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Ex situ and in situ conservation efforts for Aegilops and wild Triticum species

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Introduction

Wheat, the world's most widely grown crop, provides around 20% of food globally, and is the key commodity for approximately 2.5 billion poor people worldwide (FAO, 2008, 2012; CIMMYT and ICARDA, 2011). For countries in the Central and West Asia and North Africa (CWANA) region, wheat is the primary commodity contributing more than 60% of the calories and protein in the diets of the poorest communities (FAOSTATS, 2010). With the challenges imposed by climate change and the related emerging abiotic and biotic stresses including new races of pests and their changing virulences, substantial gains in productivity and quality will be needed to ensure the food security of the fast growing world population.

The recent report of the Intergovernmental Panel on Climate Change (IPCC, 2012) concluded that the agricultural sector is vulnerable to climate extremes which are likely to reduce wheat yields by as much as 40% at low latitudes by 2100. Yet in the light of population increase, wheat production will need to be increased by at least 60% by 2050 to ensure adequate and fair accessibility to wheat-based food for the poor (Rosegrant and Agcaoili, 2010; CIMMYT and ICARDA, 2011; FAO, 2012). While the "green revolution" has resulted in substantial gains in wheat production and productivity during the past 50 years, new approaches are needed to ensure an average gain in productivity of at least 1.6% annually considering the projected yield losses due to climate change of 16% by 2025 and 26% by 2050 (Rosegrant and Agcaoili, 2010).

This is a very challenging task considering the scarcity of water resources, the projected higher frequencies of drought and periods of extreme heat, increased soil salinity in most irrigated areas and the projected increase in prevalence and changes in virulence of major pests and diseases. Genetic resources of wheat, mainly landraces of cultivated wheat, primitive wheat species and wild relatives of wheat (wild wheats, or wheat CWR), will be highly relevant in any approach to overcome these environmental constraints to wheat productivity in the future, as they can potentially provide some of the needed adaptive traits for wheat breeding programs around the world.

Genetic variability within and between populations of a species is essential to enable it to adapt to, and survive in, changing environments through natural selection of the fittest genotypes. This genetic variability is needed for breeding efforts to sustain genetic gains in our crop plants. Use of *ex situ*-conserved wheat genetic resources, particularly landrace varieties, has enabled the broadening of the genetic base of wheat and continuing gains in yield and quality attributes. Further genetic gains in wheat improvement needed to deal with potentially complex and difficult biotic and abiotic stresses will likely require increased use of genetic resources including the wild species (wild relatives) more distantly related to cultivated wheat and belonging to different genepools (Feuillet *et al.*, 2008). This approach is particularly important in the case of wheat because of its fairly narrow genetic base presumably resulting from its evolution from a small number of individuals of the ancestral species involved in the original crosses, and because of the continuing, and apparently increasing, use of limited numbers of recurrent parents in major breeding programs.

Most international and national public and private wheat breeding programs are using germplasm of mainly cultivated species to develop elite breeding lines, but there have been several successful varieties released that were derived from crosses involving wheat wild relative species from primary, secondary and even tertiary genepools (Friebe *et al.*, 1996; Maxted and Kell, 2009). Genetic resources from cultivated forms or wild relative species, have contributed and continue to contribute useful genes for the improvement of wheat (Rajaram, 2000; Mujeeb-Kazi *et al.*, 2008; Maxted *et al.*, 2008). Although wheat is already one of the crops which has so far benefited most from the introgression of genes from wild species (Maxted and Kell, 2009; CIMMYT and ICARDA, 2011), wheat's wild relatives still represent a vast untapped reservoir of genes for further wheat improvement.

There are several reviews which summarize the traits successfully transferred from wild relatives into cultivated wheats (Rajaram, 2000; Lage *et al.*, 2003; Gill *et al.*, 2006; Maxted and Kell, 2009). Traits include resistance/tolerance to major biotic and abiotic stresses and yield and quality improvement. There are only a few breeding programs, however, with a strong dedicated pre-breeding component fully involved in introgressing genes from wheat's wild relatives as in the cases at Kansas State University and CIMMYT. The wheat/rye translocation 1B/1R is the best example of a translocation which has significantly contributed to global wheat production (Rajaram *et al*., 1983; Rajaram, 2000). The development of synthetic hexaploid wheat from crosses between durum wheat (the cultivated form of the ancestral tetraploid species) and *Aegilops tauschii* (D-genome donor to bread wheat, and one of its ancestral species) has allowed the enrichment of wheat's genepool with elite and improved germplasm having novel sources of resistance/tolerance to major biotic and abiotic stresses (Monneveux *et al*., 2000; Mujeeb-Kazi *et al*., 1993, 2008; Gill *et al*., 2006; van Ginkel and Ogbonnaya, 2007; Ogbonnaya *et al*., 2008; Trethowan and van Ginkel, 2009).

These successes call for more concerted efforts in further exploitation of wheat wild relatives to fortify wheat's resistance to major pests and diseases, and to enhance its adaptation to abiotic stresses and its use-efficiency of various inputs. Furthermore there are several insects and diseases and other complex traits of wheat for which no effective sources of resistance/tolerance have yet been found in cultivated forms (e.g. root rot complex, *Septoria*, Karnal bunt), which means that further study of wheat's wild relatives, including more distant species from the tertiary gene pool, is imperative for broadening the genetic base of wheat, and increasing its future productivity.

Although wheat breeders to date have used just a very limited portion of the available genetic resources, largely neglecting wild relatives, there is ample evidence showing that genebanks currently holding stocks are well able to supply needed sources of potentially valuable traits, thus justifying the costs of establishing, expanding and enriching these *ex situ* collections. The polyploid nature of both bread wheat and durum wheat, combined with new developments in cytogenetics and biotechnology opens new opportunities for intensive and efficient pre-breeding activities aiming to introgress useful genes from closely-related, as well as more distant, species into elite germplasm. Substantial and coordinated efforts are needed to conserve the remaining diversity of wheat wild relatives, both *ex situ* in genebanks and *in situ* under natural habitats, to ensure a robust pipeline for their effective use in wheat breeding (Maxted and Kell, 2009; FAO, 2013). The global wheat conservation strategy (CIMMYT, 2007) emphasizes the vital importance of the conservation of the existing diversity of all forms of cultivated wheat and its wild relatives.

This paper highlights the importance of the efforts already invested in the *in situ* and *ex situ* conservation of wheat wild relatives belonging to *Aegilops* and *Triticum* genera. It stresses the need for further and ongoing enrichment of the existing *ex situ* germplasm collections to ensure that the diversity of wheat is systematically and effectively recognized, collected, documented and conserved.

Wheat wild relatives: taxonomy and genepools

Knowledge of taxonomy, phylogenic relationships and intra-genepool relationships among members of the Triticeae is essential for successful introgression of genes from wild and weedy species (wild relatives) into the cultivated species.

Taxonomic treatment and distribution of wheat wild relatives

Wheat (bread wheat, *Triticum aestivum* L. subsp. *aestivum* and durum wheat, *Triticum turgidum* L. subsp. *durum* (Desf.) Husn.) belongs to the grass tribe Triticeae (Poaceae, Pooideae). The Triticeae include some of the most important cultivated cereals and their wild relatives: wheat (*Triticum, Aegilops, Amblyopyrum*), barley (*Hordeum*) and rye (*Secale*), as well as more distantly-related grasses, some useful forages, including *Elymus, Elytrigia, Roegneria, Thinopyrum, Agropyron, Eremopyrum, Dasypyrum, Leymus* (Dewey, 1984).

Triticeae taxonomy has been quite unsettled, and remains so, as evidenced by the extensive lists of synonyms for some genera, particularly *Triticum* and *Aegilops*, also *Agropyron* and *Elymus*. The Triticeae has been revised many times and 26 classification schemes have been proposed for wheat and its relatives since 1917 (Slageren, 1994), with numbers of included genera (in treatments since 1930) ranging from around 20, to almost 40 (http://www.k-state.edu/wgrc/Taxonomy/triticeaetax.html). Currently accepted genera in the Triticeae range from 19-20 (The Plant List: RBG Kew, Missouri Bot. Gardens: http://www.theplantlist.org/), c. 25 (Barkworth and Jacobs, 2011, 2013: http://www.herbarium.usu.edu/treatments/Triticeae.htm), to 30, based on molecular data and genome analysis (Yi *et al*., 2009).

Species numbers in the Triticeae are generally considered to be in the range of 400-500 (see above references) – with 50-60 (possibly up to 70) annuals, the rest perennials.

Linnaeus (1753) treated *Triticum* and *Aegilops* as separate genera and this separation has been subsequently maintained by most taxonomists and researchers, although a few have amalgamated them (together with *Amblyopyrum*) as a single genus, *Triticum,* on the basis of there being essentially no genetic barriers between them (Bowden,1959; Kimber and Feldman, 1987). More recently this group has again been treated as three separate genera: *Aegilops*, *Amblyopyrum, Triticum* (Slageren, 1994). In this paper, in accordance with Slageren (1994), 22 species of *Aegilops*, one *Amblyopyrum* and four *Triticum* species and sub-species are recognized.

Slageren (1994, pp. 81-2) considered that the genus *Amblyopyrum* possessed sufficient unique characters and deserved to be treated as separate from *Aegilops* and *Triticum*. Opinions have differed as to the taxonomic status of this taxon. Depending on whether a "lumping" (broad) or a "splitting" (narrow) taxonomic concept has been applied to wheat's closest wild relatives (the *Aegilops-Amblyopyrum-Triticum* group), this taxon has been variously treated:

– as a species of *Triticum* in a broad concept of the genus, together with all *Aegilops* and *Triticum* species, as *Triticum tripsacoides* (Jaub. and Spach.) Zhuk. (Kimber and Feldman, 1987);

– as a species of *Aegilops*, as *Aegilops mutica* Boiss. (Witcombe, 1983; Kilian *et al*., 2011);

– in a genus of its own, as *Amblyopyrum muticum* (Boiss.) Eig (Love, 1984; Slageren, 1994).

Thus, the monotypic genus *Amblyopyrum* is not universally accepted, although is currently maintained by various genebanks (e.g. GRIN (USDA); Genebank (ICARDA); IPK Gatersleben), if not by some taxonomists.

Seven species of the intergeneric hybrid genus x *Aegilotriticum* (*Aegilops* x *Triticum*) have also been described (Slageren, 1994). Comprehensive information on the taxonomy of wheat can be accessed in the website of the Wheat Genetic Resources Center at Kansas State University, Manhatten, Kansas, USA (www.k-state.edu/wgrc/).

Aegilops and *Amblyopyrum*

The genera *Aegilops* with 22 species and five non-typical varieties, is arranged taxonomically in five sections, based largely on spike morphology and genomic affinities, following Slageren (1994) (table 1). *Amblyopyrum*, a monotypic genus comprising one species (*A. muticum*) with two infraspecific varieties, is closely allied to *Aegilops* (Slageren 1994). *Aegilops* species exhibit various ploidy levels, and comprise 10 diploids, 10 tetraploids and 2 hexaploids, with *Ae. neglecta* and *Ae. Crassa* present in both tetra- and hexa-polyploid forms. *Amblyopyrum muticum* is diploid (table 1). Among *Aegilops*, only the self-incompatible *Ae. speltoides* is an obligate outcrosser, although both *Ae. markgrafii* and *Ae. longissima* are facultatively allogamous, sometimes outcrossing to a significant extent. *Amblyopyrum muticum* is also self-incompatible and obligately outcrossing (Hammer and Matzk, 1993). These outcrossing species require special arrangements by genebanks (e.g. isolation barriers) to conserve their genetic integrity during multiplication and regeneration cycles. The ploidy level, genomic constitution and the distribution of *Aegilops* and *Amblyopyrum* species are shown in table 1.

Although the center of origin of *Aegilops* is thought to be in the Transcaucasia region, the genus is now widely distributed, its natural range extending ranging from the Mediterranean basin (southern Europe, North Africa), to central and eastern Europe, southern Ukraine and the Crimea, West Asia, the Arabian Peninsular, Central Asia and the Caucasus, and east to the Tian Shan and Himalaya mountains in western China and the Indian subcontinent respectively (Slageren, 1994). The centre of diversity of *Aegilops* lies in the Fertile Crescent where Turkey and Syria each have 17 different *Aegilops* species (*Amblyopyrum* is also found in Turkey), Lebanon and Iraq with 15 each, and surrounding countries, Iran, Jordan, Palestine and Israel, Greece and Azerbaijan, have 11-12 each (Slageren, 1994). The diploid species are gene-

Table 1 ■ Information on ploidy level, genomic constitution and geographic distribution of *Aegilops* (species organized by Section) and *Amblyopyrum* species.

Section	Species	Variety	Ploidy level	Genomes*	Distribution
Aegilops L.	*Aegilops biuncialis* Vis.		Allotetraploid	$U^{bi}M^{bi}$ (UM)	Widespread; common (Med. and WA)
	Aegilops geniculata Roth		Allotetraploid	$U^{g}M^{g}$ (MU)	Widespread; common (Med.)
	Aegilops peregrina (Hack. in J. Fraser) Maire and Weiller	var. *peregrina* var. *brachyathera* (Boiss.) Eig	Allotetraploid	$U^{p}S^{p}$ (SU)	Widespread; locally common (WA and NA)
	Aegilops neglecta Req. ex Bertol.		Allotetraploid Allohexapoloid	$U^{n}X^{n}$ (UM) $U^{n}X^{n}N^{n}$ (UMN)	Widespread; abundant (Med. and CAC)
	Aegilops columnaris Zhuk.		Allotetraploid	$U^{co}X^{co}$ (UM)	Limited; rare (Med. and WA)
	Aegilops triuncialis L.	var. *triuncialis* var. *persica* (Boiss.) Eig	Allotetraploid	$U^{t}C^{t}$ (CU and UC)	Widespread; common (Med., WA and E. Europe)
	Aegilops umbellulata Zhuk.		Diploid	U (U)	Limited; rare (Med. and WA)
	Aegilops kotschyi Boiss.		Allotetraploid	$U^{k}S^{k}$ (SU)	Limited (SE-Med., WA and AP)
Comopyrum (Jaub. & Spach) Zhuk.	*Aegilops comosa* Sm. in Sibth. & Sm.	var. *comosa* var. *subventricosa* Boiss.	Diploid	M (M)	Limited; uncommon (mainly Greece, also Turkey, Bulgaria, Cyprus)
	Aegilops uniaristata Vis.		Diploid	N (N)	Limited; rare (Croatia, Adriatic coast, Greece and possibly Turkey)
Cylindropyrum (Jaub. & Spach) Zhuk.	*Aegilops markgrafii* (Greuter) K. Hammer		Diploid	C (C)	Limited to E-Med. and FC
	Aegilops cylindrica Host		Allotetraploid	$C^{c}D^{c}$ (CD)	Widespread; common (Med. Europe, WA and CAC)

Table 1 ■ Information on ploidy level, genomic constitution and geographic distribution of *Aegilops* (species organized by Section) and *Amblyopyrum* species (*continued*).

Section	Species	Variety	Ploidy level	Genomes*	Distribution
Sitopsis (Jaub. & Spach) Zhuk.	*Aegilops bicornis* (Forssk.) Jaub. & Spach	var. *bicornis* var. *anathera* Eig	Diploid	S^b (S^b)	Limited; uncommon (coastal Libya, Egypt, Cyprus, Palestine, Kuwait)
	Aegilops searsii Feldman & Kislev ex Hammer		Diploid	S^s (S^s)	Limited; uncommon (extreme south of FC: Syria, Lebanon, Palestine, Jordan)
	Aegilops longissima Schweinf. & Muschl.		Diploid	S^l (S^l)	Limited; rare (SE Med.: coastal Palestine, Egypt; rare in Jordan)
	Aegilops speltoides Tausch	var. *speltoides* var. *ligustica* (Savign.) Fiori	Diploid	S	Limited; locally common (mainly FC; also SE Balkans)
	Aegilops sharonensis Eig		Diploid	S^{sh} (S^l)	Limited; locally common (Israel/Palestine, Lebanon)
Vertebrata Zhuk. emend. Kihara	*Aegilops juvenalis* (Thell.) Eig		Allohexaploid	$X^jD^jU^j$ (DMU)	Limited; rare (WA and CAC)
	Aegilops tauschii Coss.		Diploid	D (D)	Locally common (North FC and CAC)
	Aegilops vavilovii (Zhuk.) Chennav.		Allohexaploid	$X^{va}S^{va}S^{va}$ (DMS)	Limited; uncommon to rare (FC)
	Aegilops crassa Boiss.		Allotetraploid	$X^{cr}D^{cr1}$ (DM)	Fairly widespread; locally common (FC, WA and CA)
			Allohexaploid	$X^{cr}D^{cr1}D^{cr2}$ (DDM)	
	Aegilops ventricosa Tausch		Allotetraploid	N^vD^v (DN)	Uncommon (S. Europe and NA)
Amblyopyrum (Jaub. and Spach) Eig	*Amblyopyrum muticum* (Boiss.) Eig	var. *muticum* var.*loliaceum* (Jaub. & Spach) Eig	Diploid	T	Limited; uncommon (WA: Turkey, Armenia)

* Genomic formulation proposed by Gill *et al.* 2006; ( ) Genomic formulation adopted by Slageren, 1994.
AP: Arabian Peninsula; CAC: Central Asia and Caucasus; CA: Central Asia; FC: Fertile Crescent; Med.: Around the Mediterranean Basin; NA: North Africa; WA: West Asia.

rally less widespread than the tetraploids, some having extremely restricted distributions; *Aegilops sharonensis*, for example is endemic to just a small part of northern Israel and southern Lebanon (Slageren, 1994). The two hexaploid species also have relatively limited distributions compared to the tetraploids. *Aegilops tauschii* is the only diploid species to have spread mainly eastwards from the *Aegilops* centre of origin into Turkmenistan, Kazakhstan, the mountains of Afghanistan and Pakistan, and parts of western China, perhaps carried along the old Silk Route. Some *Aegilops* species are found sporadically outside their usual areas of distribution and are termed "adventives", while others have become naturalized and widespread far from their native ranges, such as *Ae. cylindrica* in the United States of America (Damania *et al*., 1990, 1993). This study, using compiled information from various genebanks, herbaria and floras, found instances of particular species reportedly occurring well outside their native ranges (as described in Slageren, 1994). Such data can only be explained either by species being adventive or naturalized in those locations, or by errors in identification or provenance records among genebank accessions or herbarium specimens. For example, nine *Aegilops* species were recorded as being collected in France (from the compiled databases information), whereas just five species are actually known to occur there (Slageren, 1994). *Aegilops* and *Amblyopyrum* species generally occur in open habitats, commonly in disturbed areas, on field edges, roadsides, rangelands, orchards or olives groves (Hedge *et al.,* 2002).

