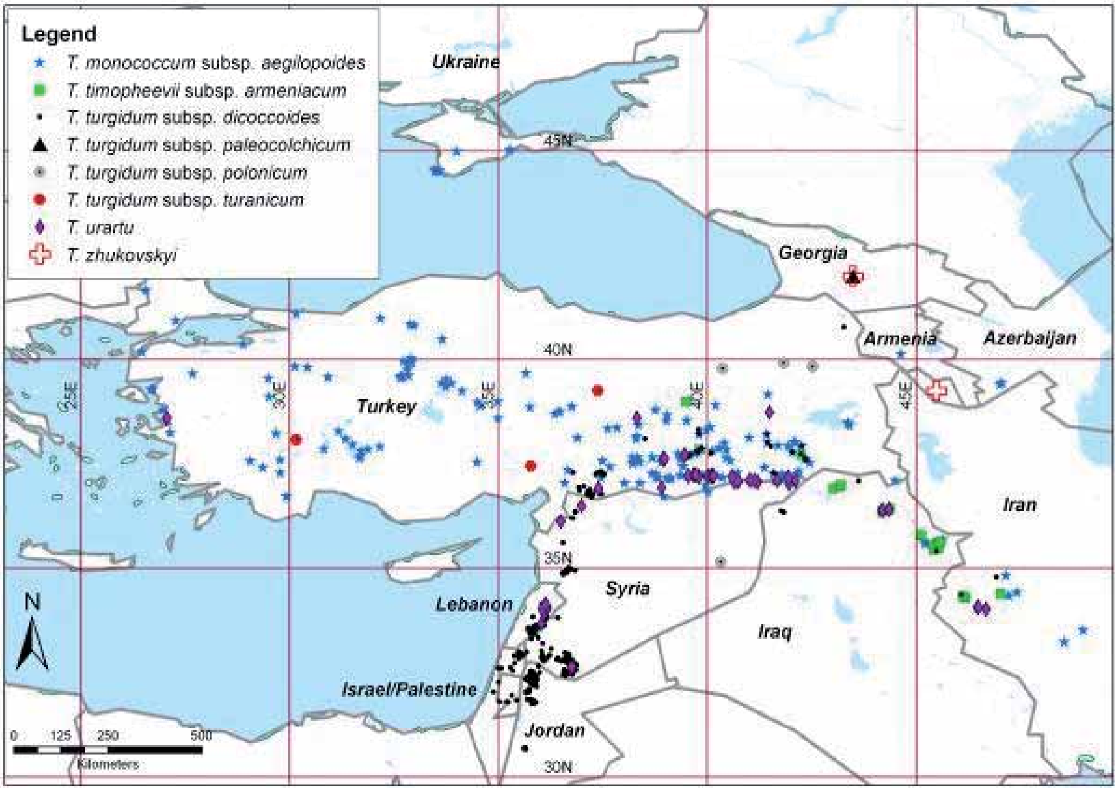
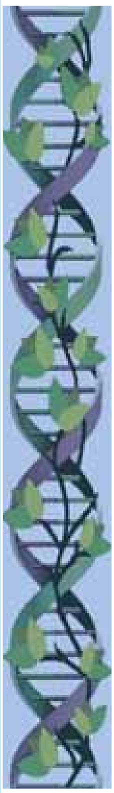


FIGURE 23

Distribution of high priority wheat wild relatives (*Triticum* spp.). Data sources: *T. monococcum* subsp. *aegilopoides, T. timopheevii* subsp. *armeniacum, T. turgidum* subsp. *dicoccoides*, subsp. *paleocolchicum, T. urartu* and *T. zhukovskyi* – USDA, ARS, National Genetic Resources Program. pcGRIN. National Germplasm Resources Laboratory, Beltsville, Maryland; *T. turgidum* subsp. *dicoccoides*, subsp. *polonicum*, subsp. *turanicum* – SINGER (accessed through GBIF data portal, http://data.gbif.org/datasets/resource/1430 29/07/2008)



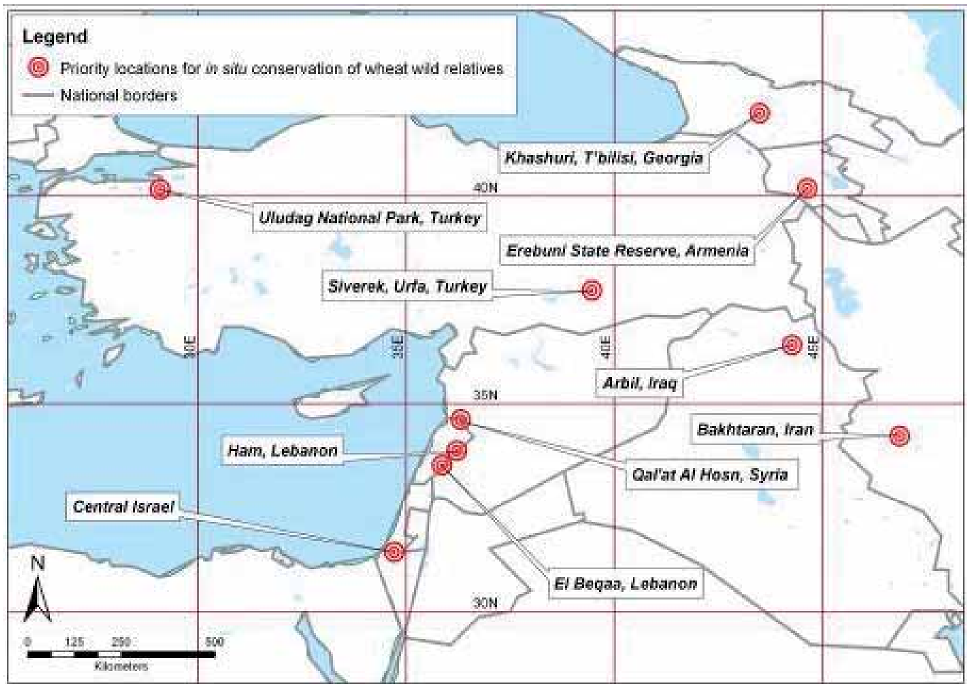


Based on the data presented in Figures 22 and 23, the following sites/locations are important for the *in situ* conservation of wheat wild relatives (see Figure 24):

- Qal'at Al Hosn, Homs province, Syria. Maxted *et al*. (2008c) identified this location as the best option for a single reserve for *Aegilops* as it has the highest concentration of taxa (14). However, there are currently no protected areas in the vicinity and a recent study (Keisa *et al*., 2008) found that this area is being developed for tourism very rapidly and is highly threatened. Designation and site protection is a priority.
- Ham, Baalbek-Hermel province, Lebanon. This would also present a good second choice for a single wheat diversity genetic reserve and the fact that it is mountainous and on the Syrian–Lebanese border means it is less likely to be threatened by future human-induced genetic erosion. The site was established as a genetic reserve under the recent Global Environment Facility funded regional project on: 'Conservation and Sustainable Use of Dryland Agrobiodiversity in West Asia' (http://www.icarda.cgiar.org/gef.html) though the current level of active conservation is unknown.
- Central Israel, possibly within Eshqol (Habsor) National Park (IUCN category V), Ha Besor Nature Reserve, Karmiyya Nature Reserve, Kurkar Gervar'am Nature Reserve, Lahav Darom Nature Reserve, Lahav Zafon Nature Reserve or Tel Qeriyyot Nature Reserve (all IUCN category IV). Although these sites have fewer total *Aegilops* species, they do contain additional endemic species.
- Uludag National Park, Bursa province. There are 8 *Aegilops* species present and two additional species to those found in West Asia.
- Erebuni State Reserve, Yerevan, Armenia. The 89 ha reserve was established in 1981 near Yerevan in foothills of the Ararat concavity and the south-western slope of Voghjaberd upland, specifically to protect wild cereals (Avagyan, 2008). The site was also included as a genetic reserve within the recent Global Environment Facility funded regional project on: '*In Situ* Conservation of Crop Wild Relatives Through Enhanced Information Management and Field Application' (http://www.cwr.am) though the current level of active conservation is unknown.
- Khashuri near Tbilisi, Georgia. Data analysis indicates that *T. turgidum* subsp. *paleocolchicum* and *T. zhukovskyi* both occur at this location. This is the only location of *T. zhukovskyi* showing in this analysis and one of two locations of wild *T. turgidum* subsp. *paleocolchicum* (the other location is in Azerbaijan). The location does not appear to be protected, though it could fall within the unknown boundaries of Nezdi Nature Sanctuary (IUCN category IV) and the Borjomi Nature Reserve (IUCN category Ia) is also close by to the southwest.
- Urfa, Turkey, 16–18 km east of Siverek. Data analysis shows this location to contain populations of *T. monococcum* subsp. *aegilopoides, T. turgidum* subsp. *dicoccoides* and *T. urartu*. This area is not currently protected but the relatively geographically close Ceylanpinar State Farm on the Syrian border was designated as a genetic reserve by the Global Environment Facility funded Turkish *In situ* Conservation of Genetic Diversity Project, which following a detailed survey was found to contain *T. monococcum, T. dicoccoides, Ae. speltoides* var. *speltoides, Ae. speltoides* var. *ligustica, Ae. tauschii, Ae. crassa, Ae. juvenalis, Ae. vavilovii, Ae. triuncialis, Ae. biuncialis, Ae. triaristata, Ae. caudata, Ae. columnaris, Ae. umhellulata, Ae. ovata, Ae. cylindrica*, along with *Hordeum spontaneum, H. bulbosum,* other *Hordeum* spp. and *Avena* spp. (Karagöz, 1998). The current level of active conservation within the site is unknown.
- Arbil, Iraq, 1 km northeast of Salahadin and 4 km northeast of Shaqlawa. *T. monococcum* subsp. *aegilopoides*, *T. timopheevii* subsp. *armeniacum* and *T. urartu* have been recorded at these locations, which are currently not protected.
- Bakhtaran province, Iran. Populations of *T. timopheevii* subsp. *armeniacum, T. urartu, T. monococcum* subsp. *aegilopoides* and *T. turgidum* subsp. *dicoccoides* have been recorded in this province. Data analysis indicates that none of these taxa are currently protected *in situ*, except perhaps for *T. monococcum* subsp. *aegilopoides*, which is on the edge of Bisotun Protected Area (IUCN category V and World Heritage Convention). This site and the neighbouring Bisotun (Varmangeh) Wildlife Refuge could however contain populations of all these taxa. Searches are required. To the southwest, searches in Ghalajeh Protected Area (IUCN category V) should also be carried out. Critically, populations of *T. timopheevii* subsp. *armeniacum* and *T. urartu* appear not to be protected in this vicinity.
- El Beqaa, Lebanon, between Kfarkouk and Aiha. *T. monococcum* subsp. *aegilopoides, T. timopheevii* subsp. *armeniacum* and *T. turgidum* subsp. *dicoccoides* have been recorded at this site, which is currently not protected.

FIGURE 24

Priority locations for wheat wild relative genetic reserve conservation



Recommendations

- Three reserves have been established in the centre of diversity specifically to conserve wild wheats—Ammiad in Israel (Anikster *et al*., 1997), Ceylanpinar in Turkey (Ertug Firat and Tan, 1997) and Erebuni in Armenia (Avagyan, 2008). There is a need to complement these existing reserves by establishing additional genetic reserves in the sites with the highest *Triticum* and *Aegilops* taxon richness. The sites/locations identified in this study (Figure 22) should be considered. Iran has significant unique *Triticum* and *Aegilops* taxa and as it is at the eastern extreme of the centre of diversity, further study should be devoted to establishing an appropriate site to conserve this diversity *in situ*. The results presented in this study should be backed up with further detailed ecogeographic surveys of the priority taxa. It is not clear from this analysis whether records of *T. turgidum* subsp. *polonicum* and subsp. *turanicum* are cultivated or wild. Further research is needed to ascertain locations of wild populations of these taxa.
- Wheat species have been relatively comprehensively surveyed and collected for *ex situ* conservation by the CGIAR centres, which have ensured that the cultivated wheats are systematically conserved *ex situ* with approximately 850 000 accessions stored, mainly of *Triticum* species (FAO, 1998). However, van Slageren (1994) comments that there is a conspicuous absence of collections from central and eastern Iran and western Afghanistan, and that it seems likely that the areas to the north of this area (Turkmenistan and Uzbekistan) are also under-collected.

2.12 Faba bean

Scientific name

Vicia faba L. (*Fabaceae*)

Principle synonyms

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

Global, regional and local importance

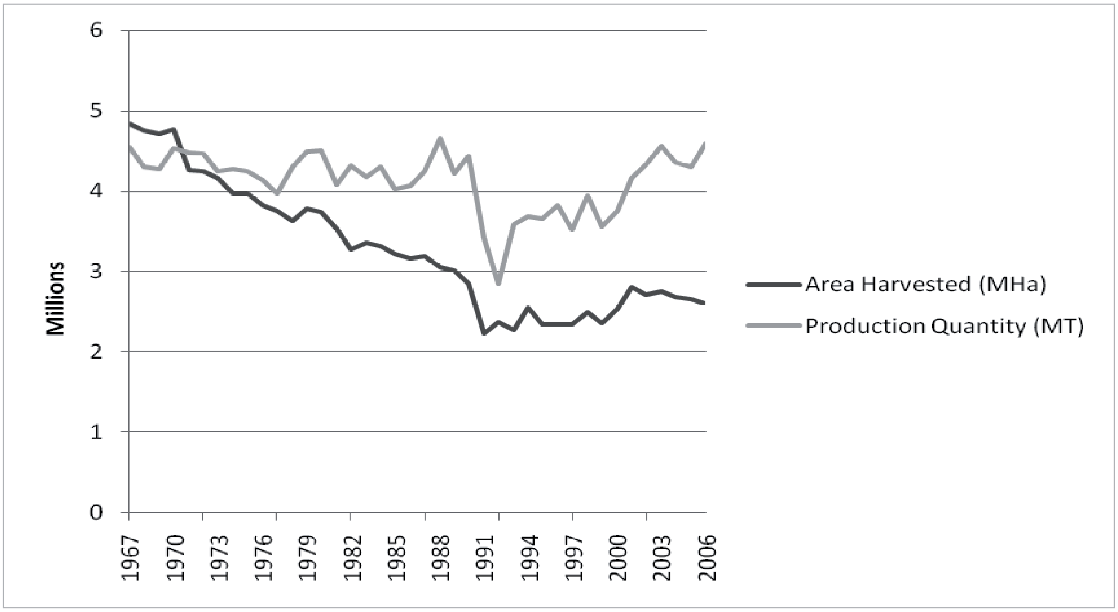
The faba bean or broad bean (*Vicia faba* L.) is an important global pulse, fodder crop and vegetable throughout the temperate world and at higher altitudes in some sub-tropical regions (Bond, 1995). It has been referred to as the 'poor man's meat' due to the fact that it may be harvested early for green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

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

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

FIGURE 25

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



Taxonomic classification

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

TABLE 9

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

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

Wild relatives

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

Primary wild relatives

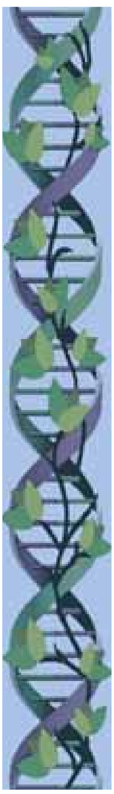
- *Vicia faba* L.
    - subsp. *paucijuga* Murat.
    - subsp. *faba*
        a. var. *minor* Beck
        b. var. *equina* Pers.
        c. var. *faba*