Wild *Triticum*

There are four species of wild *Triticum*, all self-pollinating annuals*:*

– *Triticum monococcum* subsp. *aegilopoides* (Link) Thell. (synonyms: *T. monococcum* subsp. *boeoticum, T. boeoticum, T. monococcum* var. *boeoticum, T. aegilopoides, T. thaoudar*) with A^b genome (2n=14);

– *Triticum urartu* Tumanian ex Gandilyan (synonym: *T. monococcum var. urartu*) with A^u genome (2n=14);

– *Triticum turgidum* subsp. *dicoccoides* (Korn. ex Asch. and Graebn.) Thell. (synonyms: *T. dicoccoides, T. turgidum*) with A^u and B genomes (2n=28);

– *Triticum timopheevii* subsp. *armeniacum* (Jakubz.) Slageren (synonyms: *T. turgidum* var. *timopheevii, T. timopheevii, T. araraticum, T. turgidum var. tumanianii, T. dicoccoides var. nudiglumis*) with A and G genomes (2n=28).

These wild *Triticum* species are mainly found within the Fertile Crescent center of diversity, extending from southern Jordan, Lebanon, Israel, Palestine, Syria, into southern Turkey, northern Iraq and western Iran. *Triticum turgidum* subsp. *dicoccoides* is found growing together with *T. urartu* and *T. monococcum* subsp. *aegilopoides* in some areas of Jordan, Lebanon and Syria. Three species also occur in areas to the north of the Fertile Crescent: a small population of

Triticum monococcum subsp. *aegilopoides* has been collected from eastern Greece; *Triticum urartu* is also found in the Caucasus region, particularly Armenia; *Triticum timopheevii* subsp. *armeniacum* is mainly found in the border areas between Iran, Armenia, Azerbaijan, Georgia and Turkey. Kimber and Feldman (1987) reported the occurrence of *T. monococcum* subsp. *aegilopoides*, *T. urartu* and *T. timopheevii* subsp. *armeniacum* in the north-east Mediterranean and West Asian regions, from southern Yugoslavia to southern USSR (southern Caucasus region). In Jordan, Lebanon, Syria and southern Turkey, wild *Triticum* species are mainly found in basaltic soils along field edges and roadsides, or protected from grazing among spiny bushes.

Genus x *Aegilotriticum* P. Fourn.

There are a number of natural and artificial hybrids (amphidiploids) between *Aegilops* and *Triticum* species, some with potential value in breeding (Kimber and Sears, 1987). Slageren (1994) described seven such hybrids, x *Aegilotriticum* species:

– x *Aegilotriticum erebunii* (Gandilyan) van Slageren (*Aegilops tauschii* x *Triticum urartu*);

– x *Aegilotriticum grenieri* (K. Richt.) P. Fourn. (*Aegilops neglecta* x *Triticum aestivum*);

– x *Aegilotriticum langeanum* (Amo) van Slageren (*Aegilops triuncialis* x *Triticum aestivum*);

– x *Aegilotriticum rodetii* (Trab.) van Slageren (*Aegilops ventricosa* x *Triticum turgidum* ssp. *durum*);

– x *Aegilotriticum sancti-andreae* (Degen) Soó (*Aegilops cylindrica* x *Triticum aestivum*);

– x *Aegilotriticum speltaeforme* (Jord.) van Slageren [(*Aegilops geniculata* x *Triticum aestivum*) x *Triticum aestivum*];

– x *Aegilotriticum triticoides* (Req. ex Bertol.) van Slageren (*Aegilops geniculata* x *Triticum aestivum*).

Phylogenic relationships and evolution of wheat

Wheat is a good example of the evolutionary processes of allopolyploid speciation, adaptation and domestication in plants. The evolution of primitive wheats and cultivated bread and durum wheats depended mainly on hybridization between species (polyploidization) and on the accumulation of mutations. The phylogenic relationships among *Aegilops* and *Triticum* species have been investigated using morphological, genetic, ecogeographic and palaeobotanical studies. Cytogenetics and molecular techniques have contributed significantly in further elucidating these relationships (Gill *et al*., 2006). Molecular techniques using both nuclear and cytoplasmic DNA have been highly instrumental in defining the origin of the cytoplasm and also the evolutionary pathways of various species.

Chloroplast evidence has shown that *Ae. speltoides* is the donor of two plasmons forming all allopolypoid wheat species and that there are three variants within the diploid A genome *Triticum* (Goncharov *et al*., 2008). Detailed information on cytogenetics and evolution of wheat is given in the recent reviews by Gill *et al.* (2006) and Peng *et al.* (2011). Estimates of phylogenic relationships among various diploid species of *Aegilops* and *Triticum*, and tetraploid and hexaploid *Aegilops* and *Triticum* cultivated and wild species, in terms of both cytoplasmic and nuclear DNA origins, has led to the following proposal for the evolution of cultivated wheats (Gill *et al*., 2006).

The progenitor of the B genome (close to the S genome of *Aegilops speltoides*) crossed with wild einkorn containing the A genome (*Triticum urartu*) to produce wild emmer (*Triticum turgidum* subsp. *dicoccoides*, BBAA) around 350,000 years ago, and the domestication of cultivated emmer (*Triticum turgidum* subsp. *dicoccon*; BBAA) occurred around 10,000 years before the present time (BP). *Triticum turgidum* subsp. *dicoccon* crossed naturally with *Aegilops tauschii*, donor of the D genome, most likely the form of *Ae. tauschii*, sometimes referred to as subsp. (or var.) *strangulata,* from Transcaucasia and regions south-west of the Caspian Sea, to produce spelt wheat (*Triticum aestivum* subsp. *spelta*; BBAADD) around 9,000 BP (Dvorak *et al*., 1998; Wang *et al*., 2013). The free-threshing grain wheats, tetraploid durum wheat (*T. turgidum* subsp. *durum*, BBAA) and hexaploid bread wheat (*T. aestivum* subsp. *aestivum,* BBAADD) were later selected (by early farmers) and their cultivation extended outwards from the Fertile Crescent to other regions (Zohary and Hopf, 2000; Ozkan *et al*., 2002). Several primitive tetraploid (BBAA) and hexaploid (BBAADD) wheat forms differing by a few major genes were also domesticated and some are still cultivated in very limited areas (MacKey, 1966). Other cultivated *Triticum* species, einkorn (*Triticum monococcum* subsp. *monococcum*) and *T. timopheevii* subsp. *timopheevii*, derive from their wild progenitors, *T. monococcum* subsp. *aegilopoides* and *T. timopheevii* subsp. *armeniacum* respectively, the latter considered to be derived from a cross between *T. urartu* and B-genome progenitor (*Aegilops speltoides* with different plasmon). The primitive wheat *Triticum zhukovskyi* is derived from a cross between the two primitive wheats *T. timopheevii* subsp. *timopheevii* and *T. monococcum* subsp. *monococcum* (Gill *et al*., 2006).

A recent study using genome assemblies of bread wheat and five of its diploid wild relatives has clarified the evolutionary relatedness and divergence times, and revealed that A and B genomes diverged from a common ancestor ~7 million years ago and that these genomes gave rise to the D genome 1 to 2 million years later (Marcussen *et al*., 2014).

Wheat and barley were among the first domesticated crops, most likely being first domesticated in different locations within the Fertile Crescent (Brown *et al*., 2008; Eckardt, 2010; Peng *et al*., 2011), and this has marked the subsequent development and radiation of human civilizations with the transition to agriculture coupled with a more sedentary existence. There are also important secondary centers of diversity (high landrace diversity) for bread wheat in China and several European countries (Italy, Greece), and for durum wheat in Ethiopia and North African countries (Morocco, Algeria, Tunisia).

Wheat genepools

Crop plant genetic resources can be divided into a number of different groups (Frankel, 1977; FAO, 1983) as follows:

– elite breeding germplasm having useful traits;

– modern varieties, still being cultivated and often used as recurrent parents in new crosses;

– obsolete cultivars, developed by breeders and replaced by new cultivars;

– landraces, local populations that have developed their distinctive traits within farming systems;

– wild relatives, species belonging to the same tribe as the cultivated species, commonly the same genus, thus closely-enough related to enable the transfer of their genes into cultivated crop species;

– primitive wheat species which are the earliest cultivated forms having the same genomes as commonly cultivated species such as, eikorn, emmer and spelt wheats;

– genetic and cytogenetic stocks, including mutants, differentials and aneuploids, and possibly TILLING and molecular mapping populations.

Zohary and Feldman (1962) and Kimber and Feldman (1987) grouped *Aegilops* and *Triticum* species into three clusters based on their pivotal genomes (A, D, and U). Plant genetic resources can also be classified using the genepool concept (Harlan and De Wet, 1971) or, where the gene pool or inter-crossing information is unavailable, using the taxon concept (Maxted *et al*., 2006) in which the grouping of species into three genepools according to their phylogenetic closeness is used as a proxy for the ease of transfering their useful genes into cultivated species.

Harlan and de Wet (1971) proposed classifying each crop and its related species by gene pools rather than by formal taxonomy[1]:

– primary gene pool (GP-1): Members of this gene pool are probably in the same "species" (in conventional biological usage) and can inter-mate freely.

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[1] Source: http://en.wikipedia.org/wiki/Gene_pool#cite_note-Harlan.26DeWet1971-1.

Harlan and de Wet wrote, “Among forms of this gene pool, crossing is easy; hybrids are generally fertile with good chromosome pairing; gene segregation is approximately normal and gene transfer is generally easy”. They also advised subdividing each crop gene pool in two:

- subspecies A (GP 1A): Cultivated races,
- subspecies B (GP 1B): Spontaneous races (wild or weedy);

– secondary gene pool (GP-2): Members of this pool are probably normally classified as different species than the crop species under consideration (the primary gene pool). However, these species are closely related and can cross and produce at least some fertile hybrids. As would be expected by members of different species, there are some reproductive barriers between members of the primary and secondary gene pools:

- hybrids may be weak,
- hybrids may be partially sterile,
- chromosomes may pair poorly or not at all,
- recovery of desired phenotypes may be difficult in subsequent generations,
- however, “The gene pool is available to be utilized, however, if the plant breeder or geneticist is willing to put out the effort required”;

– tertiary gene pool (GP-3): Members of this gene pool are more distantly related to the members of the primary gene pool. The primary and tertiary gene pools can be intermated, but gene transfer between them is impossible without the use of «rather extreme or radical measures» such as:

- embryo rescue (or embryo culture, a form of plant organ culture),
- induced polyploidy (chromosome doubling),
- bridging crosses (e.g., with members of the secondary gene pool).

Opinions differ slightly as to the make-up (included taxa) of the three wheat genepools, particularly the secondary and tertiary genepools (Mujeeb-Kazi and Rajaram, 2002). Recent determination of the gene pools for bread wheat (*Triticum aestivum* subsp. *aestivum*) has been based on genomic composition and recombination (Gill *et al*., 2007) so that the primary genepool (GP-1) comprises all ABD-genome-containing land races and subspecies, the AB-genome containing tetraploid durum wheat landraces and subspecies, and the D-genome donor diploid *Ae. tauschii* (the D-genome of *Ae tauschii* once introduced into bread wheat, through direct crosses or via synthetic wheats, freely recombines with the D-genome of bread wheat); the secondary genepool (GP-2) comprises wild *Triticum* and *Aegilops* species (mostly polyploids) that share one genome closely related to the ABD genomes of cultivated wheats, including the wild and cultivated diploid A-genome species, the wild and cultivated AAGG genome species and D-genome carrier polyploid *Aegilops* species (although these species share a genome with polyploid wheat, the shared genome is modified, for example, 4A chromosome of polyploid wheat is highly rearranged compared to A-genome of diploid wheat); the tertiary genepool (GP-3) comprises the more distantly-related species of *Aegilops* and species in other Triticeae genera that have non-homologous genomes and for which gene introgression requires radical techniques.

Species in the primary genepool of bread and durum wheat

– Cultivated species: *Triticum aestivum* L. subsp. *aestivum* (common or bread wheat) and *Triticum turgidum* subsp. *durum* (Desf.) Husn. (macaroni or durum wheat).

– Primitive hexaploid wheats: subspecies of *Triticum aestivum* L.: subsp. *compactum* (Host) MacKey (club wheat); subsp. *macha* (Dekapr. and Menabde) MacKey; subsp. *spelta* (L) Thell. (large spelt or dinkel wheat); subsp. *sphaerococcum* (Percival) MacKey (Indian dwarf wheat) (ABD genomes).

– Primitive (and wild) tetraploid wheats: subspecies of *Triticum turgidum* L.:subsp. *turgidum* (pollard wheat); subsp. *carthlicum* (Nevski) A. Love & D. Love (Persian wheat); subsp. *dicoccum* (Schrank) Thell. (emmer wheat); subsp. *paleocolchicum* (Menabde) A. Love & D. Love; subsp. *polonicum* (L.) Thell. (Polish wheat); subsp. *turanicum* (Jakubz.) A. Love & D. Love (Khorassan wheat); subsp. *dicoccoides* (Körn. ex Asch. & Graebn.) Thell. (wild emmer) (AB genomes) *Aegilops tauschii* Coss., included here for bread wheat (D-genome).

Species in the secondary genepool of bread and durum wheat

The species in this pool share at least one genome in common with polyploid wheat that may recombine but not as efficiently as the genomes of the species of the primary gene pool. The polyploid species or man-made amphiploids that contain a second and a different genome than A, B or D genomes also are listed as a part of the tertiary gene pool.

– Cultivated species: *Triticum monococcum* L. subsp. *monococcum* (einkorn or small spelt wheat); *Triticum timopheevii* (Zhuk.) Zhuk. subsp. *timopheevii*.

– Wild species: *Triticum monococcum* L. subsp. *aegilopoides* (Link) Thell.; *Triticum urartu* Tumanian ex Gandilyan (A-genome); *Triticum timopheevii* (Zhuk.) Zhuk. subsp. *armeniacum* (Jakubz.) Slageren (A-genome).

– Primitive species: *Triticum zhukovskyi* Menabde & Ericz (AG genomes).

– Species belonging to section *Tricosecale* including the subtriticale (*T. semisecale* Mac Key with AARR genomes) and hexaploid (BBAARR genomes) and octaploid (BBAADDRR genomes) triticales.

– The D-genome cluster of *Aegilops* species: *Ae. cylindrica* (CD); *Ae crassa* (DM; DDM); *Ae ventricosa* (ND), *Ae juvenalis* (DMU), and *Ae vavilovi* (DMS).

– *Aegilops speltoides* in the *Aegilops* sect. Sitopsis whose S-genome is closely related to B and G genomes of polyploid wheats.

Species in the tertiary genepool of bread and durum wheat

This genepool contains a large number of species and includes the remaining 15 *Aegilops* species and all other Triticeae species that are not included in GP1and GP2, in genera such as *Amblyopyrum, Secale*, *Dasypyrum*, *Thinopyrum*, *Agropyron, Eremopyrum, Elymus*, *Elytrigia*, *Hordeum* and *Leymus*. The transfer of genes from these species to cultivated wheat requires sophisticated techniques, including induced translocations and homoeologous recombination (Qi *et al*., 2007).