Secondary wild relatives

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

Tertiary wild relatives

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



Distribution and centre of diversity

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

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

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

Known uses of wild relatives in crop improvement

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

Priority taxa

High priority taxa

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

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

Other priority taxa

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

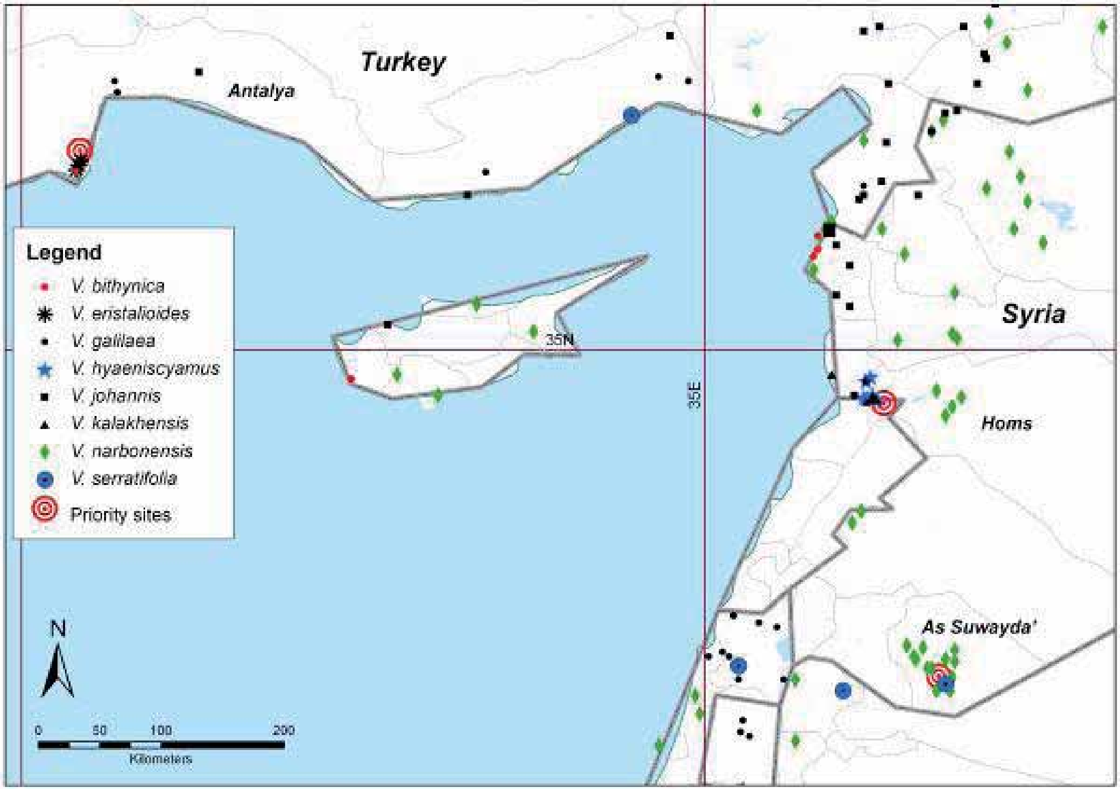
Priority sites

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

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

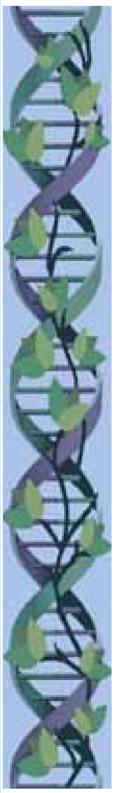
FIGURE 26

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



Recommendations

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



2.13 Cowpea

Scientific name

Vigna unguiculata (L.) Walp.

Principle synonyms

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

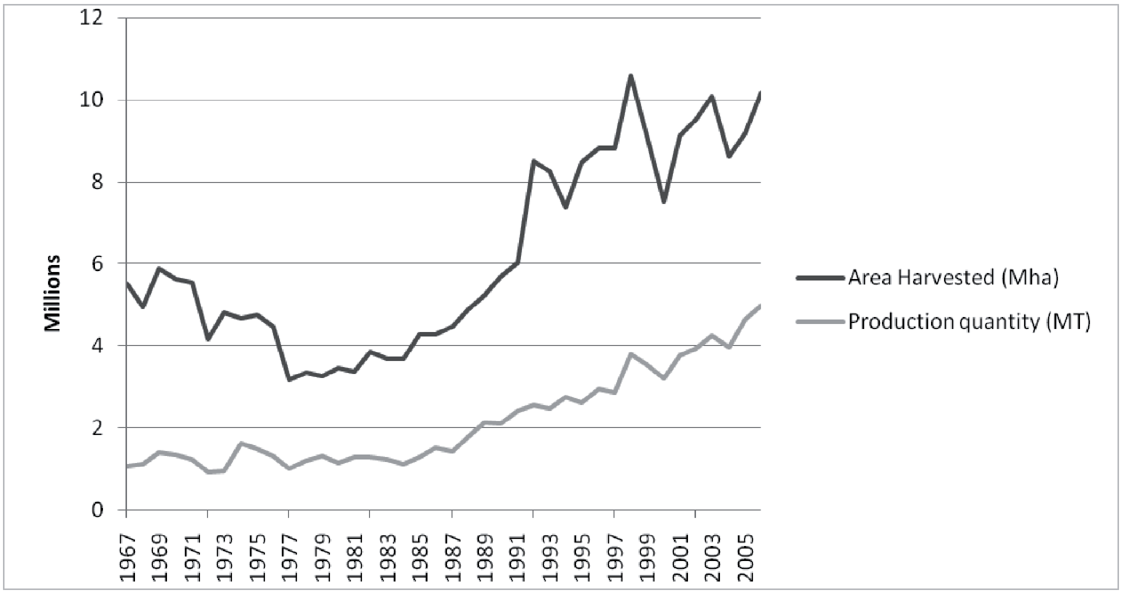
Global, regional and local importance

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

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

FIGURE 27

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

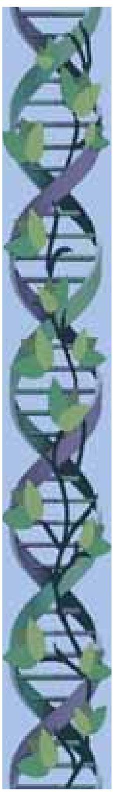


Although plant breeders have striven to enhance and improve production (IITA, 2004), exploitation has been hampered by a lack of:

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

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

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



Taxonomic classification

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

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

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

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

Wild relatives

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

Primary wild relatives

Group A

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

Group B

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

Secondary wild relatives

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

Tertiary wild relatives

Other *Vigna* subgenus *Vigna* species

Distribution and centre of diversity

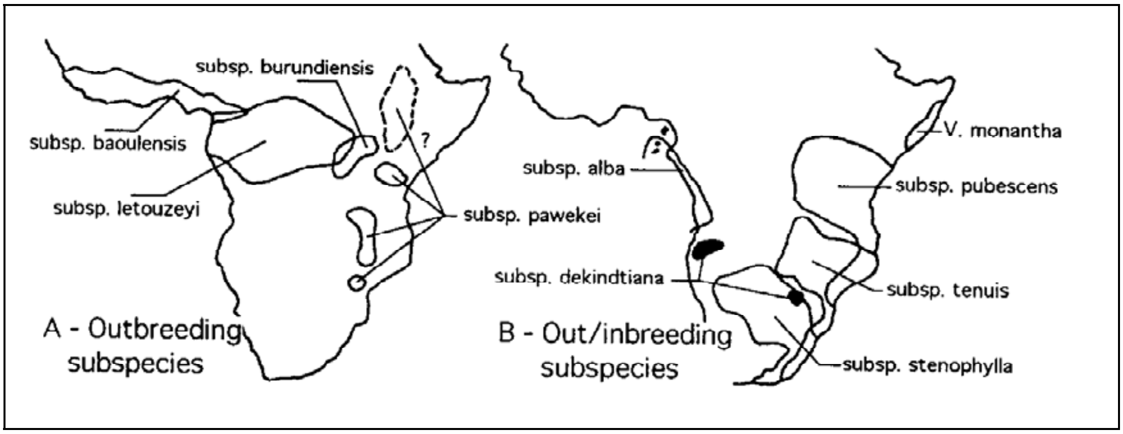
Cultivated cowpea originated in Africa—the only continent where wild relatives are encountered (Maréchal *et al*., 1978). Wild and cultivated forms cross readily. Sauer (1952) argues a solely Ethiopian centre of origin, followed by subsequent evolution predominantly in the ancient farming systems of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

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

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

FIGURE 28

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



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

TABLE 10

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

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

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

Known uses of wild relatives in crop improvement

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

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

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

Priority taxa

High priority taxa

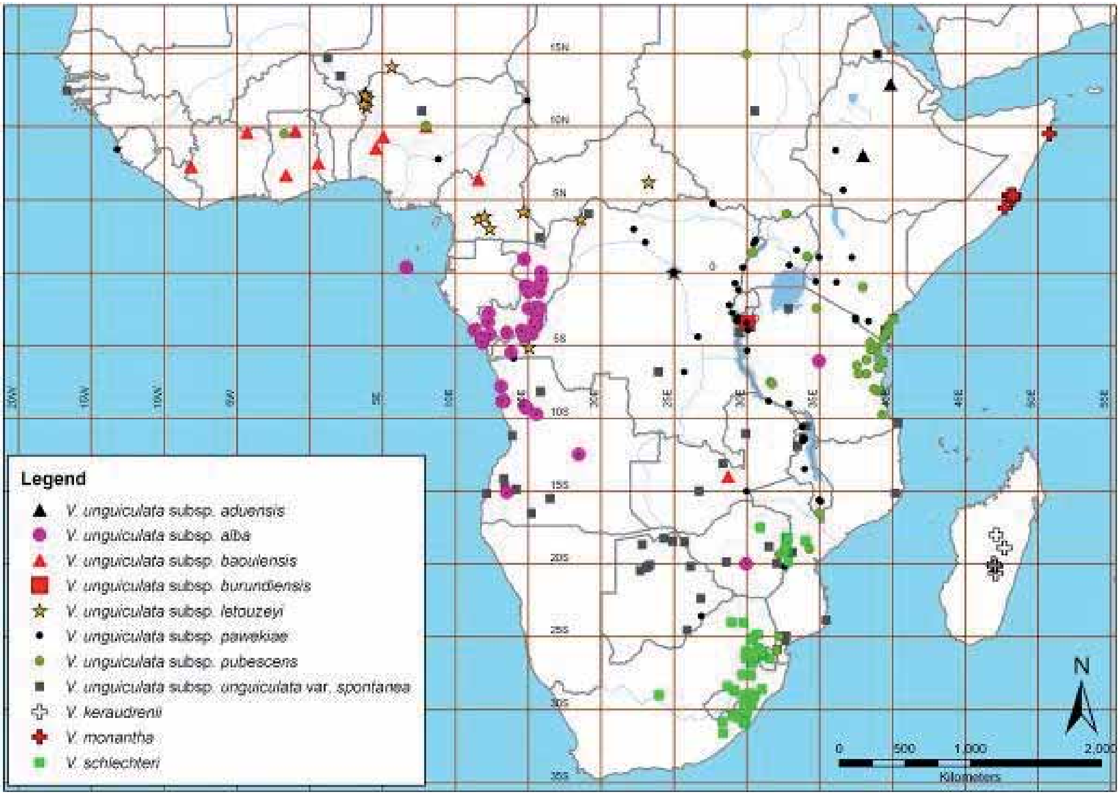
- *V. unguiculata* subsp. *aduensis*
    - subsp. *alba*
    - subsp. *baoulensis*
    - subsp. *burundiensis*
    - subsp. *letouzeyi*
    - subsp. *pawekiae*
    - subsp. *pubescens*
    - subsp. *unguiculata* var. *spontanea*

Other priority taxa

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

FIGURE 29

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



Priority sites

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

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

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

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

Recommendations

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

2.14 Maize

Scientific name

Zea mays L.

Principle synonyms

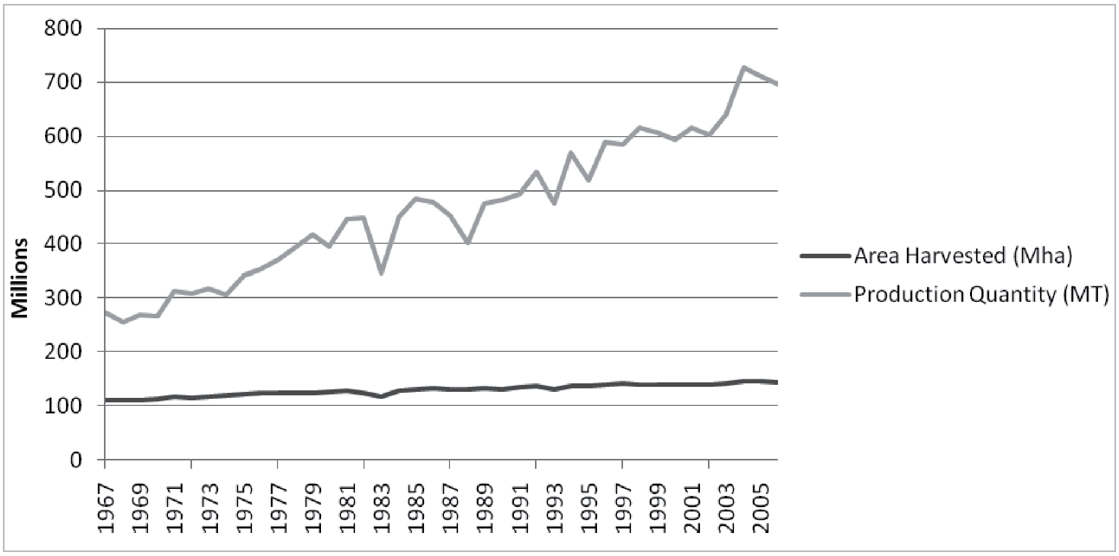
Zea curagua Molina, *Zea indentata* Sturtev., *Zea indurata* Sturtev., *Zea japonica* Van Houtte, *Zea saccharata* Sturtev.

Global, regional and local importance

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

FIGURE 30

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

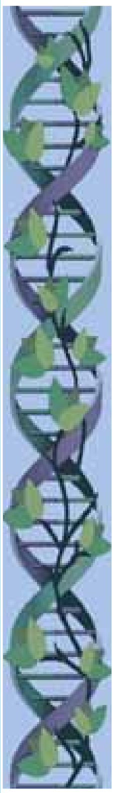


It is believed that maize was domesticated well before 4000 BC in Tehuscán, Puebla Tstae, Mexico (MacNeish, 1985). There is pollen of maize, teosinte (*Zea luxurians* (Durieu and Ascherson) Bird) and their common ancestor from 60,000–80,000 years ago from around Mexico City (Goodman, 1988), and maize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