Genetic transformation however, has now enabled us to go beyond the limits of the genepool concept by allowing the transfer of genes between very distantly related, or even quite unrelated, species, including micro-organisms. Natural gene flow among various sympatric species within genepools is known, and artificial interspecific and intergeneric crosses are continuously being investigated by researchers involved in pre-breeding and cytogenetic studies. Thus the whole Triticeae tribe can now be considered a source of potentially useful genetic resources for the improvement of wheat and other major cultivated cereals (von Bothmer *et al.,* 1992).

Conservation of *Aegilops* and wild *Triticum* genetic resources

Vavilov was among the first scientists to recognize the significance of crop wild relatives (CWR) in breeding and he collected many of these species during his wide-ranging expeditions. An FAO technical meeting organized in 1961 recognized the need for concerted efforts to conserve the gene-centers and the wild relatives of crops. Subsequently, the Convention on Biological Diversity (CBD, 1993) and the International Treaty on Plant Genetic Resources for Food and Agriculture (FAO-ITPGRFA, 2001), both international binding agreements, stressed the importance of conserving CWR, and recommended the implementation of both *ex situ* and *in situ* approaches for the conservation of biodiversity (Meilleur and Hodgkin, 2004). More recently, The European Strategy for Plant Conservation (Planta Europa, 2008), the Global Strategy for CWR Conservation and Use (Heywood *et al*., 2008), the CBD Strategic Plan (CBD, 2010a), the FAO Global Plan of Action for the Conservation and Sustainable Utilization of PGRFA (FAO, 2011) have also stressed the importance of *in situ* conservation of crop wild relatives and recommended the establishment of CWR *in situ* genetic reserves (protected areas where CWR genetic conservation is given priority). In addition, they recommended that further gap analysis studies be undertaken in order to prioritize diversity gaps to be filled with *ex situ* CWR collections.

Serious efforts to collect and conserve *ex situ* a range of CWR started in the 1970s, and although the push for *in situ* conservation of CWR began later, in the mid-1990s (Maxted *et al*., 1997), only few established reserves are specifically targeting the *in situ* conservation of wheat wild relatives such as Erebuni reserve in Armenia and Ceylanpinar State Farm located in south-eastern Turkey.

Maxted and Kell (2009) proposed the establishment of a worldwide network of *in situ* genetic reserves independent of national political borders, focussing on worldwide priority crop genepools, with complementary *ex situ* storage of genetically representative population samples. Recently the FAO Commission on Genetic Resources for Food and Agriculture (CGRFA) held a Technical Workshop to debate the establishment of a global network *in situ* conservation (FAO, 2013) and recommended the establishment of a global network to provide the necessary platform to raise awareness of the social and economic value of *in situ* conservation in partnerships with national- and regional-level activities.

CWR conservation and use provides an excellent means of simultaneously addressing the dual Millennium Development Goals of biodiversity conservation and poverty alleviation. Wheat wild relatives have been given high priority among the 1,392 most important wild species of relevance to global food security, and to date they remain among the most widely used in breeding (Vincent *et al*., 2013). The updated Global Plan of Action for the Conservation and Sustainable Utilization of Plant Genetic Resources for Food and Agriculture (GPA-PGRFA), derived from the FAO second report on the State of the World of Plant Genetic Resources (FAO, 2012) recommended substantial efforts be made to conserve crop wild relatives both *ex situ* and *in situ* and to promote their use.

Both *ex situ* and *in situ* conservation efforts should extend across the whole ecogeographic range of the species targeted to enable identification of areas of high species diversity and those with potential for harbouring populations with valuable adaptive or other sought-after traits. Attention should also be given to endemic species, uncommon species, those with only few accessions present in genebanks holdings, and species which are threatened by loss of their natural habitats. Conservation efforts will therefore require in-depth knowledge of the natural distribution of species, genetic diversity among different populations, and the causal factors of degradation of their natural habitats.

Geographic distribution of *Aegilops*, *Amblyopyrum* and wild *Triticum* species

Combined information from floras, herbaria, botanical surveys, and genebank databases has been used to study the ecogeographic distribution of species. Geo-referenced collection site data taken from genebank accessions and herbarium specimens was used here to determine the geographic distribution of *Aegilops* and wild *Triticum* species using DIVA-GIS 7.5.0. Clearly spurious data was eliminated from the database, as was data from naturalized or cultivated specimens. The results of this analysis confirms that the genus *Aegilops* is a Mediterranean–Western Asiatic element as previously described (Slageren, 1994), and that wild *Triticum* occurs mainly within the Fertile Crescent. The range of distribution of wheat wild relatives extends from the Canary Islands to China, and from southern Russia to northern Pakistan and India (Slageren, 1994). However, the major centres of diversity for *Aegilops* and wild *Triticum* occur in the countries of the Fertile Crescent (Iraq, Iran, Jordan, Lebanon, Palestine, Syria, Turkey), South Eastern Europe (Bulgaria, Croatia, Greece), Caucasus and Central Asia (Armenia, Azerbaijan, Georgia, Turkmenistan, Uzbekistan). The differences in species distributions reported here, with those described by Slageren (1994), may be explained by unwitting inclusion of poor quality data in the analysis, most likely deriving from cases of mis-identification and incorrect collection site information for some specimens/accessions.

Distribution of species in Section Aegilops L. (figures 1 to 3)

– ***Aegilops biuncialis***: a widespread geographic distribution extending from Morocco and Spain to Central Asia, with the highest concentrations in south-eastern Europe, the Fertile Crescent and the Caucasus region. There were no records of this species from Algeria, Egypt, Georgia, Israel or Palestine in the database compiled during this study, although it has previously been collected, very rarely, in Algeria, Georgia and Palestine (Slageren, 1994).

– ***Aegilops columnaris***: occurs in the countries of the Fertile Crescent except Palestine and Israel, Armenia and Azerbaijan in the Caucasus; records from Central Asia (Turkmenistan) are most likely incorrect.

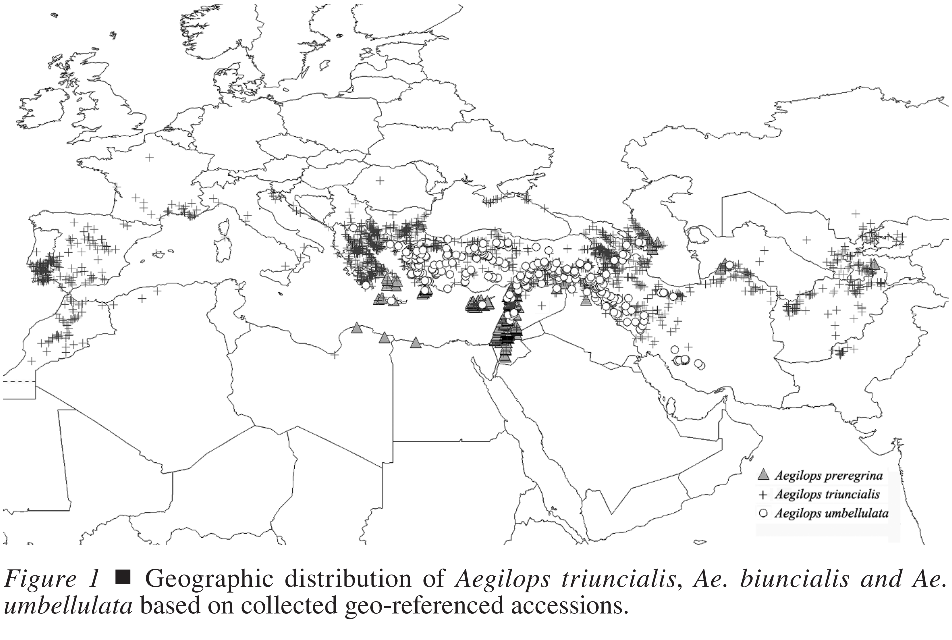

Figure 1 ■ Geographic distribution of *Aegilops triuncialis*, *Ae. biuncialis and Ae. umbellulata* based on collected geo-referenced accessions.

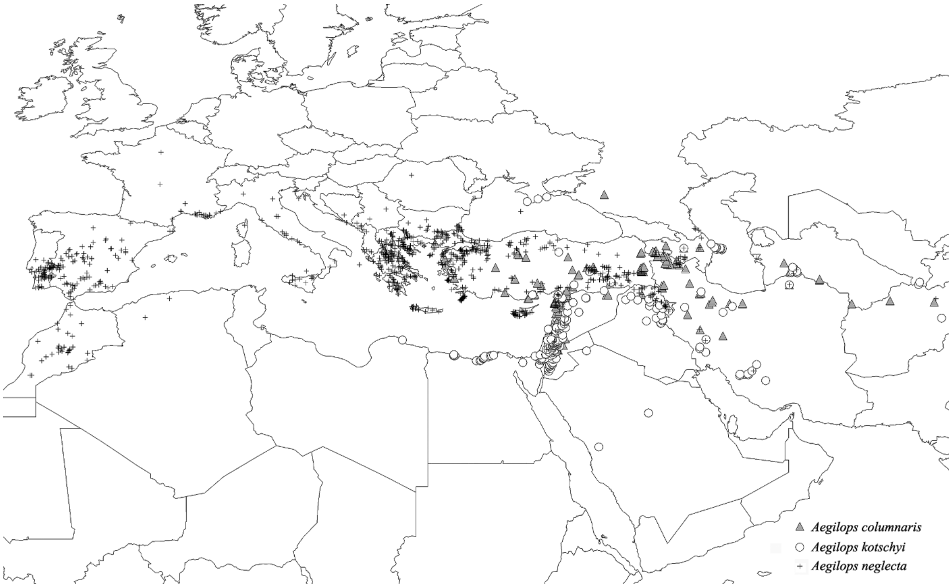

Figure 2 ■ Geographic distribution of *Aegilops columnaris*, *Ae. kotschyi* and *Ae. neglecta* based on collected geo-referenced accessions.

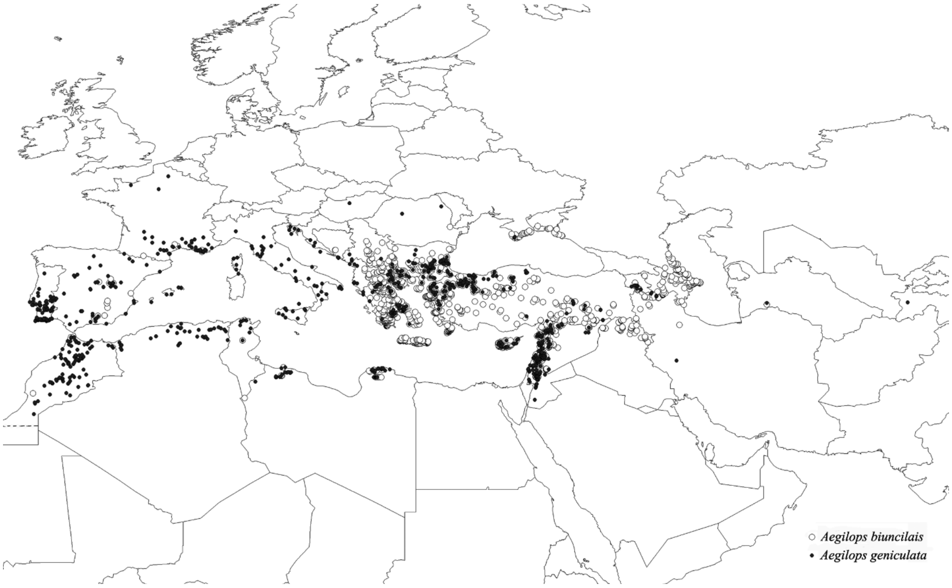

Figure 3 ■ Geographic distribution of *Aegilops biuncialis* and *Ae. geniculata* based on collected geo-referenced accessions.

– ***Aegilops geniculata***: an extended distribution around the Mediterranean Basin, central Europe, and the Fertile Crescent. There were no records of this species from Azerbaijan, Egypt or Georgia, although it has been found, very rarely, in all three (Slageren, 1994).

– ***Aegilops kotschyi***: occurs mainly in the driest areas of the Fertile Crescent, with some collections from Egypt, Saudi Arabia, Turkmenistan and Uzbekistan.

– ***Aegilops neglecta***: widely distributed from Morocco and southern Europe to the Fertile Crescent, Caucasus and Central Asia.

– ***Aegilops peregrina***: occurs mainly in the Fertile Crescent, Greece, Cyprus and Central Asia but is rare in Caucasus.

– ***Aegilops triuncialis***: the most common and widely distributed species, occurring in most countries around the Mediterranean Basin (except Egypt, Libya, Tunisia), southern and eastern Europe, the Fertile Crescent, Caucasus and Central Asia. No records for this species were seen for Egypt, Israel and Palestine, despite it being reported from Palestine (Slageren, 1994).

– ***Aegilops umbellulata***: confined largely to the Fertile Crescent and southern Caucasus regions, although not recorded in Jordan, Israel or Georgia.

Distribution of species in Section Comopyrum (Jaub. & Spach) Zhuk. (figure 4)

– ***Aegilops comosa***: mainly found in Greece and western Turkey, also Cyprus.

– ***Aegilops uniaristata***: mainly found in Greece; the reports from Cyprus, Turkmenistan, Iran and central Turkey are probably cases of misidentification. Slageren (1994) recorded it from coastal Croatia, Greece, Albania and Italy with 1-2 old records, but no recent collections, from western Turkey.

Figure 4 ■ Geographic distribution of *Aegilops comosa* and *Ae. uniaristata* based on collected geo-referenced accessions.

Distribution of species in Section Cylindropyrum (Jaub. & Spach) Zhuk. (figure 5)

– ***Aegilops markgrafii***: occurs mainly in Greece (including islands) and Turkey; sporadic in the Fertile Crescent. Its distribution is similar to that of some species in the Section Sitopsis (e.g. *Ae. speltoides*).

– ***Aegilops cylindrica***: widely distributed from western Europe to southern Russia, Caucasus and Central Asia, with a high concentration in Turkey and northern parts of the Fertile Crescent; almost absent from Greece (inexplicably?) (Slageren, 1994). This species is naturalized in parts of China and the United States of America.

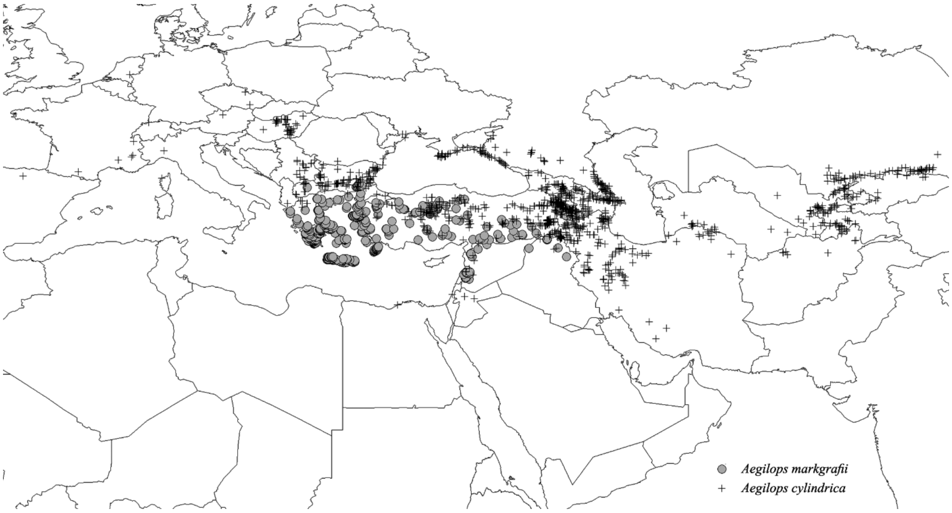

Figure 5 ■ Geographic distribution of *Aegilops markgrafii* and *Ae. cylindrica* based on collected geo-referenced accessions.

Distribution of species in Section Sitopsis (Jaub. and Spach) Zhuk. (figure 6)

This includes some species which have good tolerance to salinity.

– ***Aegilops bicornis***: very limited distribution in some coastal saline areas of Cyprus, southern Jordan, northern Egypt and north-eastern Syria. Records of this species occurring in the extreme north-east of Iran, in data used for this study, are probably incorrect.

– ***Aegilops longissima***: restricted to small area in Israel, Jordan, Palestine and Syria; records from Turkey, Iran and Afghanistan are probably incorrect.

– ***Aegilops searsii***: very limited distribution in Jordan, Lebanon and Syria.

– ***Aegilops sharonensis***: restricted to a small region in northern Israel and southern Lebanon; records from Armenia and Turkey shown on map below are no doubt incorrect.

– ***Aegilops speltoides***: widely distributed across the entire Fertile Crescent; scattered in northern Turkey and eastern Greece.

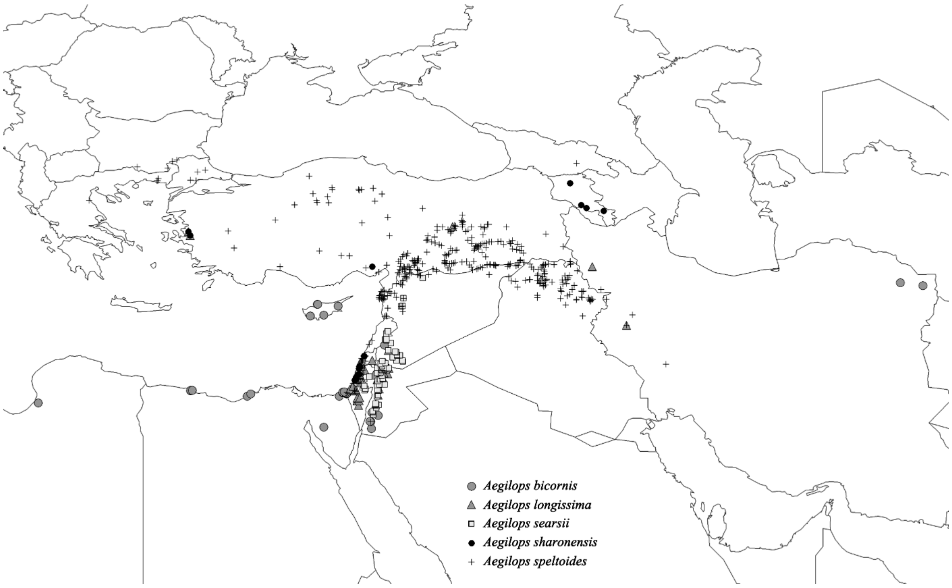

Figure 6 ■ Geographic distribution of *Aegilops* species from the Section Sitopsis based on collected geo-referenced accessions.

Distribution of species in Section Vertebrata Zhuk. emend. Kihara (figure 7)

This section includes species found growing under extreme drought and heat conditions.

– ***Aegilops crassa***: distributed along the Fertile Crescent, also found in Armenia, Central Asia and Afghanistan, mainly in dry areas. The records from Egypt should be checked as this species is sometimes confused with *Ae. ventricosa*.

– ***Aegilops juvenalis***: scattered distribution, mainly in northern Iraq, Syria and Central Asia (Turkmenistan, Uzbekistan), occasionally in Iran and Turkey, although this species was previously considered absent from Iran and adventive in Turkey (Slageren 1994).

– ***Aegilops tauschii***: concentrated in the Caucasus, and to the west and south of the Caspian Sea, but also occasionally found in the dry areas of Syria, even Afghanistan, Pakistan and India. Reports of *Ae. tauschii* from Germany, China and Japan probably refer to adventive plants, possibly locally naturalized, or introduced breeding material.

– ***Aegilops vavilovii***: found mainly in the driest parts of the western arc of the Fertile Crescent. The records from Central Asia need to be re-checked.

– ***Aegilops vavilovii***: found mainly in the driest parts of the western arc of the Fertile Crescent. Records from Armenia, Central Asia and Afghanistan could well be actually *Ae. crassa* or *Ae. juvenalis*, as both are sometimes mistaken for *Ae. vavilovii*.

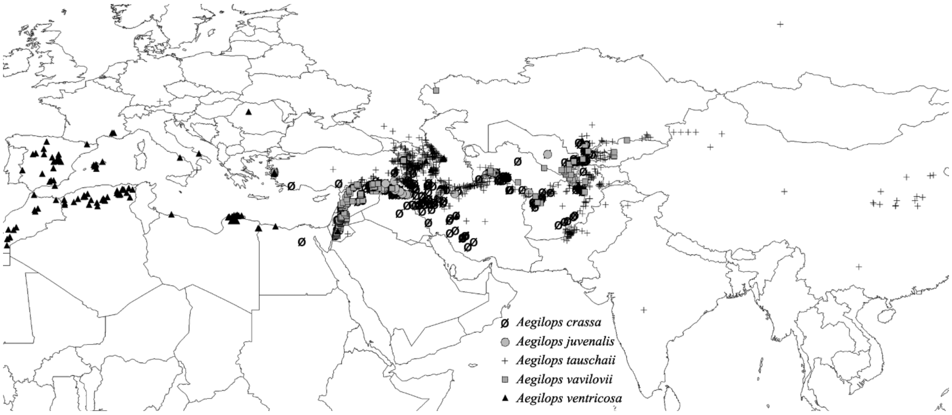

Figure 7 ■ Geographic distribution of *Aegilops crassa*, *Ae. juvenalis*, *Ae. tauschii*, *Ae. vavilovii* and *Ae. ventricosa* based on collected geo-referenced accessions.

– ***Aegilops ventricosa***: occurs mainly in dry areas of North Africa and southern Europe. The few records reported from Central Asia and the Fertile Crescent should be re-checked as this typically western Mediterranean species can be confused with *Ae. crassa*.

Distribution of Amblyopyrum species

GENESYS (https://www.genesys-pgr.org/welcome) as a total of 207 accessions (not unique), 51 of them listed as *Aegilops mutica*, 15 as *Triticum muticum* (15) and 74 as *Amblyopyrum muticum* (74), only 50 have coordinates. ICARDA conserves 32 accessions, 10 of them issued from collecting missions and 22 acquired from USDA. Most of the accessions are collected from Turkey (figure 8).

Figure 8 ■ Geographic distribution of *Amblyopyrum muticum* species based on collected geo-referenced accessions

Distribution of wild Triticum species (figure 9)

Wild *Triticum* species are mainly found within the Fertile Crescent (the arc linking south Jordan, through Palestine, Israel, Lebanon, Syria, southern Turkey to western Iran and northern Iraq).

– ***Triticum monococcum* subsp. *aegilopoides***: distributed across eastern Europe, Armenia, Azerbaijan, Iran and Turkey, extending into Lebanon and Syria. Reported collections from Morocco, far beyond its natural geographic distribution, require further investigation.

– ***Triticum turgidum* subsp. *dicoccoides***: occurs mainly in southern Syria, northern and southern Jordan, Israel, Palestine, southern Turkey; also Armenia and Iraq. This species may also occur in Iran (GRIN Taxonomy, USDA).

– ***Triticum timopheevii* subsp. *armeniacum***: occurs mainly in Armenia, Azerbaijan, northern Iraq, western Iran and eastern Turkey. Records from Lebanon and western Turkey need further investigation as there could be a possible confusion with *Triticum turgidum* subsp. *dicoccoides.*

– ***Triticum urartu***: occurs mainly in the Fertile Crescent, and northwards into Armenia. Records from Tunisia, far from its native range, require further investigation.

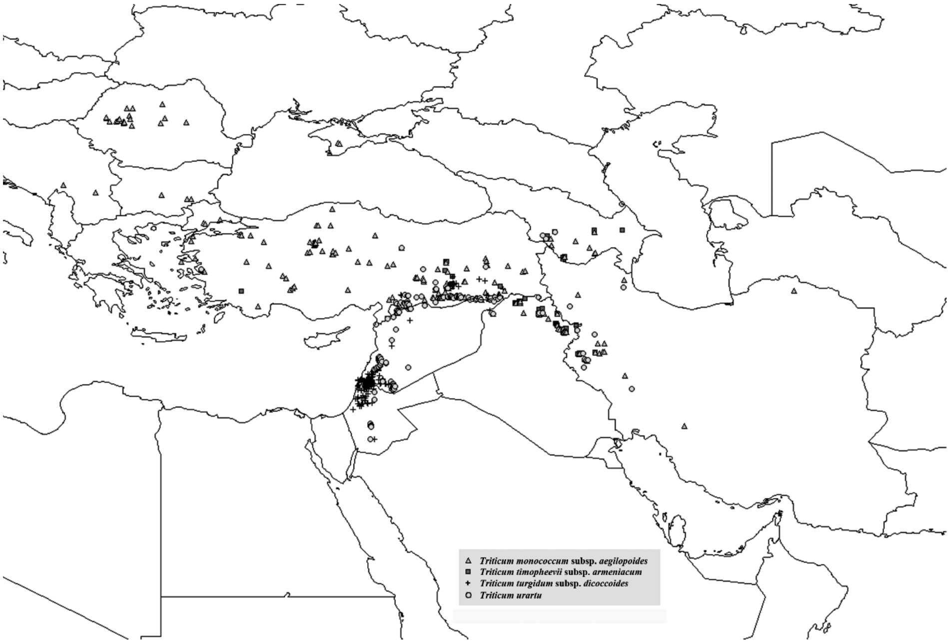

Figure 9 ■ Geographic distribution of wild *Triticum* species based on collected geo-referenced accessions.

Status of *ex situ* conservation of *Aegilops* and wild *Triticum*

Since the 1970s many national, regional and international genebanks have been established. The FAO Commission on Genetic Resources for Food and Agriculture (CGRFA) in its Second Report on the State of the World Plant Genetic Resources for Food and Agriculture (2010) reported more than 1,750 individual genebanks holding more than 7.4 million seed accessions, approximately 45% of which is held by genebanks in just seven countries (Australia, China, India, France, Germany, Russia, United States of America) and 12% by the genebanks of the CGIAR Centers (Africa Rice, CIAT, CIMMYT, CIP, ICARDA, ICRISAT, IITA, ILRI, IRRI Biodiversity International and ICRAF) (FAO, 2010). The Svalbard Global Seed Vault (http://www.nordgen.org/sgsv/), a global initiative started in 2008 by the Norwegian government to ensure long-term storage and back-up as "black boxes" of crop diversity, already holds more than 774,600 accessions. The Global Crop Diversity Trust (GCDT) established in 2004 to support *ex situ* conservation, in collaboration with CGIAR centers and other partners, has developed regional and crop conservation strategies, and in 2011 launched an important project targeting the collection and conservation of crop wild relatives and their use in pre-breeding (GCDT, 2011).

Species belonging to the Triticeae (tribe of cereal grasses and their wild relatives) make up the largest proportion of overall genebank holdings (Genesys, 2012; Knupffer, 2009; WIEWS, 2007). A comprehensive database containing information on 1,284,000 conserved accessions (c. 300 species in 35 genera) of Triticeae taxa (*Triticum, Hordeum,* × *Triticosecale, Aegilops, Amblyopyrum, Secale, Elymus, Agropyron*, etc.) has been compiled using data from diverse sources, including 295 genebanks from 83 countries (Knupffer, 2009). It contains 31,401 accessions of *Aegilops* and 17,575 accessions of the four wild *Triticum* species, from 61 and 58 genebanks respectively. The World Information and Early Warning System (WIEWS) database compiled by FAO (FAO, 2007) includes 25,242 *Aegilops* and 6015 wild *Triticum* accessions. In the "Crop Strategy for Wheat", conducted in 2007 by the GCDT, CGIAR centers and other partners reported around 750,000 wheat accessions held in over 80 genebanks, of which 4% were wild relatives, although no detailed information on *Aegilops* and wild *Triticum* was included (http://www.croptrust.org/documents/cropstrategies/WheatStrategy.pdf).

Sources of information

ICARDA holds a global database of *Aegilops* and wild *Triticum* accessions and is fully involved with other partners in the recent efforts to develop a reliable wild wheat database. The ICARDA global database prepared for this wheat wild relatives conservation strategy contains a total of 25,681 accessions, made up of 22,630 *Aegilops* and 3,051 wild *Triticum* accessions, of which 18% and 50% respectively, are currently held by the ICARDA genebank. The updated global database is based largely on the previous Global Database of wheat wild relatives (ICARDA, Syria), with additional information from GENESYS and other sources such as Kansas State University Wheat Genetics Resource Center and Kyoto University.

GENESYS (https://www.genesys-pgr.org) is the global genetic resources information portal developed by the GCDT, Bioversity International and other partners, comprising aggregated data from the System-wide Information Network for Genetic Resources (SINGER), now defunct or delisted, the European Plant Genetic Resources Internet Search Catalogue (EURISCO, http://eurisco.ecpgr.org/index.php), and the US National Plant Germplasm System (Germplasm Resources Information Network – http://www.ars-grin.gov/cgi-bin/npgs/html/index.pl). GENESYS contains 2,773,082 accession records including 404,322 wheat (cultivated *Triticum*), 16,409 *Aegilops*, and 16,005 wild *Triticum*. Information from collections compiled by Maxted *et al.* (2008) and from the holdings of the Wheat Genetics Resource Center (WGRC) at Kansas State University (provided by Dr. Bikram Gill) were also used in the compilation of the global wild wheats database for this study. Accessions were assigned geo-reference coordinates based on available site information using online gazetteers. A summary of *Aegilops* and wild *Triticum* accession data used in the preparation of the global wild wheats database is presented in table 2.

Table 2 ■ Summary of the total, geo-referenced and unique accessions of *Aegilops* and wild *Triticum* accessions included in different databases.

Source of data	**Total Wheat**	***Aegilops***			**Wild *Triticum***		
		Total	**Georeferenced**	**Unique**	**Total**	**Georeferenced**	**Unique**
WIEWS (2007)	856,167	28,181	–	–	11,668	–	–
Genesys (2012)	404,322	16,409	7,087	5,902	845	845	248
Maxted *et al.* (2008b)	–	14,662	14,662	9,375	–	–	NA
Knupffer *et al.* (2009)	763,662	31,401	?	?	17,575	?	?
ICARDA Global wild wheat database	–	43,000	22,630	11,643	21,000	3,051	747

–: not available or not studied, ?: not distinguished

Data from different sources were standardized to taxon level based on the taxonomic classification in Slageren (1994). In order to retain only unique and fully geocoded accessions in the database, all duplicates were removed, as were accessions incompletely identified. Additional information on species distribution is available through the Global Biodiversity Information Facility (GBIF) data portal.

Clearly, errors cannot be completely avoided when species information is gathered by simply mining databases without first examining and confirming identification of each specimen. Doubtless, a certain proportion of genebank accessions (and herbarium specimens) are mis-identified, compounded to a certain degree by errors in associated passport data. An invaluable and comprehensive monograph of *Aegilops* and *Amblyopyrum* (Slageren, 1994) lists c. 20,000 herbarium specimens from many institutions (c. 70-80% of the world's preserved *Aegilops* specimens at that time), examined and identified by the author. These specimens are depicted as points on distribution maps, and although not geo-referenced, it is hoped in the future that much of this specimen data might be incorporated in the newly-updated Global wild wheat database maintained at ICARDA database. This would increase the overall amount and reliability of data for *Aegilops* occurrence, and would confirm the value of herbarium collections, trained taxonomists, and careful plant identification in this enormous task of global conservation of crop plant biodiversity.

The global wild wheat database compiled for this study initially included around 43,000 *Aegilops* and 21,000 wild *Triticum* records. Following the standardization of taxonomic names, elimination of duplicates and accessions incompletely identified or with spurious collection site data, there remain 11,643 and 747 unique records of *Aegilops* and wild *Triticum* occurrences respectively (table 2). This database is maintained by ICARDA.

It is apparent that wild relatives species represent only a small portion of the existing wheat germplasm collections, and that only few genebanks (notably ICARDA-Genetic Resources Section and the Wheat Genetics Resource Center at Kansas State University, US) are specialized in long-term conservation, regeneration and distribution of these species. In order to compile an increasingly comprehensive, accurate and useful database of wild wheats (*Aegilops*, *Amblyopyrum* and *Triticum*), more work with existing germplasm collections is clearly still needed. Priority should be given to identifying the large number of unidentified or mis-identified accessions and geo-referencing accessions where data is missing, in order to reduce errors in species distribution data. Future collaborative work with other genebanks with substantial holdings of wild wheats, such as those in Iran, Turkey, Israel and Russia, and access to the relevant data about their holdings, is highly recommended.

Number of accessions conserved in genebanks

According to the WIEWS database, there are 28,181 records of *Aegilops* species reported by the genebanks in 47 countries (table 3). The highest numbers of records are reported from Israel (9,482 from 15 species) and Turkey (3,932 from 21 species). Greatest species diversity of *Aegilops* is again shown to lie within the countries of the Fertile Crescent (Jordan, Palestine, Israel, Lebanon, Syria, Turkey, Iraq, Iran), and somewhat lower in the Caucasus and Central Asian regions. Other significant *Aegilops* collections are reported from France, Portugal, Spain and Yugoslavia. The most commonly recorded species in the WIEWS database are *Ae. triuncialis, Ae. tauschii, Ae. speltoides, Ae. cylindrica, Ae. geniculata* and *Ae. sharonensis,* with more than 2,000 accessions of each.

Table 3 ■ Number of seed accessions of different *Aegilops* species conserved *ex situ* and reported by different countries.