Taxonomic classification

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

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



Wild relatives

Primary wild relatives

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

Secondary wild relatives

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

Tertiary wild relatives

Tripsacum species

Distribution and centre of diversity

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

TABLE 11

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

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

Known uses of wild relatives in crop improvement

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

Priority taxa

High priority taxa

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

Other priority taxa

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

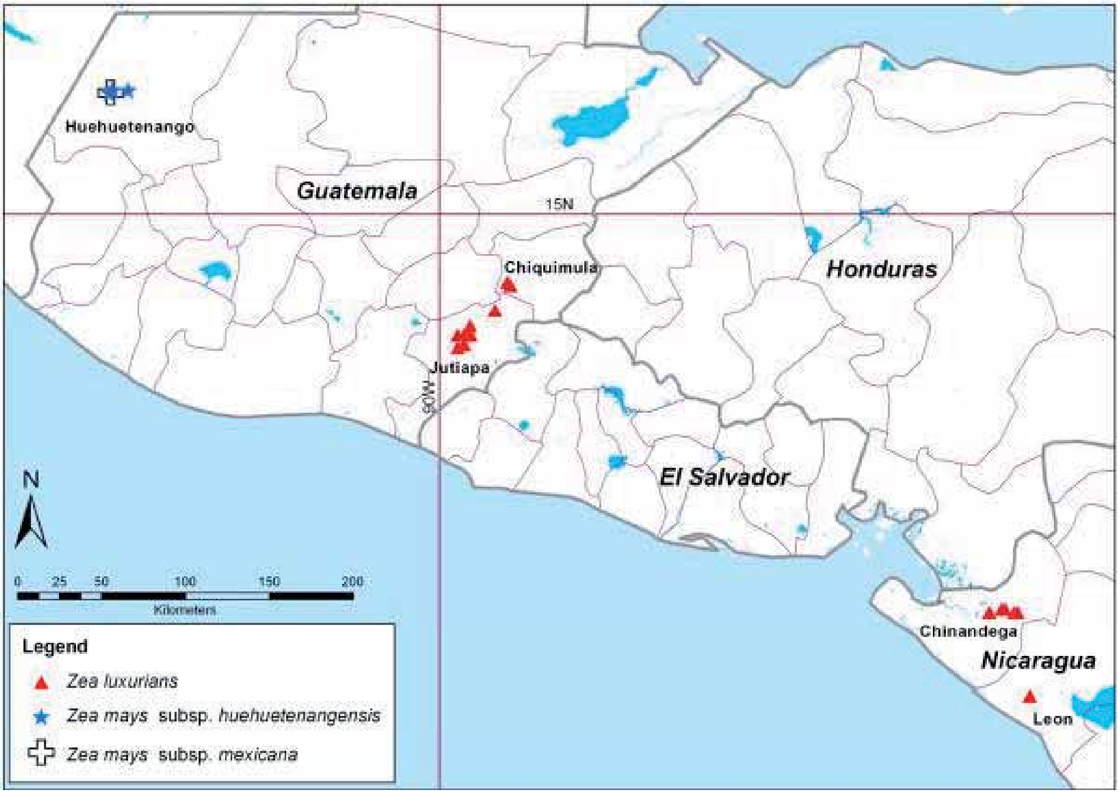
Priority sites

Zea luxurians

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

FIGURE 31

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



Zea mays subsp. *huehuetenangensis*

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

Zea diploperennis

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

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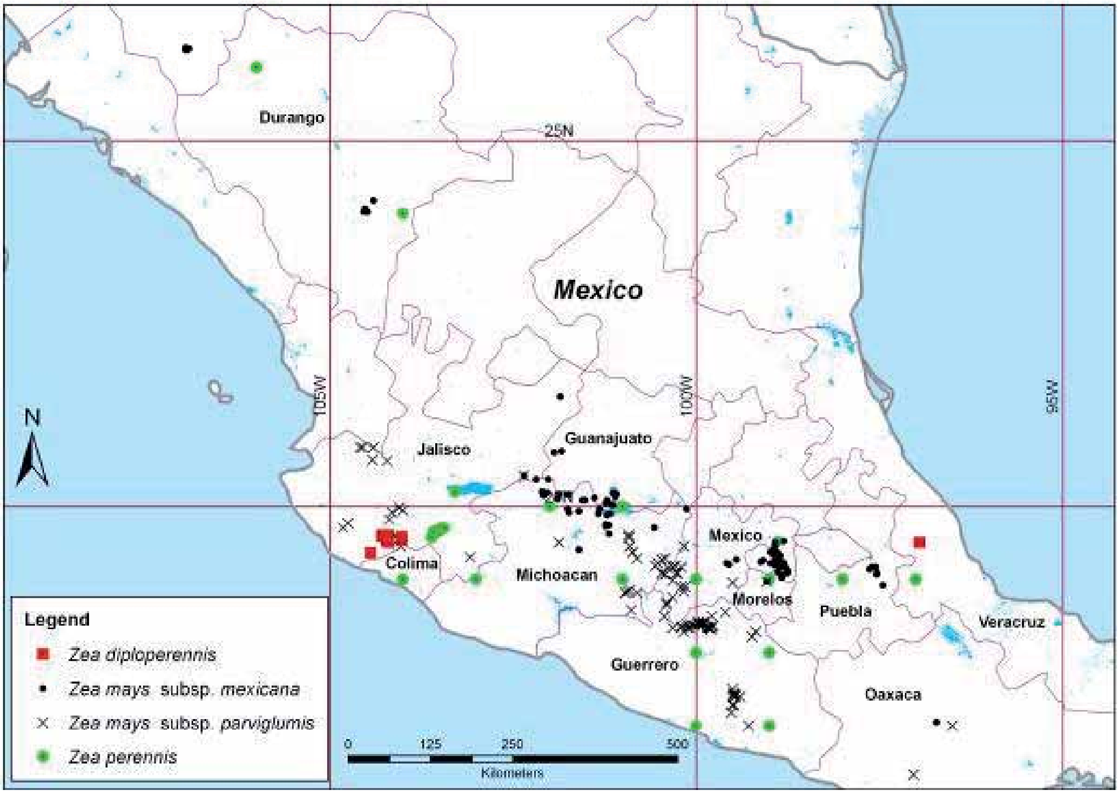
[33] Data sources: J.F. Doebley, Wisconsin, pers. comm., 2008; USDA, ARS, National Genetic Resources Program. pcGRIN. National Germplasm Resources Laboratory, Beltsville, Maryland; Missouri Botanical Garden (accessed through GBIF data portal, http://data.gbif.org/datasets/resource/621 09/08/2008); The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

FIGURE 32

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



Zea mays subsp. *mexicana*

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

Zea mays subsp. *parviglumis*

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

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

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

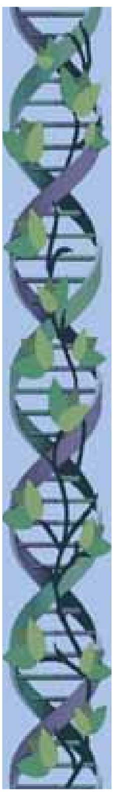
Manantlán Biosphere Reserve, where *Z. diploperennis* and *Z. perennis* are also found. Another population is very close to (c. 2 km outside) the eastern boundary of Insurgente Jose Maria Morelos National Park (IUCN category II), Northeast Michoacan.

Zea perennis

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

Recommendations

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



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

3. Important areas and conservation gaps: synthesis

3.1 Establishing the global network: first steps

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

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

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

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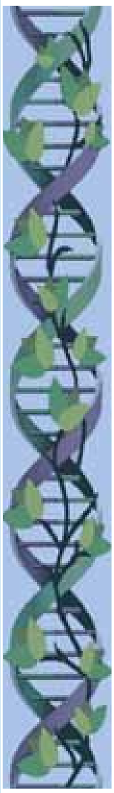
[36] In cases where data were not readily available for analysis, recommendations have been made for further study.