Country	*Ae. bicornis*	*Ae. biuncialis*	*Ae. markgrafii*	*Ae. columnaris*	*Ae. comosa*	*Ae. crassa*	*Ae. cylindrica*	*Ae. geniculata*	*Ae. juvenalis*	*Ae. kotschyi*	*Ae. longissima*	*Ae. neglecta*	*Ae. peregrina*	*Ae. searsii*	*Ae. sharonensis*	*Ae. speltoides*	*Ae. tauschii*	*Ae. triuncialis*	*Ae. umbellulata*	*Ae. uniaristata*	*Ae. vavilovii*	*Ae. ventricosa*	**Total**
Afghanistan				1		14	3			2							394	84			12		510 (7)*
Albania		2					2	7				34						4					49 (5)
Algeria								60				5	1					6				64	136 (5)
Armenia		30		81		28	740	4				25	1			10	408	500	2		1		1,830 (12)
Austria							3																3 (1)
Azerbaijan	1	183		22	1	4	296	1	3	35		49	11		1		742	393	41	1	1	8	1,793 (18)
Bosnia		6						1				6											13 (3)
Bulgaria		107	10	1	5	1	112	40	1			126	2			5	5	166	1				582 (14)
China				1			1									1	41	1					45 (5)
Croatia								11				11						5					27 (3)
Cyprus	5	46			2			34					23					31					141 (6)
Czech Republic			1				8					1				4		3					18 (5)
Egypt	35	1								16			2				4					4	62 (6)
France		2					20	101				43				2	2	51			1	6	228 (9)
Georgia							55										55	33					143 (3)
Greece		458	238	3	291	1	9	102		1		279	12			8		428	5	16		2	1,853 (15)
Hungary			1				113	2				2				2	2	2					124 (7)
India																	24						24 (1)
Iran		5		17		112	126		4	14		9				14	554	212	31	1		12	1,111 (13)
Iraq		19	2	2		48	4	1	12	5	1	14	2			96	12	72	18		2		310 (16)
Israel	529	111		5		1	3	420		216	1871		1164	307	3053	1612	84	76			30		9,482 (15)
Italy		1			1		1	102				12				2		13	1	1		1	135 (10)
Jordan	13	41		14		9	4	72		60	25		181	122		1	6	9			141	1	699 (15)
Kazakhstan		1				5	83					1					29	8			2	2	131 (8)
Kyrgyzstan						2	16										19	7			4		48 (5)
Lebanon		49	21	23			5	72					29	4		3		56	5		15		282 (11)

Table 3 ■ Number of seed accessions of different *Aegilops* species conserved *ex situ* and reported by different countries (*continued*).

Country	*Ae. bicornis*	*Ae. biuncialis*	*Ae. markgrafii*	*Ae. columnaris*	*Ae. comosa*	*Ae. crassa*	*Ae. cylindrica*	*Ae. geniculata*	*Ae. juvenalis*	*Ae. kotschyi*	*Ae. longissima*	*Ae. neglecta*	*Ae. peregrina*	*Ae. searsii*	*Ae. sharonensis*	*Ae. speltoides*	*Ae. tauschii*	*Ae. triuncialis*	*Ae. umbellulata*	*Ae. uniaristata*	*Ae. vavilovii*	*Ae. ventricosa*	**Total**
Libya	2	29		1				36		1			2				2					41	114 (8)
Macedonia		14					7	4				15						24					64 (5)
Malta								1															1 (1)
Montenegro								4				7						1		1			13 (4)
Morocco						1		196				35				1	4	75				20	332 (7)
Pakistan																	114	13					127 (2)
Palestine			1					2		2	2	1	5	1	1	1			2		1		19 (11)
Poland																		1					1 (1)
Portugal				2				323				46				3	2	231					607 (6)
Romania	1	1	1	1		2	10	9								4	2	5				6	45 (11)
Russia	3	38	1	2	1		75			1	1	11	1			9	95	29	1	1			269 (15)
Serbia		12					12	1				1						7	1				34 (6)
Spain	1	9					1	72				116						110				36	345 (7)
Syria		111	14	41		33	16	93	1	24		6	96	36		138	16	130	17		47		819 (16)
Tajikistan						11	72						1				152	103			3		342 (6)
Tunisia		2						8															10 (2)
Turkey	2	216	129	87	29	12	403	310	5	4	6	458	17		3	503	229	1265	234	16	1	3	3,932 (21)
Turkmenistan		1		9		35	14		3	3		2	3				219	62	1		3	1	356 (13)
Ukraine		43	1				47	3		3		3				2		20					122 (8)
Uzbekistan	4	1				25	68		14	2	2			1		6	112	66		2	23	1	327 (14)
Yugoslavia		6						10				7					3	5					31 (4)
Totals	596	1556	420	314	330	366	2393	2105	45	391	1911	1332	1555	471	3058	2434	3599	4396	361	44	293	211	28,181

( )* number of different species
(Source: WIEWS, 2007)

The unexpectedly, and probably misleadingly, high number (3,035) of *Ae. sharonensis* records, all from Israel, reflects very high sampling density and single-plant collections. Most other records most likely refer to populations rather than individual plants, which underlines the fact that data cannot be taken at face value or correctly compared without understanding it more deeply.

The WIEWS database contains 11,668 records of wild *Triticum* from 14 countries (table 4). All four wild *Triticum* species were recorded from several countries within the Fertile Crescent (Iraq, Iran, Lebanon and Turkey), while Jordan and Syria recorded three species, lacking *T. timopheevii* subsp. *armeniacum*. The absence of *T. monococcum* subsp. *aegilopoides* and *T. urartu* in Israel and Palestine needs to be further investigated.

It is essential to try and obtain more detailed information from genebanks about the correct identification and origin of the *Aegilops* (and wild *Triticum*) accessions, the accession type (i.e. sampling strategy - seeds from a single plant vs. from a population) and the issue of duplications. The information provided by WIEWS is updated when preparing the report on the FAO-State of the World for PGRFA.

Genebanks with major holdings of *Aegilops* and wild *Triticum* germplasm accessions are listed in table 5. Israel (ISR003) has the highest number of accessions for both *Aegilops* and wild *Triticum* genera and this could be due to the fact that large numbers of accessions are derived from single plant sampling.

Table 4 ■ Number of accessions of wild *Triticum* species per country.

Country	*Triticum timopheevii* subsp. *armeniacum*	*Triticum monococcum* subsp. *aegilopoides*	*Triticum turgidum* subsp. *dicoccoides*	*Triticum urartu*	Totals
Armenia	190	247	–	74	511 (3)*
Azerbaijan	152	36	–	–	188 (2)
Bulgaria	–	16	–	–	16 (1)
Greece	–	108	–	–	108 (1)
Iran	79	92	16	29	216 (4)
Iraq	545	687	6	77	1,315 (4)
Israel	–	–	1,864	–	1,864 (1)
Jordan	–	3	556	28	587 (3)
Lebanon	88	17	56	566	727 (4)
Poland	–	3	–	–	3 (3)
Syria	–	37	416	257	710 (3)
Turkey	3,999	548	220	617	5,384 (4)
Ukraine	–	16	–	–	16 (1)
Russia	16	1	1	5	23 (3)
Totals	**5,069**	**1,811**	**3,135**	**1,653**	**11,668**

()* total number of species
(Source: WIEWS, 2007)

Table 5 ■ Genebanks with the highest number of accessions of *Aegilops* and wild *Triticum* species.

Code	**Institution**	***Aegilops***		**Wild *Triticum***	
		Number of species	**Number of accessions**	**Number of species**	**Number of accessions**
ISR003	Lieberman Germplasm Bank-Institute for Cereal Crops Improvement- Tel-Aviv University	20	9,143	4	2,841
SYR002	International Centre for Agricultural Research in Dry Areas	22	4,015	4	1,564
JPN003	Department of Genetic Resources I-National Institute of Agrobiological Resources	20	2,396	4	962
RUS001	N.I. Vavilov All-Russian Scientific Research Institute of Plant Industry	21	2,229	4	417
USA029	National Small Grains Germplasm Research Facility USDA-ARS	21	2206	4	2,275
DEU146	Genebank Leibniz Institute of Plant Genetics and Crop Plant Research	20	1,412	4	286
MEX002	Centro Internacional de Mejoramiento de Maíz y Trigo	21	1,294	4	2,006
ARM035 and 036	Laboratory of Plants Gene Pool and Breeding	9	1,106	4	274
TUR001	Plant Genetic Resources Department Aegean Agricultural Research Institute	11	1,075	4	536
CZE122	Genebank Department Division of Genetics and Plant Breeding-Research Institute of Crop Production	21	982	4	123
IND001 and 046	National Bureau of Plant Genetic Resources and Punjab Agricultural University	21	955	4	330
USA109	Department of Botany and Plant Sciences	21	688	4	1,477
GRC005	Greek Genebank Agricultural Research Center of Macedonia and Thrace National Agricultural Research Foundation	12	676	1	44
BGR001	Institute for Plant Genetic Resources "K.Malkov"	21	602	2	34
NLD037	Centre for Genetic Resources the Netherlands Plant Research International	12	488	1	257
JOR006	National Centre for Agricultural Research and Technology Transfer	11	267	3	564
CAN004	Plant Gene Resources of Canada Saskatoon Research Centre-Agriculture and Agri-Food	15	138	4	1,666
	Wheat Genetic Resources Center, Kansas State University, USA	22	1436	4	1381

(Source: FAO-WIEWS, 2007)

Status of *in situ* conservation of *Aegilops* and wild *Triticum*

One of the most difficult aspects in the preparation of the State of the World on Plant Genetic Resources for Food and Agriculture (SoWPGRFA 2010, http://www.fao.org/agriculture/crops/thematic-sitemap/theme/seeds-pgr/sow/sow2/en/) was the assessment and monitoring of the state of *in situ* biodiversity. Very little information is available and very limited efforts have been invested in *in situ* conservation of crop wild relatives. Scattered observations show that *Aegilops* and wild *Triticum* populations, and thus their infraspecific diversity, are under threat. Damania *et al*. (1993) reported that some wild *Triticum* taxa in Iran appeared to be almost lost in areas where large populations were previously reported. Similar observations were reported by Amri *et al*. (2005) for *T. urartu* in the Beka'a Valley in Lebanon and for *T. turgidum* subsp. *dicoccoides* in the northern parts of Syria. These are worrying reports.

The Global Environment Facility (GEF) has funded a few projects dealing with *in situ* conservation of CWR. ICARDA coordinated such a regional project called "Conservation and Sustainable Use of Dryland Agrobiodiversity in the Fertile Crescent" funded by GEF/UNDP, which assessed and monitored CWR (including *Aegilops* and wild *Triticum*) species' richness, abundance, frequency and the factors associated with the observed degradation of their natural habitats (Amri *et al*., 2005). Ecogeographic and botanic surveys were conducted in 55 monitoring areas in the drylands and mountainous areas of Jordan, Lebanon, Palestine and Syria during the period of 2000-2010. The results showed continuing habitat degradation, due mainly to overgrazing (table 6) and land reclamation for agricultural and urbanization purposes. Rock quarrying caused almost total loss of natural vegetation in some localized areas, and fires continue to impact areas of native vegetation along roadsides and within forests.

Table 6 ■ Percent of monitoring areas affected by different levels of major factors of degradation in 55 sites in Jordan, Lebanon, Palestine and Syria, during 2000 and 2010.

Level of degradation	**No degradation**		**Low degradation**		**Medium degradation**		**High degradation**	
Factor of degradation/year	**2000**	**2010**	**2000**	**2010**	**2000**	**2010**	**2000**	**2010**
Overgrazing	1.8	1.8	14.5	7.3	40.0	18.2	43.6	72.7
Overuse other than grazing*	34.5	16.4	29.1	20.0	23.6	27.3	12.7	36.4
Land reclamation**	40.0	21.8	14.5	12.7	34.5	21.8	10.9	43.6
Urbanization	63.6	41.8	14.5	14.5	14.5	18.2	7.3	25.5
Quarries	72.7	70.9	18.2	18.2	3.6	3.6	5.5	7.3
Fire	76.4	72.7	12.7	12.7	7.3	7.3	3.6	7.3

* Includes cutting and up-rooting vegetation.
** Includes cultivation for crops and orchards.

The results of the surveys undertaken in the south-east of Turkey between 2006 and 2009 showed that natural habitat loss and fragmentation, due to overgrazing and frequent droughts thought to be associated with climate change, are threatening the conservation of wild relatives of wheat. In spite of this, some important biodiversity hotspot areas with a large number of *Aegilops* and wild *Triticum* species still remain. In this area of Turkey there are few protected areas and limited efforts have been directed towards the *in situ* conservation of CWR, including *Aegilops* and wild *Triticum*. The Ceylanpinar State Farm located in south-eastern Turkey, designated to conserve *Aegilops* species, is an exception (Firat and Tan, 1997; Karagoz, 1998).

In the larger Fertile Crescent region, however, a number of protected areas have been established specifically for the *in situ* conservation of certain CWR or suites of CWR:

– Ammiad reserve in Galilee, Israel, for conservation of wild *Triticum*, particularly *T. turgidum* subsp. *dicoccoides* (Anikster *et al.*, 1997; Kaplan, 2008);

– Miyanjangal-e-Fasa, a protected area in the Fars province of Iran, for conservation of crop wild relatives including several *Aegilops* species;

– Al-Lujat biosphere reserve, established in 2008 in southern Syria, for the *in situ* conservation of wild relatives of cereals, legumes and fruit trees;

– Erebuni nature reserve, northeast of Yerevan in Armenia, established on the recommendation of Vavilov, for *in situ* conservation of *Triticum urartu*, *T. monococcum* subsp. *aegilopoides, T. timopheevii* subsp. *armeniacum*, several *Aegilops* species and *Amblyopyrum muticum*.

There are several other protected areas and national parks located within the area of natural distribution of wheat wild relatives, likely to contain a number of important species. The *in situ* conservation of CWR in these areas is more or less passive and "accidental" and the extent to which these areas are contributing to the conservation of *Aegilops* and wild *Triticum* needs to be assessed.

Gaps in *ex situ* and *in situ* conservation of *Aegilops* and wild *Triticum*

Gap analysis is increasingly used to identify gaps in existing collections and to guide future actions of seed collecting and *in situ* conservation of genetic resources (Margules and Pressey, 2000; Balmford, 2003; Brooks *et al.*, 2004; Riemann and Ezcurra, 2005). This methodology for gap analysis was adapted for CWR by Maxted *et al.* (2008), and follows four steps:

– identifying priority taxa;

– using distributional data to identify ecogeographic breadth and complementary hotspots;

– matching current conservation actions with the identified ecogeographic breadth and complementary hotspots to existing protected area networks (identifying the so-called "gaps");

– formulating a revised *in situ* and *ex situ* conservation strategy.

Gap analysis has been used previously in order to plan an efficient conservation strategy for *Aegilops* and wild *Triticum*, using 11,647 and 734 unique accessions of *Aegilops* and wild *Triticum* species respectively (Maxted *et al.*, 2008). Potential geographic species distribution can be predicted using environmental similarity analysis based on 19 climatic variables using the Bioclim method (Hijmans *et al.*, 2005). The addition of further layers of information such as edaphic data and collection site elevation that may be gleaned from herbarium specimens and botanical literature including local Floras, can further improve the analysis. A predicted distribution map for wild *Triticum* species has been generated using this method (figure 10).

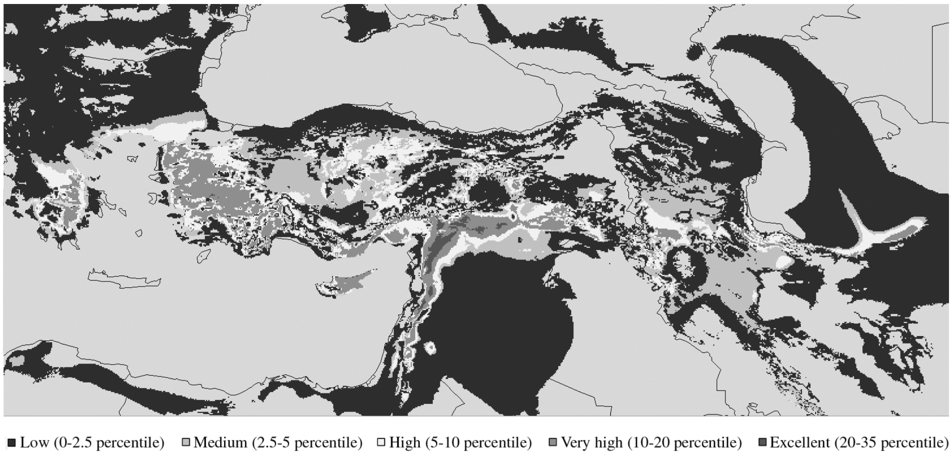

Figure 10 ■ Predicted distribution map of wild *Triticum* species.

Gaps in *ex situ* collections

Gaps in existing *ex situ* germplasm collections of *Aegilops* germplasm were determined by comparing the collection locations of all available accessions with the known natural range of each species This analysis requires an extensive herbarium survey such as that undertaken by Slageren (1994). Future collecting missions can then be planned to target certain species according to the priority levels (below) as outlined in Maxted *et al.* (2008):

– high priority: species with 200 or fewer conserved accessions and/or species which are under-sampled in their natural range;

– medium priority: species with 200-500 conserved accessions, with only a few identified under-sampled regions;

– low priority: species with more than 500 conserved accessions, well-sampled over most of their geographic range.