TABLE 12

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

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



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

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

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

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

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

TABLE 13

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

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

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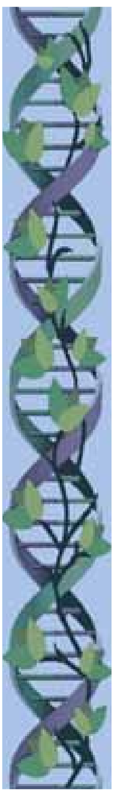
[42] – = no global Red List assessment published



Figures 33–36 show the priority locations for CWR genetic reserve establishment identified in this study in each of four regions: Africa, the Americas, the Middle East, and Asia and the Far East. The symbols shown on the maps indicate the highest priority locations for *in situ* conservation of the wild relatives within each of the 14 crop case studies. These maps are provided to give an overview of priority sites for inclusion in the global network in terms of the individual crop case studies and regional priorities—for taxon and site details, the reader should refer to the individual crop case studies. In each case study, we have identified priority sites that are likely to be within the boundaries of existing protected areas, as indicated by data analysis. However, important sites that are probably outside of existing protected areas are also included where known taxon locations are very limited. Options for the complementary conservation of taxa outside of existing protected areas will have to be investigated on a case by case basis.

It is important to stress that the potential genetic reserve locations shown in Figures 33–36 are for a limited number of crop complexes (those included in this study) and within these, for the highest priority CWR taxa only. Within each crop complex, there are other taxa that could eventually be included in the global CWR genetic reserve network[43], once the complementary conservation of the highest priority taxa is secured. Further, the wild relatives of other crops will be included in the network over time, based on further global crop case studies and priorities arising from national CWR strategies. While the results of the 14 crop complex analyses (with the exception of the Middle East and Eastern Congo) show few obvious opportunities for multi-crop gene pool CWR genetic reserves, further research on other crop complexes is likely to identify additional potential multi-taxon CWR genetic reserves. Therefore, the results of this analysis should be considered as a first step in the process of establishing the global network with a view to carrying out further research in the future.