Based on these criteria, there are 10 "high-priority" *Aegilops* species (*Ae. bicornis, Ae. columnaris, Ae. juvenalis, Ae. kotschyi, Ae. longissima, Ae. searsii, Ae. sharonensis, Ae. uniaristata, Ae. vavilovii*, *Ae. ventricosa*) and two "high-priority" wild *Triticum* species (*T. timopheevii* subsp. *armeniacum*, *T. turgidum* subsp. *dicoccoides*). Each has fewer than 200 germplasm populations in total, in global collections, and urgently needs collecting (figures 11 and 12). "Medium-priority" species include the remaining wild *Triticum* species (*T. monococcum* subsp. *aegilopoides* and *T. urartu*), with fewer than 250 accessions, and six *Aegilops* species (*Ae. comosa, Ae. crassa, Ae. markgrafii, Ae. peregrina, Ae. speltoides* and *Ae. umbellulata*), all of which also need to be further collected for *ex situ* conservation. The remaining six *Aegilops* species (*Ae. biuncialis, Ae. cylindrica, Ae. geniculata, Ae. neglecta, Ae. tauschii, Ae. triuncialis*) are considered to be "low priority" however, additional populations can be collected with potential of having adaptive traits such as drought and salinity tolerance.

Continued and targeted germplasm collecting is still needed in the regions where wheat wild relatives are native (Waines and Skovmand, 1996). The wheat genetic resources conservation strategy (CIMMYT, 2007) identified priority regions and certain "target" wild wheat relatives on which to base future collection missions, including:

– Albania, Greece and Former Yugoslavia, which have 13 species including *Ae. uniaristata* known to possess tolerance to heavy metals;

– Iran, Jordan, Pakistan and Syria, very dry areas, for heat- and drought-tolerant *Ae. searsii, Ae. tauschii* and *Ae. vavilovii*;

– Iran, in the mountains near Shiraz and near Esfahan, along the Zagros mountains and in the desert and salt affected areas, all wild *Triticum* and *Aegilops* species, for drought- and salt-tolerance.

Other recommendations for further and urgent collections of wheat wild relatives include:

– Algeria, Cyprus, Egypt, Greece, Iran, Israel, Libya, Pakistan, Palestine, Spain, Syria, Tajikistan, Tunisia, Turkey, Turkmenistan, Uzbekistan, targeting *Ae. bicornis, Ae. comosa, Ae. juvenalis, Ae. kotschyi, Ae. peregrina, Ae. sharonensis, Ae. speltoides, Ae. uniaristata* and *Ae. vavilovii* (Maxted *et al*., 2008);

– Aegean region, western Mediterranean region (France, Portugal, Spain), North Africa, Iran and Syria (Skovmand *et al.,* 2006).

We consider that further collecting is needed for all *Aegilops* and wild *Triticum* species, even for the "low-priority" species identified in our study with many accessions already conserved (*Ae. biuncialis, Ae. cylindrica, Ae. geniculata, Ae. neglecta, Ae. tauschii, Ae. triuncialis*). They are relatively widespread and locally-common species, meaning many more accessions are required, from across their entire geographic ranges, to ensure complete sampling to target potentially valuable traits.

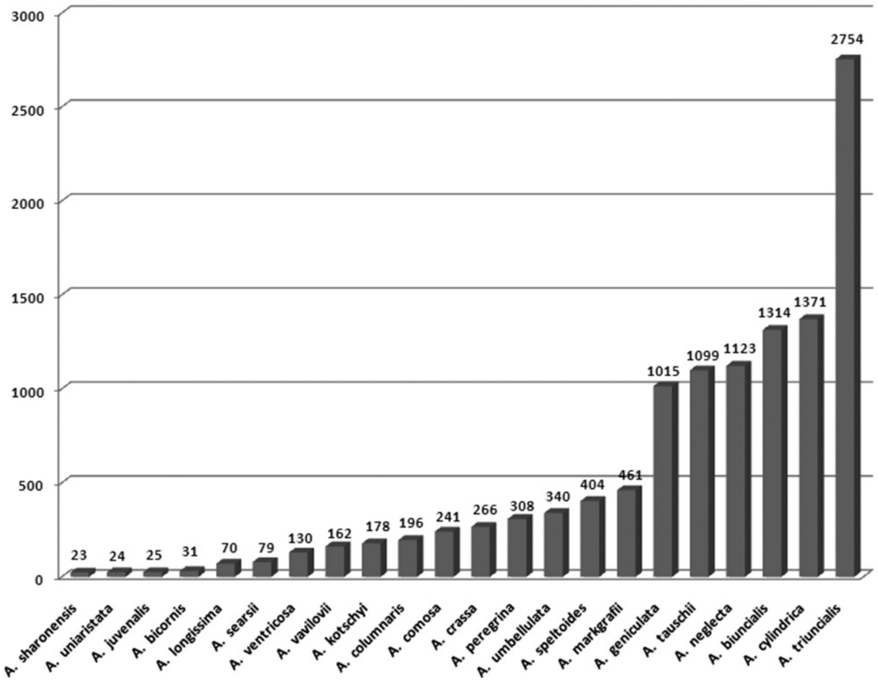

Figure 11 ■ Number of unique accessions for each of the 22 species of *Aegilops* distributed within their geographic range.

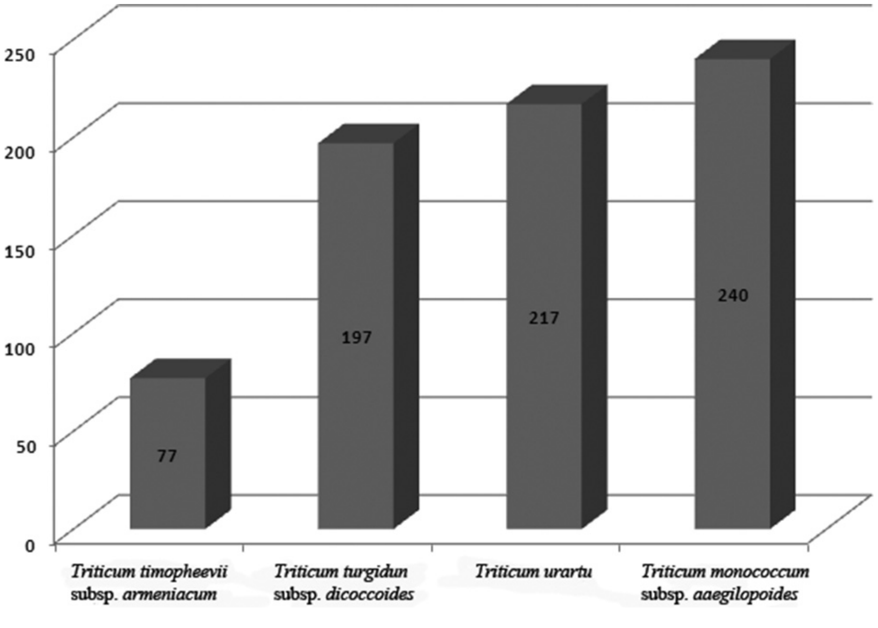

Figure 12 ■ Number of unique accessions for each of the four species of wild *Triticum* distributed within their geographic range.

Germplasm collection priorities can also be based on other factors including the extent of the loss of or threat to, existing populations, a species' place in the crop genepools, and on particular useful traits which can be transferred from the wild relatives. Considering this, all wild *Triticum* species and all *Aegilops* species with S and D genomes should be targeted in areas subject to heavy environmental degradation. The direct wild ancestors of cultivated wheats, namely *Ae. tauschii*, *Ae. speltoides*, *T. urartu, T. monococcum* subsp. *aegilopoides*, *T. turgidum* subsp. *dicoccoides* and *T. timopheevii* subsp. *armeniacum*, are commonly negatively affected by overgrazing and disturbance by cultivation.

For all wild species, *Aegilops* and *Triticum*, special collecting missions should be organized to sample populations surviving under harsh environments subject to extreme drought, heat, cold, and saline conditions; for example, by targeting *Ae. sharonensis, Ae. tauschii* and *Ae. bicornis* for salt tolerance; *Ae. crassa, Ae. searsii, Ae. tauschii*, *Ae. vavilovii* and *Ae. ventricosa* for drought and heat tolerance (figure 13); and *Ae. speltoides, T. timopheevii* subsp. *armeniacum*, *T. monococcum* subsp. *aegilopoides* and *T. urartu* for cold tolerance and winter hardiness needed to extend durum wheat cultivation to cold winter areas.

Following gap analysis and the analysis of *Aegilops* distribution along the aridity gradient, ICARDA initiated since 2010 several collaborative collecting missions, to Armenia, Cyprus, Georgia, Greece, Jordan, Libya, and Tajikistan, mainly to fill collection gaps in crop landraces and CWR, and to target popu-

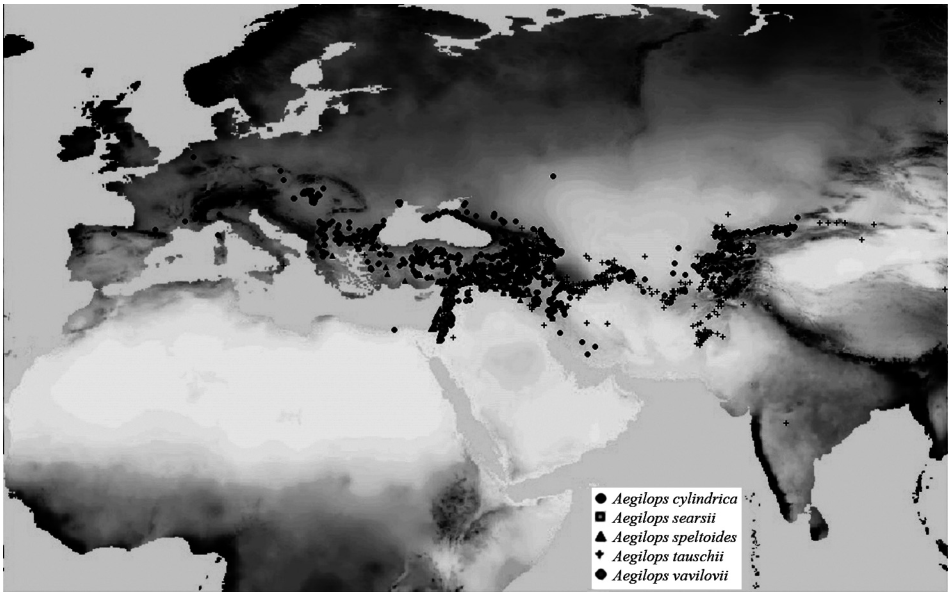

Figure 13 ■ Distribution of some *Aegilops* species along the aridity gradient using aridity index.

lations with potential traits for tolerance to heat, drought and salinity stresses. Further searching is also urgently needed in other regions, such as Palestine and Israel for *Triticum urartu* and *T. monococcum* subsp. *aegilopoides*; Cyprus and most south-east European countries for several *Aegilops* species and *T. monococcum* subsp. *aegilopoides*; and Afghanistan, Iraq and Iran, the heart of the natural range of wheat's wild relatives, from where very few *Aegilops* accessions have been collected and conserved in genebanks.

Gaps in *in situ* conservation

DIVA-GIS version 7.5.0 (www.diva-gis.org) was used to portray the distribution of species, calculate the species richness and conduct complementary analysis to identify species diversity hotspots and where best to establish future *in situ* conservation reserves for maximum species diversity conservation (Hijmans *et al.*, 2005). The iterative procedure (Rebelo and Siegfried, 1992) used in the "reserve selection" manner, as described by Hijmans *et al.* (2005), identifies the minimum number of 100 x 100 km^2 grid cells that are complementary to each other in maximizing conserved diversity of *Aegilops* and wild *Triticum* species. The identified hotspots were checked to see if they fall within existing protected areas using the World Database on Protected Areas (WDPA – www.unep-wcmc.org).

The species richness analysis highlighted two areas ("hotspots"?) having the highest number of *Aegilops* species (at least 15): one in the vicinity of the border between Syria and Lebanon and the other in western Turkey (figure 14). Six areas with 12-14 *Aegilops* species are located in western Jordan, northern Iraq, western Iran, Israel/Palestine and northern Syria/ southern Turkey.

No particular site in the analysis contained all four species of wild *Triticum* together, although several areas within the Fertile Crescent had three species:

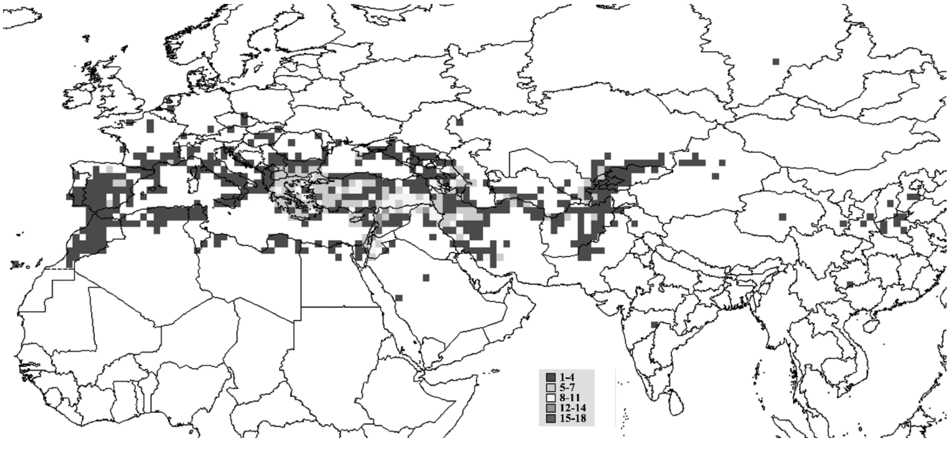

Figure 14 ■ Species richness analysis for *Aegilops* species using DIVA-GIS program.

the border between Lebanon and Syria; the southern Sweida region in Syria where *T. turgidum* subsp. *dicoccoides*, *T. urartu* and *T. monococum subsp. aegilopoides* can be found growing together; Armenia, northern Iraq and southern Turkey, where *T. timopheevii* subsp. *armeniacum* and *T. monococum subsp. aegilopoides* are found, together either with *T. turgidum* subsp. *dicoccoides* or *T. urartu* (figure 15).

Species richness analysis identified five complementary regions of high *Aegilops* diversity: in western Syria and northern Lebanon, central Israel, and north-west Turkey. Additional high species richness areas identified in Turkmenistan and southern France are questionable and need further checking. Within these areas, 16 IUCN-recognized protected areas are found and these are potentially valuable sites in which to establish genetic reserves. Unfortunately, the "premier" *Aegilops* hotspots on the Syrian/Lebanese border are not coincident with any existing internationally-recognized protected areas, and there is an urgent need to establish a new protected area in that region. These results confirm those of the study conducted by Maxted *et al.* (2008).

Reserve analysis using DIVA-GIS identified species diversity hotspots for wild *Triticum* in southern Turkey, and for *Aegilops*, the border region between Syria and Lebanon, and western Turkey. Ideally these hotspot areas should be included in protected conservation areas, or genetic reserves, for *in situ* conservation of wild *Triticum* and *Aegilops* species diversity (figure 16). None of these hotspots are at present included in existing protected areas, but the establishment a new protected area in the valley of Qal'at Al Hosn in Syria as recom-

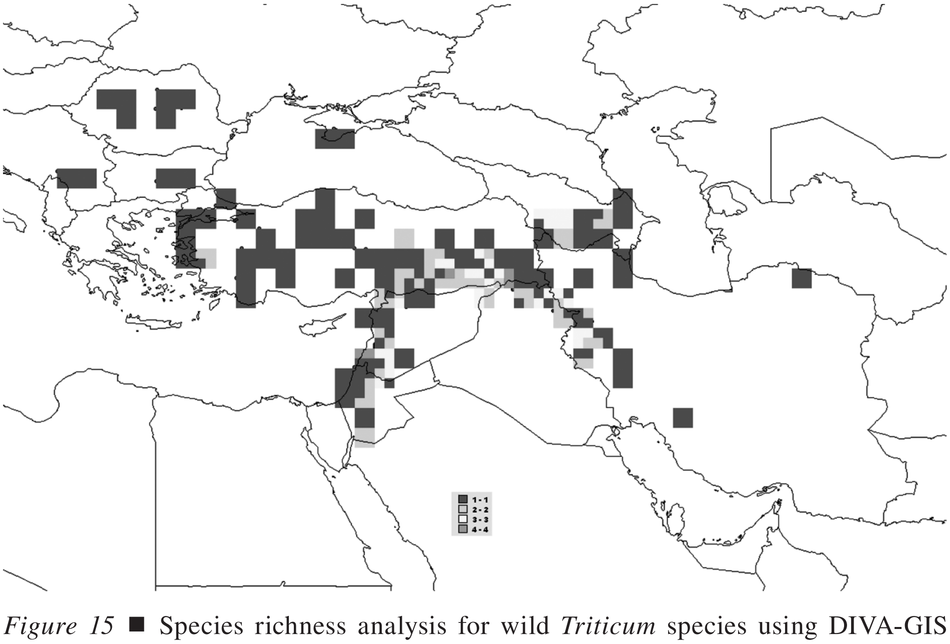

Figure 15 ■ Species richness analysis for wild *Triticum* species using DIVA-GIS program.