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

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

FIGURE 33

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

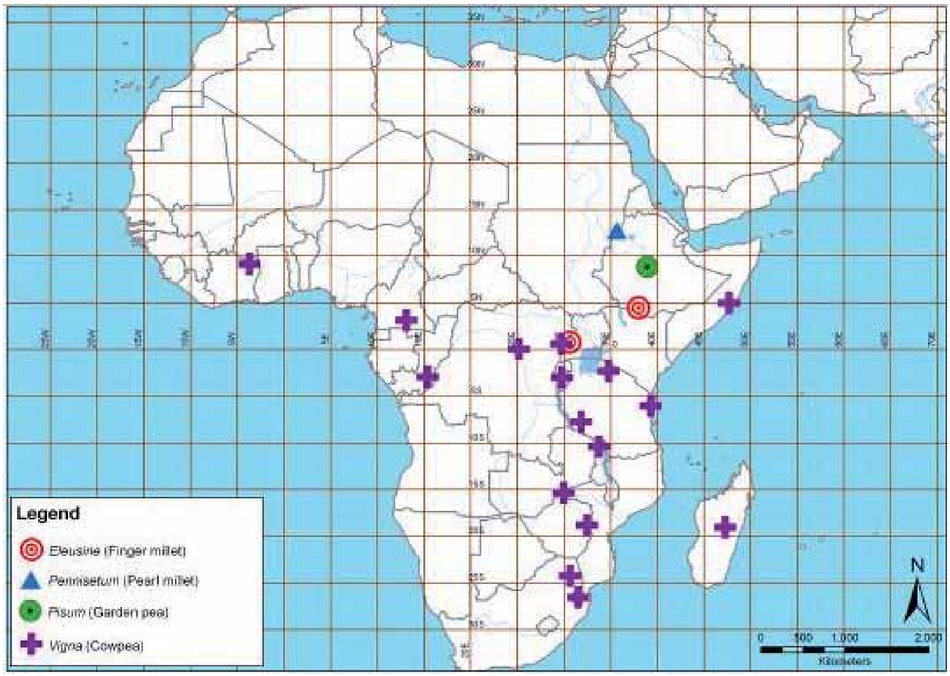


FIGURE 34

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

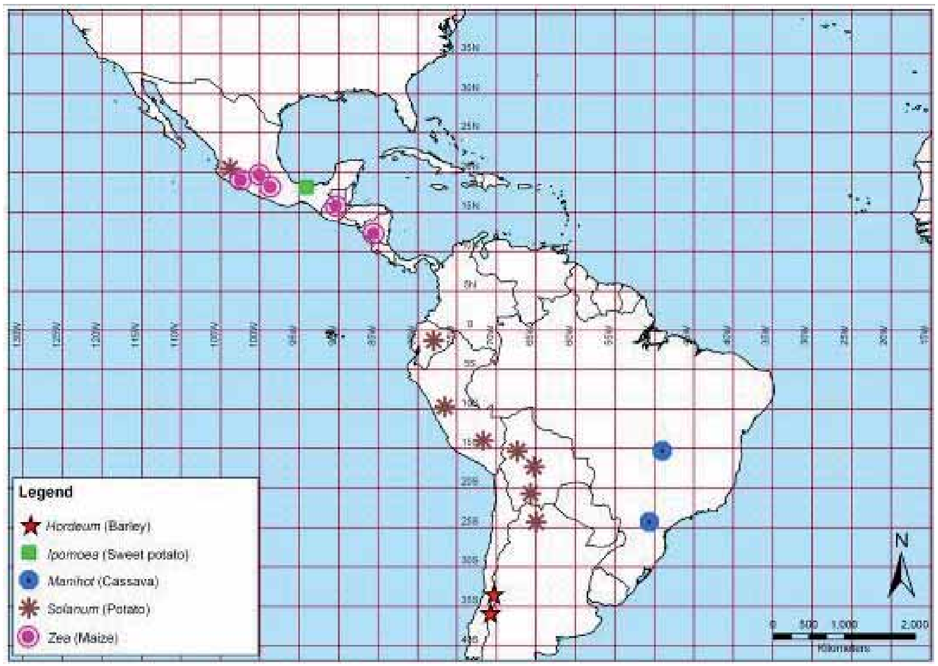


FIGURE 35

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

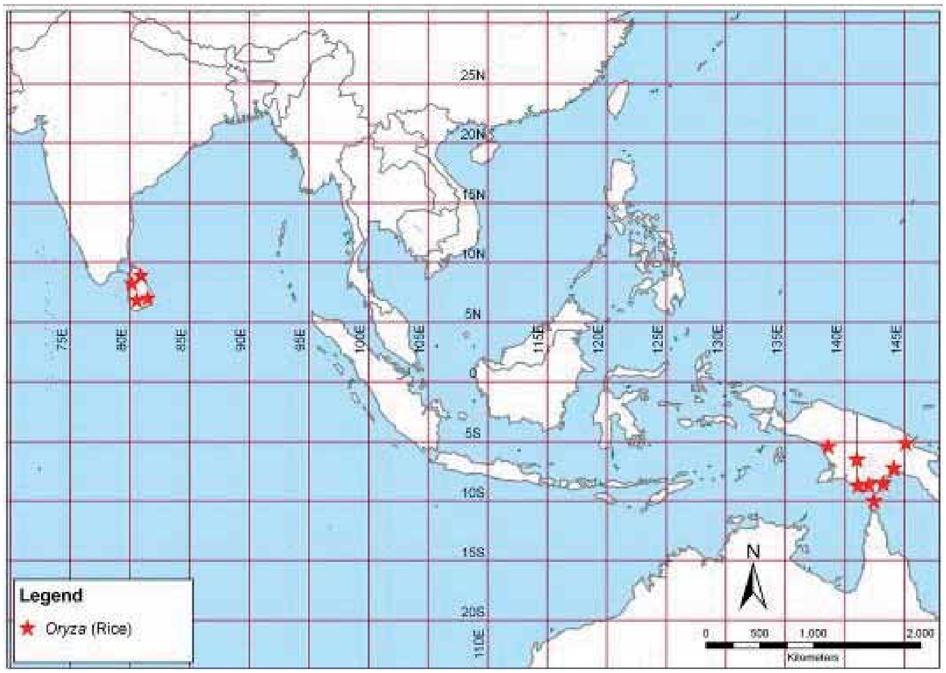
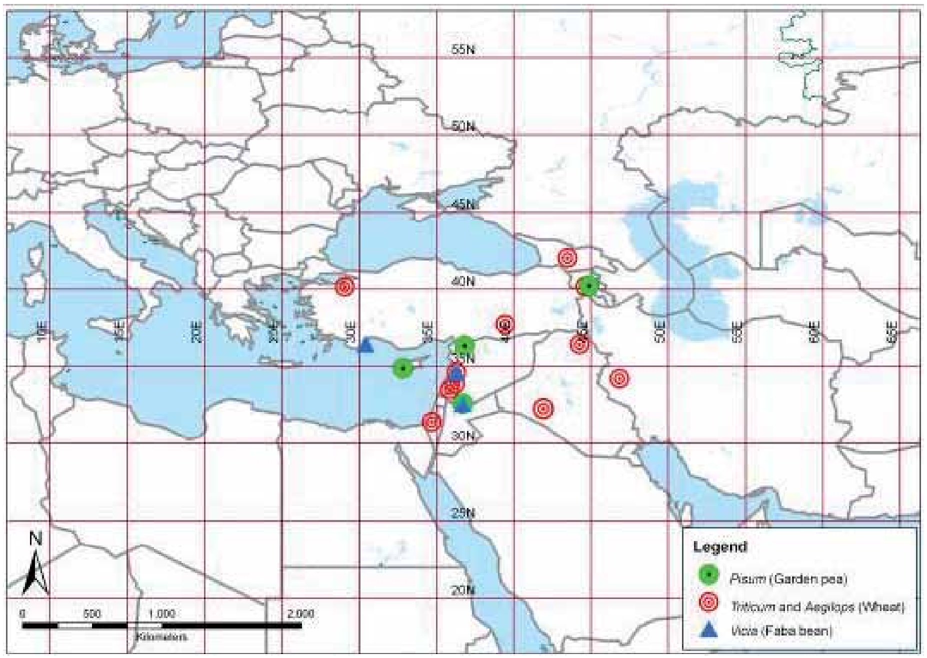


FIGURE 36

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



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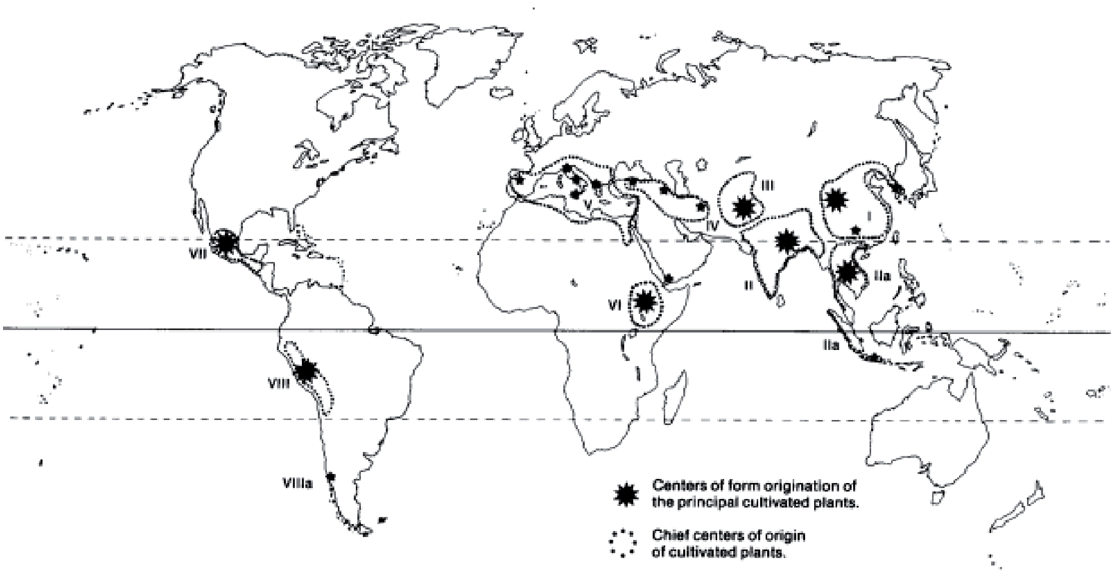
[44] The wild relatives of banana/plantain (*Musa* spp.) also have their centre of distribution in Asia (extending into Australasia). Priority sites for Musa species are not shown as data were not readily available for analysis.

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

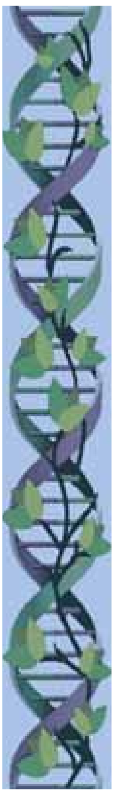
FIGURE 37

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



3.2 Overview of crop gene pool priorities by region

As already noted, the potential genetic reserve locations presented in Figures 33–36 are based only on 14 crop case studies and the highest priority CWR within each group. Options for the establishment of genetic reserves, both within and outside existing protected areas will have to be investigated on a case by case basis. It is evident from this study that there are relatively few options for the establishment of multi-crop complex genetic reserves for the highest priority taxa, probably because these taxa are of restricted distribution range and adapted to specific ecological conditions and therefore less likely to overlap. However, multi-taxon sites within crop gene pools have been identified where possible (for details, see the individual crop case studies). To maximize the efficiency of the global *in situ* network, the establishment of genetic reserves for the high priority taxa treated in this study should also be supported with further research to investigate whether other CWR occur at the same locations to give greater weight to justification for reserve establishment. These additional CWR taxa may be more common and widespread but their conservation *in situ* is also necessary to ensure that the widest pool of genetic diversity of CWR is protected and as a buffer for the impact of climate change. Here, we briefly summarize the genetic reserve locations for high priority CWR taxa for the 14 crop gene pools treated in this study, on a regional basis.



Africa

Figure 33 shows priority genetic reserve locations for finger millet (*Eleusine* spp.), pearl millet (*Pennisetum* spp.), garden pea (*Pisum* spp.) and cowpea (*Vigna* spp.) wild relatives in Africa.

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

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

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

The Americas

Figure 34 shows priority genetic reserve locations for barley (*Hordeum* spp.), sweet potato (*Ipomoea* spp.), cassava (*Manihot* spp.), potato (*Solanum* spp.) and maize (*Zea* spp.) wild relatives in the Americas.

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

Identification of specific sites for the conservation of potato wild relatives will involve further research due to the large number of taxa in the genus and the fact that nearly all of them can be crossed relatively easily with the crop in breeding programmes. As shown in the *Solanum* case study, several species rich areas have been identified in Mexico, Ecuador, Peru, Bolivia and Argentina. The identification of suitable genetic reserve sites in these areas is recommended. However, the majority of potato wild relatives have very restricted distributions, many of which do not overlap, and this presents a major challenge in terms of *in situ* conservation. However, it is possible that many of these species have already been afforded some degree of protection if they are within the boundaries of existing protected areas. A detailed analysis of distribution data overlaid with protected area shapefiles is needed to begin to formulate an appropriate *in situ* conservation strategy for this group.

The Middle East

Figure 35 shows priority genetic reserve locations for garden pea (*Pisum* spp.), wheat (*Triticum* spp. and *Aegilops* spp.) and faba bean (*Vicia* spp.) wild relatives in the Middle East.

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

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

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

Asia and the Far East

Figure 36 shows high priority genetic reserve locations for rice (*Oryza* spp.). The four highest priority taxa, which are of extremely restricted distributions, are found in Sri Lanka, Indonesia (Irian Jaya) and Papua New Guinea and all require urgent conservation attention.