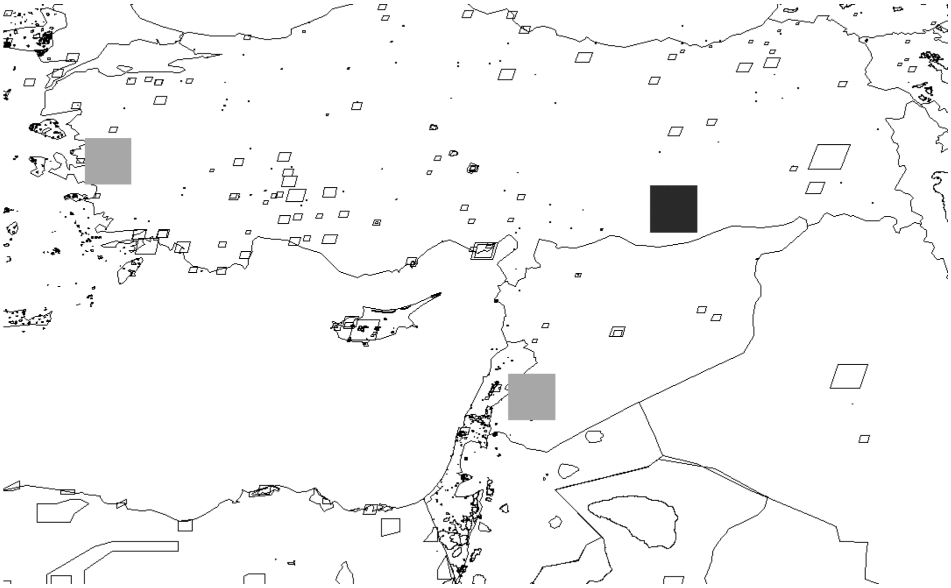

Figure 16 ■ Regions for establishing genetic reserves for the conservation of *Aegilops* species (grey) and wild *Triticum* species (black), with the scatter of the existing protected areas.

mended by Maxted *et al.* (2008) would be an excellent first step in the *in situ* conservation of *Aegilops.*

There is a need to assess the extent to which existing protected areas are contributing to the conservation of wheat wild relatives. Preliminary observations in Jordan, Lebanon and Syria showed that none of the recognized protected areas are specifically targeting the *in situ* conservation of *Aegilops* and wild *Triticum* species, although many of them contain some of these species. The Dana reserve in Jordan did not contain any of the wild *Triticum* species found in the adjacent region, while the protected areas in Jabal Abdulaziz and Sweida, in Syria, contained several *Aegilops* and wild *Triticum* species. In 1999 the Syrian government restricted grazing by sheep and goats in the Sweida region, and in 2007 established a biosphere reserve in Al-Lujat in Houran region and an *in situ* conservation site of 10,000 hectares close to the border between Lebanon and Syria, about 30 km from Homs, to conserve wild relatives and range species.

Several other areas have been recommended as suitable for the *in situ* conservation of wheat wild relatives and other species by the GEF-funded, ICARDA-coordinated agriobiodiversity project (table 7). The establishment of these protected areas could target a number of species including wild relatives of crops, rangeland and medicinal plants, and some neglected fruit trees. Several less-disturbed areas, in the Golan heights, in the border areas between Lebanon and Syria, and between Turkey and Syria, were identified as being ideal for the establishment of genetic reserves for wheat wild relatives and other CWR.

Table 7 ■ Areas recommended for *in situ* conservation of crop wild relatives and range species in Jordan, Lebanon, Palestine and Syria.

Target area	**Monitoring area**	**Major threats**	**Important CWR species**
Ajloun	Samta (privately owned land, fenced)	Land reclamation for fruit orchards	*T. turgidum* subsp. *dicoccoides* and 8 *Aegilops* species occurring with *Trifolium, Medicago, Lathyrus, Hordeum, Allium, Pistacia, Amygdalus* wild species and several medicinal plants species
Aarsal	Wadi Saweid (privately owned by members of local community)	Land reclamation for fruit orchards, urbanization, grazing pressure, quarry expansion	A limited population of *T. turgidum* subsp. *dicoccoides* and 6 *Aegilops* species occur within the disturbed forest containing large population of *Pyrus syriaca*, few plants of wild *Amygdalus, Crataegus, Prunus, Pistacia* and others; also *Trifolium, Medicago* and *Vicia* species
Nabha	Bishwet (Owned by the Church or common land with the right of use)	Overgrazing, land reclamation for agriculture and urbanization	*T. turgidum* subsp. *dicoccoides, T. urartu* and *T. monococcum* subsp. *aegilopoides* occur in the *Quercus*-dominated forest; also large number of legumes and cereal CWR, and wild fruit tree species
Ham/ Maaraboun	Talat Sawdah (privately owned by Ham Mokhtar)	Overgrazing, land reclamation for agriculture	There are several patches which are rich in herbaceous species including three wild *Triticum* species (*T. turgidum* subsp. *dicoccoides, T. urartu* and *T. monococcum* subsp. *aegilopoides*), 8 *Aegilops* and forage legume species
Jenin	Tayassir (Land owned by patriarchate and used by local communities)	Overgrazing, land reclamation for agriculture	Rangeland species including 6 *Aegilops* and many forage legume species
Hebron	Wadi Sair (privately owned by farmers from different surrounding villages)	Overgrazing, land reclamation for agriculture and urbanization, rapid quarry expansion	Large number of herbaceous species including 7 *Aegilops*, 3 *Hordeum*, 9 *Medicago*, 13 *Trifolium*, 5 *Vicia*, 3 *Lathyrus* species and a limited population of *T. turgidum* subsp. *dicoccoides*; also small populations of wild *Amygdalus*, *Pistachia and Crataegus, Olea, Ficus* and *Catania* species
Sweida	Natural reserve between Sale and Rsheida (government forested area with pine trees)	Dense plantations of introduced species, impacting native herbaceous vegetation	This is the richest site for *T. turgidum* subsp. *dicoccoides* of all the 75 sites monitored in Jordan, Lebanon, Palestine and Syria

(Source: Amri et al., 2005)

Conclusions and future prospects

Development of reliable global *Aegilops* and wild *Triticum* databases

Further work is still needed to develop and maintain reliable global databases for wheat wild relatives, including:

– gathering more data through further eco-geographic surveys and analysis of existing herbarium collections and Floras, and additional secondary information related to surveys of species richness, abundance and threats;

– accessing information on unique accessions held by national genebanks especially in the countries located within the centers of wild wheat diversity;

– assigning geo-reference coordinates to accessions where needed;

– correctly identifying genebank accessions and herbarium specimens that are either not completely identified or misidentified;

– increasing availability of the accession information to collaborating partners.

Monitoring *Aegilops* and wild *Triticum* distribution and diversity and threats to them

Substantial efforts are needed to assess and monitor the diversity of the remaining populations of *Aegilops* and wild *Triticum* species, particularly in areas identified as biodiversity hotspots in this analysis. This includes:

– continuing and increased monitoring of wheat wild relatives in collaboration with partners, mainly in the countries of Central and West Asiatic and North Africa (CWANA) region, including measurement of genetic diversity and accurate identification of major threats to diversity. There is an urgent need for the development of more accurate approaches for assessing and monitoring changes, and threats, to genetic diversity of wild populations;

– increased research into the population biology and ecology of the ancestors and wild relatives of wheat, and into the dynamics of species under the effects of climate change. ICARDA has monitored *in situ* conservation simulation sites in Syria since 1992 in order to study the population dynamics of wild relatives of barley, chickpea, lentil, vetch and wheat (Valkoun and Damania,1992). Assessing the extent to which existing protected areas are contributing to the *in situ* conservation of wheat wild relatives and reviewing the management plans to optimize their conservation;

– identification of potential additional natural reserve areas for protection of wheat wild relatives, and recommendation of these to national programs that these areas would form vital links in a future extensive global network of *in situ* reserves for wild wheat conservation.

Application of best practices for conservation of *Aegilops* and wild *Triticum*

Careful handling is needed to ensure reliable conservation of wheat's wild relatives. Many of the existing *Aegilops* and wild *Triticum ex situ* collections in countries of the West Asia, North Africa, Caucasus and Central Asiatic regions are under constant threat to their long-term viability, reliability and thus usefulness (Global Wheat Conservation Strategy; CIMMYT, 2007). Some of the problems identified are:

– lack of adequate medium- and long- term cold storage facilities, shortage of back-up generators in case of electricity cuts and lack of humidity control;

– inadequate pre-storage drying of seed accessions required to optimize long-term seed health and viability;

– poor multiplication/regeneration practices, including planting too few seeds, thus compromising genetic integrity/diversity, and using no, or inadequate, isolation barriers when multiplying outcrossing species such as *Ae. speltoides* and *Ae. mutica* (*Amblyopyrum muticum*);

– passport data and characterization information sometimes inadequate and/or inaccurate. All documentation must be detailed, careful and accurate, including correct taxonomic identification of species. A need for increased return of evaluation data/exchange of information from ICARDA's collaborating partners;

– lack of safety duplication of unique collections held by national genebanks;

– need for both *ex situ* and *in situ* conservation approaches to be used in tandem for conservation of genetic diversity of wild wheats, using quality standards for *in situ* genetic reserves of crop wild relatives according to Iriondo *et al.* (2012).

Efficient gene mining and utilisation of the collections

Conservation of genetic resources should be tightly linked with their use in breeding, research and rehabilitation of degraded natural habitats. *Aegilops* and wild *Triticum* species potentially hold a rich reservoir of genes needed to overcome existing and future biotic and abiotic challenges posed to wheat breeding programs around the world.

Efficient use of these species in wheat breeding will require:

– targeting adaptive traits *in situ* during collecting missions by sampling populations evolving under major constraints, such as drought, heat and salt stress;

– efficient identification of sources of desired traits through the use of the newly developed approach of Focused Identification of Germplasm Strategy

(FIGS). By the use of complex algorithms describing the relationships between environmental factors and certain plant traits, FIGS identifies the best subsets of accessions most likely to exhibit the desired traits. FIGS is an alternative to the establishment of core collections, and has demonstrated its usefulness in identifying sources of resistance to major diseases and insects, and tolerance to drought and salinity (Mackey and Street, 2004; Street *et al*., 2008; El-Bouhssini *et al*., 2009, 2010; Endresen *et al*., 2011, 2012). Allelic variation can be identified using molecular markers through eco-TILLING;

– proper evaluation of *Aegilops* and wild *Triticum* collections for adaptive traits prior to their use in interspecific crosses. Selecting accessions from different origins could lead to novel genes for a given trait. Feedback of crossing and evaluation information into the database is critical to the effective use of genetic diversity conserved in genebanks;

– development of strong pre-breeding activities to enable broadening of genetic diversity of wheat and the development of adapted parental germplasm from intergeneric and interspecific crosses.

Proposed Strategic Initiatives

In view of the above review and survey of wheat genetic resources, it is suggested that ICARDA, CIMMYT and WGRC under the auspices of GCBT and in consultation with other Gene Banks and research organizations should take a lead in the conservation and utilization of Wheat CRWs.

This plan should be modeled on the ongoing WGRC and ICARDA CIMMYT programs in CRWs:

– establish working collections for all wheat CRWs where all organizations and/or individuals holding significant and unique wheat wild species collections will contribute to the working collection. Only those collections should be accepted for which precise and accurate passport data on collection sites is available;

– genotype the working collection by GBS (genotyping by sequencing) for identifying centers of genetic diversity and detecting duplicate collections to establish world's unique working collection for each species;

– perform phenotyping of unique working collections for abiotic and biotic stress, morphological, physiological, nutritional and quality traits by tapping a team of researchers drawn from world centers of wheat research. Identify hotspots of genetic diversity for each phenotypic trait and overlay with genotypic data;

– based on this data together with the many types of data discussed earlier, determine the needs and goals of *in situ* and *ex situ* conservation research;

– establish a value chain from nature to nurture for the benefit of the custodians of genetic diversity and those who profit from it.

References

Amri AM, Monzer A, Al-Oqla N, Atawneh A, Shehahdeh and Konopka J (2005). Status and Threats to Crop Wild Relatives in Selected Natural Habitats in West Asia Region. Proceedings of the International Conference on: "Promoting Community-driven Conservation and Sustainable Use of Dryland Agrobiodiversity", ICARDA, Aleppo, Syria, 18-21 April 2005.

Anikster Y, Feldman M and Horovitz A (1997). The Ammiad experiment. *In*: Maxted N, Ford-Lloyd BV and Hawkes JG (eds). *Plant Genetic Conservation: The in situ Approach*. London: Chapman & Hall, pp. 239-253.

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

Barkworth M and Jacobs S (2011). The Triticeae (Poaceae) in Australasia. *Telopea* **13**(1-2): 37-56.

Bowden WM (1959). The taxonomy and nomenclature of the wheats, barleys, and ryes and their wild relatives. *Canadian Journal of Botany* **37**: 657-684.

Brooks TM, Bakarr MI, Boucher T, Da Fonesca GAB, Hilton-C and Hoekstra JM (2004). Coverage provided by the global protected area system: is it enough? *Bioscience* **54**: 1081-1091.

Brown TA, Jones MTK, Powell W and Allaby RG. (2008). The complex origins of domesticated crops in the Fertile Crescent. *Trends in Ecology and Evolution* **24**(2): 103-109.

CBD (2010a). Global Strategy for Plant Conservation 2011-2020. Secretariat of the Convention on Biological Diversity, Montreal, Quebec, Canada.

CBD (2010b). Strategic Plans for Biodiversity 2011-2020 and the Aichi Targets. Secretariat of the Convention on Biological Diversity, Montreal, Quebec, Canada. http://www.cbd.int/doc/strategic-plan/2011-2020/Aichi-Targets-EN.pdf [Accessed 1 January 2013].

CIMMYT (2007). Global Strategy for the *ex situ* conservation with enhanced access to wheat, rye and triticale genetic resources. International Maize and Wheat Improvement Center (CIMMYT), Mexico. http://www.croptrust.org/documents/web/Wheat-Strategy-FINAL-20Sep07.pdf. Accessed Jan 2008.

CIMMYT and ICARDA (2011). Global Alliance for Improving Food Security and the Livelihoods of the Resource-poor in the Developing World. www.wheat.org.

Clayton WD, Vorontsova MS, Harman KT, Williamson H (2006). GrassBase – The Online World Grass Flora. http://www.kew.org/data/grasses-db.html.

Convention on Biological Diversity (2002). Global strategy for plant conservation. Secretariat of the Convention on Bilogical Diversity, Montreal, Quebec, Canada.

Damania AB (1990). Evaluation and documentation of genetic resources in cereals. *Advances in Agronomy* **44**: 87-111.

Damania AB (1994). *In situ* conservation of biodiversity of wild progenitors of cereal crops in the Near East. *Biodiversity Letters* **2**: 56-60.

Damania AB, Slageren M, Nikpour M, Khaghani N, Soltani A and Lessani N (1993). Collecting genetic resources of wheat and barley in Iran. *Plant Genet. Resour. Newsl.* **96**: 39-44.

Dewey DR (1984). The genomic system of classification as a guide to intergeneric hybridization in the perennial Triticeae. *In*: Gustafson JP (ed). Gene manipulation in plant improvement, New York, USA, Plenum Press, pp. 209-279.

Dvorak J, Luo MC and Yang ZL (1998). Genetic evidence on the origin of *Triticum aestivum* L. *In*: Damania AB, Valkoun J, Willcox G and Qualset CO (eds). *The Origins of Agriculture and Crop Domestication*. Aleppo, Syria: ICARDA, pp. 235-251.

Eckardt NA (2010). Evolution of Domesticated Bread Wheat. *Plant Cell* **22**: 993; http://www.plantcell.org/content/22/4/993.full.html#ref-list-1.

El-Bouhssini M, Street K, Amri A, Mackay M, Ogbonnaya FC, Omran A, Abdalla O, Baum M, Dabbous A and Rihawi F (2010).

Sources of resistance in bread wheat to Russian wheat aphid (*Diuraphis noxia*) in Syria identified using the Focused Identification of Germplasm Strategy (FIGS). *Plant Breeding* **130**: 96-97.

El-Bouhssini M, Street K, Joubi A, Ibrahim Z and Rihawi F (2009). Sources of wheat resistance to Sunn pest, *Eurygaster integriceps* Puton, in Syria. *Genetic Resources and Crop Evolution* **56**(8): 1065-1069.

Endresen DTF, Street K, Mackay M, Bari A and De Pauw E (2011). Predictive association between biotic stress traits and ecogeographic data for wheat and barley landraces. *Crop Science* **51**: 2036-2055.

Endresen DTF, Street K, Mackay M, Bari A, Amri A, De Pauw E, Nazari K and Yahyaoui A (2012). Sources of resistance to stem rust (Ug99) in bread wheat and durum wheat identified using focused identification of germplasm strategy. *Crop Science* **52**(2): 764-773. DOI: 10.2135/cropsci 2011.08.0427.

Ertug Firat A and Tan A (1997). *In situ* conservation of genetic diversity in Turkey. *In*: Maxted N, Ford-Lloyd BV and Hawkes JG (eds). *Plant Genetic Conservation: the* In Situ *Approach*. London: Chapman and Hall, pp. 254-262.

FAO (1983). Commission on plant genetic resources. Resolution 8/83 of the 22nd session of the FAO conference. Rome.

FAO (2007). FAOSTAT. Food and Agriculture Organization of the United Nations. http://www.faostat.fao.org.

FAO (2008). Climate Change and Biodiversity for Food and Agriculture. Rome, Italy: Food and Agriculture Organization of the United Nations.

FAO (2011). Global Plan of Action for the Conservation and Sustainable Utilization of PGRFA. Rome, Italy: Food and Agriculture Organization of the United Nations.

FAO (2012). FAO Integrated Food Security Support Service. Rome, Italy: Food and Agriculture Organization of the United Nations.

FAO (2012). The State of the World's Plant Genetic Resources for Food and Agriculture. Second report, Rome, Italy: Food and Agriculture Organization of the United Nations.

FAO (2013). Towards the establishment of a global network for in situ conservation and on-farm management of PGRFA. Report of Technical Workshop held in Rome, Italy 13th November, 2012. Food and Agriculture Organisation of the UN, Rome Italy. Available at: http://www.fao.org/agriculture/crops/core-themes/theme/seeds-pgr/itwg/6th/technical-workshop/en.

FAO-ITPGRFA (2001). International Treaty on Plant Genetic Resources for Food and Agriculture.

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

Frankel OH (1977). Genetic resources. The genetic basis of epidemics in agriculture. *Annals of NY Academy of Science* **287**: 332-344. DOI:10.111/j.1749-6632.1977.tb34251.x.

GCDT (2011). $50 million pledge for climate change adaptation. Global Crop Diversity Trust, Rome, Italy. Available at: www.croptrust.org/main/index.php?itemid=908 (accessed 1 January 2013).

GENESYS. Gateway to Genetic Resources: http://www.genesys-pgr.org/ (accessed 10/01/2014).

Gill BS, Freibe B, Raupp WJ, Wilson DW, Cox TS, Sears RG, Brown-Guedira GK and Fritz AK (2006). Wheat Genetics Resource Center: the First 25 years. *Advances in Agronomy* **89**: 73-136.

Goncharov NP, Golovnina KA, Kilian B and Glushkov S (2008). Evolutionary history of wheats-the main cereal of mankind. In: Dobretsov N *et al*. (eds). *Biosphere Origin and Evolution*. Springer, pp. 407-419.

GRIN Taxonomy: http://www.ars-grin.gov/cgi-bin/npgs/html/taxgenform.pl (accessed 10/01/2014).

Hammer K, Matzk F (1993). Variation in breeding systems in the Triticeae. *In*: Damania AB (ed). *Biodiversity and Wheat Improvement*. ICARDA, Wiley.

Harlan JR and De Wet JMJ (1971). Toward a rational classification of cultivated plants. *Taxon*. **20**: 511-514.

Harlan JR, De Wet JMJ and Price EG (1973). Comparative evolution of cereals. *Evolution; International Journal of Organic Evolution* **27**: 311-325.

Hedge SG, Valkoun J and Waines JG (2002). Genetic diversity in wild and weedy *Aegilops*, *Amblyopyrum* and *Secale* species – preliminary survey. *Crop Science* **42**: 608-614.

Heywood VH, Kell SP and Maxted N (2008). Towards a global strategy for the conservation and use of crop wild relatives. *In*: Maxted N, Ford-Lloyd BV, Kell SP, Iriondo J, Dulloo E and Turok J. (eds.). Crop Wild Relative Conservation and Use, CAB International, Wallingford, pp. 653-662.

Hijmans RJ, Guarino L, Jarvis A, O'Brien R, Mathur P, Bussink C, Cruz M, Barrantes I and Rojas E (2005). DIVA-GIS version 5.2 Manual. Accessed at www.diva-gis.org.

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

IPK Gatersleben: http://www.ipk-gatersleben.de/en/resources/genebank-information-system/ (accessed 10/01/2014).

Iriondo JM, Maxted N, Kell SP, Ford-Lloyd BV, Lara-Romero C, Labokas J and Magos Brehm J (2012). Quality standards for genetic reserve conservation of crop wild relatives. *In*: Maxted N, Dulloo ME, Ford-Lloyd BV, Frese L, Iriondo JM and Pinheiro de Carvalho MAA (eds). *Agrobiodiversity Conservation: Securing the Diversity of Crop Wild Relatives and Landraces*. CAB International, Wallingford, pp. 72-77.

Kaplan D (2008). A designated nature reserve for *in situ* conservation of wild emmer wheat (*Triticum dicoccoides* Korn.). *In*: Maxted *et al*. Crop wild relatives conservation and use book. ISBN 978-1-84593-307-4 (ebook).

Karagoz A (1998). *In situ* conservation of plant genetic resources in the Ceylanpinar State Farm. *In*: Zencirci N, Kaya Z, Anikster Y and Adams WT (eds). The Proceedings of International Symposium on *in situ* Conservation of Plant Diversity. Ankara, Turkey: Central Research Institute for Field Crops, pp. 87-91.

Kilian B, Mammen K, Millet E, Sharma R, Graner A, Salamini F, Hammer K, Ozkan H (2011). *Aegilops*. Chapter 1. *In*: Kole C (ed.). *Wild Crop Relatives: Genomic and Breeding Resources. Cereals*. Springer.

Kimber G and Feldman M (1987). *Wild Wheat. An Introduction*. Coll. Agric. Univ. Missouri-Columbia, Spec. Rep. 353, pp. 129-131.

Kimber G and Sears ER (1987). Evolution in the genus Triticum and the origin of cultivated wheat. *In*: Heyne EG (ed). *Wheat and wheat improvement*, 2nd ed. American Society of Agronomy, Madison, WI, pp. 154-164.

Knüpffer H (2009). *Triticeae* genetic resources in *ex situ* genebank collections. *In*: Feuillet C and Muehlbauer G (eds). *Genetics and Genomics of the* Triticeae. *Plant Genetics and Genomics: Crops and Models* **7**. London: Springer, pp. 31-79.

Lage J, Warburton ML, Crossa J, Skovmand B and Anderson SB (2003). Assessment of genetic diversity in synthetic hexaploid wheats and their *Triticum dicoccum* and *Aegilops tauschii* parents using AFLP's and agronomic traits. *Euphytica* **134**: 305-317.

Linnaeus C (1753). *Species plantarum* (ed. 1) **2**(996): 1050-1051.

Mac Key M (1966). Species relationship in *Triticum*. *In*: MacKey JH (ed). Second Int. Wheat Gene. Symp. *Hereditas (suppl)* **2**: 237-275.

Mackay MC and Street K (2004). Focused identification of germplasm strategy – FIGS. *In*: Black CK, Panozzo JF, Rebetzke GJ (eds..) Proceedings of the 54th Australian Cereal Chemistry Conference and the 11th Wheat Breeders' Assembly. Royal Australian Chemical Institute, Melbourne, Australia, pp. 138-141.

Manners GR and Slageren MW (1998). Research and Production: Cereal Taxonomy Used in Rachis. *Rachis* **17**(1-2): 1-6.

Margules CR and Pressey RL (2000). Systematic conservation planning. *Nature* **405**: 243-253.

Maxted N and Kell SP (2009). Establishment of a Global Network for the *In Situ* Conservation of Crop Wild Relatives: Status and Needs. FAO Commission on Genetic Resources for Food and Agriculture, Rome, Italy, 266 p.

Maxted N, Dulloo E, Ford-Lloyd BV, Iriondo JM and Jarvis A (2008a). Gap analysis: a tool for complementary genetic conservation assessment. *Diversity and Distributions* **14**: 1018-1030.

Maxted N, White K, Valkoun J, Konopka J and Hargreaves S (2008b). Towards a conservation strategy for *Aegilops* species. *Plant Genetic Resources* **6**: 126-141.

Meilleur BA and Hodgkin T (2004). *In situ* conservation of crop wild relatives: status and trends. *Biodiversity and Conservation* **13**: 663-684.

Monneveux P, Zaharieva M, Rekika D, Royo C, Nachit MM, Fonzo ND and Araus JL (2000). The utilisation of *Triticum* and *Aegilops* species for the improvement of durum wheat. *Options Méditerranéennes. Serie A, Séminaires Méditerraneens* **XX**: 71-81.

Mujeab-Kazi A (1993). Interspecific and intergeneric hybridization in the Triticeae for wheat improvement. *In*: Damania AB (ed). *Biodiversity and Wheat Improvement*, John Wiley and Sons, Chichester, UK, pp. 95-102.

Mujeeb-Kazi A, Gul A, Farook M, Rizwan S and Ahmad I (2008). Rebirth of synthetic hexaploids with global implications for wheat improvement. *Australian Journal of Agricultural Research* **59**: 391-398.

Ogbonnaya FC, Imtiaz M, Bariana HS, McLean M, Shankar M, Hollaway JJ, Trethowan R, Lagudah ES and van Ginkel M (2008). Mining synthetic hexaploids for multiple disease resistance to improve wheat. *Aust. J. Agric. Res.* **59**:421-431.

Ozkan *et al*. (2002). AFLP analysis of a collection of tetraploid wheats indicates the origin of emmer and hard wheat in southeast Turkey. *Mol. Biol. Evol.* **19**: 1797-1801.

Peng JH, Sun D and Nevo E (2011). Domestication evolution, genetics and genomics in wheat. *Mol Breeding* **28**: 281-301. DOI 10.1007/s11032-011-9608-4.

Planta Europa (2008). A Sustainable Future for Europe; the European Strategy for Plant Conservation 2008-2014. Plantlife International (Salisbury, UK) and the Council of Europe (Strasbourg, France).

Rajaram S (2000). International wheat breeding: past and present achievements and future directions. Warren E. Kronstad Symposium. Oregon State University Special Report 1017.

Rajaram S, Mann CE, Ortiz-Ferrara G and Mujeeb-Kazi A (1983). Adaptation, stability, and high yield potential of certain 1B/1R CIMMYT wheats. *In*: SaSakamoto S (ed). Proc. 6th Int. Wheat Genetics Symp., Kyoto, Japan, 28 Nov-3 Dec, p. 613-621.

Rebelo AG (1994). Iterative selection procedures: centres of endemism and optimal placement of reserves. *Strelitzia* **1**: 231-257.

Rebelo AG and Siegfried WR (1992). Where should nature reserves be located in the Cape Floristic Region, South Africa? Models for the spatial configuration of a reserve network aimed at maximizing the protection of floral diversity. *Conservation Biology* **6**: 243-252.

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

Rosegrant MW and Agcaoili M (2010). Global food demand, supply, and price prospects to 2010. International Food Policy Research Institute, Washington, D.C. USA.

Simon BK, Clayton WD, Harman KT, Vorontsova M, Brake I, Healy D, Alfonso Y (2011). GrassWorld, http://grassworld.myspecies.info/ (accessed 11/01/2014).

Skovmand B, Rajaram S, Ribaut JM and Hede AR (2006). Wheat genetic resources. http://www.fao.org//docrep/006/y4011e/y4011e08.htm. pp: 1-16.

Street K, Mackay M, Zuev E, Kaur N, El Bouhssini M, Konopka J and Mitrofanova O (2008). Diving into the genepool: a rational system to access specific traits from large germplasm collections. *In*: Appels R, Eastwood R, Lagudah E, Langridge P, Mackay M (eds). Proceedings of the 11th International Wheat Genetics Symposium: Brisbane, Australia), pp. 28-31.

Trethowan RM and van Ginkel M (2009). Synthetic Wheat – an Emerging Genetic Resource. *In*: Carver B (ed). *Wheat Science and Trade, Section III: Making of a Wheat Cultivar.* Chapter 16, Wiley-Blackwell, pp. 369-385.

van Ginkel M and Ogbonnaya FC (2007). Novel genetic diversity from synthetic wheats in breeding cultivars for changing production conditions. *Field Crops Research* **104**: 86-94.

Van Slageren MW (1994). Wild Wheats: A Monograph of *Aegilops* L. and *Amblyopyrum* (Jaub. & Spach) Eig (Poaceae). Wageningen, The Netherlands: Wageningen Agricultural University.

Vavilov NI (1951). Phytogeographic basis of plant breeding. *In:* The origin, variation, immunity and breeding of cultivated plants (K.S. Chester, transl.). *Chronica Botanica* **13**: 14-54.

Vincent H, Wiersema J, Kell SP, Dobbie S, Fielder H, Castañeda Alvarez NP, Guarino L, Eastwood R, León B and Maxted N (2013). A prioritised crop wild relative inventory as a first step to help underpin global food security. *Biological Conservation* **167**: 265-275.

von Bothmer R, Seberg O and Jacobsen N (1992). Genetic resources in the Triticeae. *Hereditas* **116**: 141-150.

Waines G and Skovmand B (1996). Unpublished report to the Wheat Crop Germplasm Committee, Manhattan, KS, USA.

Witcombe JR (1983). *A Guide to the species of* Aegilops *L. Their taxonomy, morphology and distribution*. IBPGR, Rome, Italy.

Zohary D and Feldman M (1962). Hybridization between amphiploids and the evolution of polyploids in the wheat (*Aegilops-Triticum*) group. *Evolution* **16**: 44-61.

Zohary D and Hopf M (2000). *Domestication of plants in the old world. The origin and spread of cultivated plants in West Asia, Europe and the Nile Valley*, 3rd ed., Oxford University Press: New York, NY, USA, 328 p.

Internet sources

Bioversity International (2007). Bioversity Directory of Germplasm Collections. http://www.bioversityinternational.org/Information_Sources/Germplasm_Databases/Gerplasm_Collection_Directory/index.asp.

CBD (2006). Homepage of the Convention on Biological Diversity. www.biodiv.org.

CIMMYT (2007). Global Strategy for the *ex situ* conservation with enhanced access to wheat, rye and triticale genetic resources. International Maize and Wheat Improvement Center (CIMMYT), Mexico. http://www.croptrust.org/documents/web/Wheat-Strategy-FINAL-20Sep07.pdf.

DIVA (2006). Homepage of DIVA-GIS mapping program providing a downloadable version of the DIVA GIS program, additional materials and data. Accessed throughout the project. www.diva-gis.org.

EURISCO (2006). EURISCO web catalogue providing access to all the *ex situ* plant genetic resources information in Europe. Site hosted and maintained by Bioversity International on behalf of the Secretariat of the ECP/GR (European Cooperative Programme for Crop Genetic Resources Networks. http://eurisco.ecpgr.org/index.php.

FAO-SoWPGRFA (2011). Report on the State of the World's Plant Genetic Resources for Food and Agriculture. Food and Agriculture Organization of the United Nations, Rome, Italy. www.fao.org/AG/AGp/agps/Pgrfa/pdf/swrshr_e.pdf.

FAO-WIEWS (2007). World Information and Early Warning System. http://apps3.fao.org/wiews/institute_query.htm.

GBIF (2008). Global Biodiversity Information Facility Data Portal. http://www.gbif.net.

GENESYS (2011). Accession Level Information System. www.genesys-pgr.org.

GRIN (2006). Homepage of the USDA, ARS, National Genetic Resources Program. *Germplasm Resources Information Network - (GRIN)* [Online Database]. National Germplasm Resources Laboratory, Beltsville, Maryland. Accessed throughout the project – Data downloaded in July 2006. http://www.ars-grin.gov/cgi-bin/npgs/html/index.pl.

GRIN-Taxonomic Nomenclature Checker. http://pgrdoc.bioversity.cgiar.org/taxcheck/grin index.html.

ICARDA (2012). Global database of wheat wild relatives. Available at ICARDA-Genetic Resources Unit.

Plant List (Kew, Missouri Botanical Garden). www.theplantlist.org (accessed 11/01/2014).

SINGER (2006). Homepage for the System-wide Information Network for Genetic Resources (SINGER), which is an information exchange network for plant genetic resources. http://singer.grinfo.net/ (Replaced by GENESYS in 2012).

Thomas Marcussen, Simen R. Sandve, Lise Heier, Manuel Spannagl, Matthias Pfeifer, The International Wheat Genome Sequencing Consortium,† Kjetill S Jakobsen, Brande B H Wulff, Burkhard Steuernagel, Klaus F X Mayer, Odd-Arne Olsen (2014). Ancient hybridizations among the ancestral genomes of bread wheat. *Science* 345, Read the full article at http://dx.doi.org/10.1126/science.1250092.

WDPA (2006). World Database on Protected Areas providing a dataset on protected areas worldwide. This site is managed by UNEP-WCMC in partnership with the IUCN World Commission on Protected Ares (WCPA) and the World Database on Protected Areas Consortium. www.unep-wcmc.org/wdpa.