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

Asia and the Far East is also the centre of distribution of banana/plantain wild relatives in the genus *Musa*. Priority locations for *in situ* conservation of this genus are not shown in Figure 36 because distribution data were not readily available for analysis. However, ten priority banana/plantain wild relatives have been identified in this study. They occur in India, Bhutan, China, Myanmar, Thailand, Vietnam, Sumatra, Papua New Guinea and the Philippines. The highest priority areas for *in situ* conservation based on the known distribution ranges of the priority species are Assam (India), Bhutan, Papua New Guinea, Sumatra and the Philippines. Further research is needed on the priority taxa to order to ascertain their *in situ* conservation status and identify genetic reserve sites for inclusion in the network.

3.3 Coordinating the establishment of the CWR genetic reserve network

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

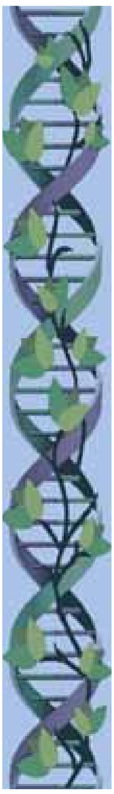
The Global Network could build in a largely uncoordinated ad hoc manner but it would be more effective if an agency with an international remit led the systematic establishment of such a network—the FAO Commission on Genetic Resources for Food and Agriculture would be ideally placed to lead such an initiative.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

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

- **Consultation with crop-based experts** – It would be wise to engage in a dialogue with crop-based specialists for each of the 14 crop case studies prepared to confirm that they support the sites/areas recommended for the establishment of CWR genetic reserves. This is necessary because of the variability in the quantity and quality of information available when preparing the case studies. For some case studies, such as finger millet (*Eleusine* spp.), cassava (*Manihot* spp.) and pearl millet (*Pennisetum* spp.), limited data were available, while for others, such as wheat (*Triticum* and *Aegilops* spp.), faba bean (*Vicia* spp.), cowpea (*Vigna* spp.) and maize (*Zea* spp.), significant data sets were available.
- **Crop case study extension** – The CGRFA could use the crop case studies provided in this study as a template for each of the ITPGRFA Annex I list of Crops Covered Under the Multilateral System, so that over time the Global Network could be extended from those sites identified in this study to provide a comprehensive network of *in situ* genetic reserves that conserve the world's CWR diversity.
- **Financing genetic reserve location and implementation** – As already noted, the Global Network sites are almost exclusively likely to be located in developing countries, many of which may have limited technical and financial resources to take responsibility for maintaining the genetic reserves. As acknowledged in the ITPGRFA (FAO, 2001), the onus is on developed countries to work with developing countries to help conserve CWR diversity. Therefore, a funding mechanism should be put in place to help meet the cost of genetic reserve location and implementation, so that the additional cost does not fall solely on developing country economies.
- **Harmonization of crop case studies with national CWR conservation strategies** – As already stressed in this study, the effective global complementary conservation of CWR diversity must involve efforts at national level, both to effect the conservation of the priority CWR taxa identified in the global crop case studies but also to implement national CWR strategies, which will take a floristic approach and consider national priorities. Therefore, a dialogue between the coordinating body of the Global Network of CWR Genetic Reserves and National PGRFA

Coordinators will be essential for the success of the Network. The publication of the current study and subsequent inclusion of *in situ* CWR conservation priorities in the Second Report on the State of the World's PGRFA and *Global Plan of Action* should go a long way towards meeting this need; however, there is a need to plan ahead for the provision of arenas for specific dialogue between those involved in the establishment and management of the Network, both through face to face communication at meetings and via electronic means. Web tools dedicated to providing such an arena, as well as access to guidance documents and contacts could be made available.

- **Protected area manager dialogue** – To avoid the substantial costs of purchasing new sites, genetic reserves should be established within the boundaries of existing protected areas where possible. However, existing protected area management plans will need to be amended to permit the *in situ* genetic conservation of CWR diversity; therefore, there will be a need for a dialogue between those with overall responsibility for managing the Global Network of CWR Genetic Reserves and individual protected area managers. It is likely that this dialogue will need to involve or be mediated by the National PGRFA Coordinators.
- **Guidelines for *in situ* genetic conservation of CWR diversity** – To ensure the efficient and effective *in situ* genetic conservation of CWR diversity, genetic reserve managers will need to be supplied with guidelines on how to adapt current management plans to allow for genetic conservation of CWR. Iriondo *et al*. (2008) already offers such generic guidance but it may be thought appropriate to supply more specific guidelines to meet the specific needs of CWR genetic reserve managers. A practical manual providing the minimum guidance needed would be beneficial.
- **Training for CWR genetic reserve managers** – Whether the reserves are established within or outside of existing protected areas, training of reserve managers and staff will be beneficial, in addition to the provision of the guidelines suggested above. Genetic reserve management training will be a particular requirement in developing countries where the bulk of the Global Network is likely to be located.



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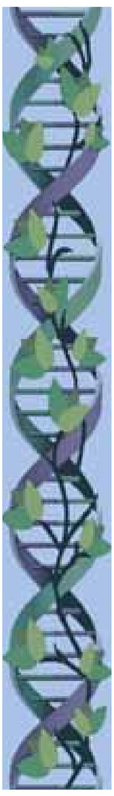

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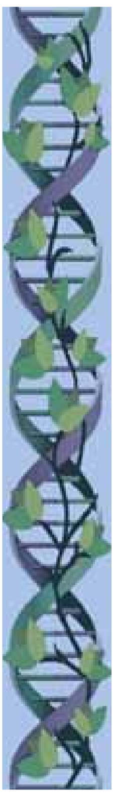

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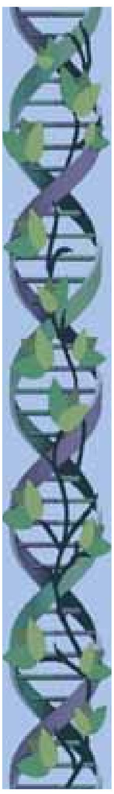

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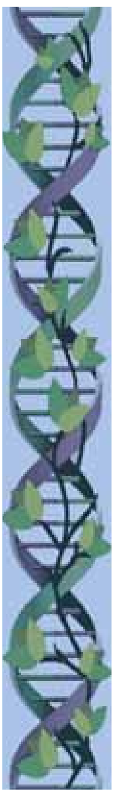

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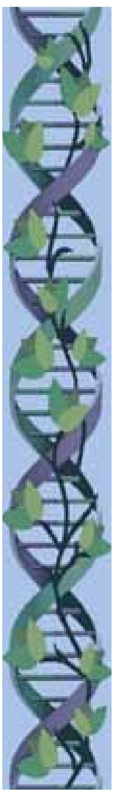

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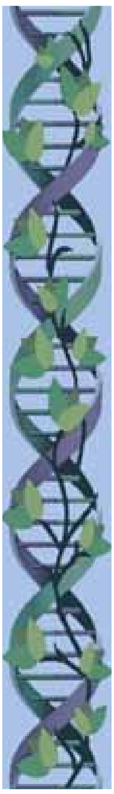

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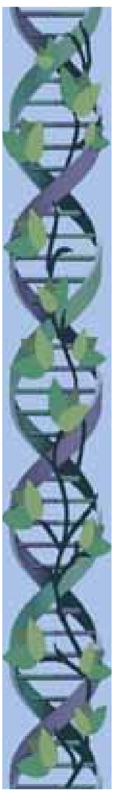

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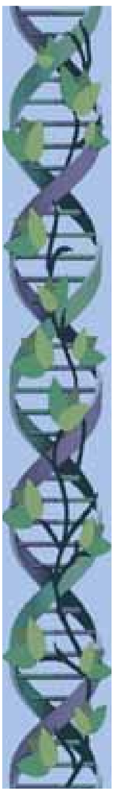

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