Evaluation of Diversity in Wild Relatives of Wheat

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Abstract: Wild relatives of common wheat, *Triticum aestivum* L, are potential sources of valuable genetic materials for wheat improvement. In the center of origin of wheat, the Fertile Crescent, diploid and polyploid wheat species exhibit huge morphological and ecological diversity. Iran constitutes a part of this center, where the first cereals were domesticated. A collection of twenty-four *Triticum* and *Aegilops* accessions belonging to four diploid (*T. monococcum*, *Ae. umbellulata*, *Ae. caudata* and *Ae. squarrosa*), five tetraploid (*T. dicoccoides, T. dicoccum, Ae. crassa* (4*x*), *Ae. cylindrica, Ae. triuncialis*) and two hexaploid (*T. compactum*, *Ae. crassa* (6*x*)) species and sampled from different eco-geographical regions of Iran were evaluated for diversity in morphological and agronomical characters. Four synthetic hexaploid wheat lines provided by CIMMYT, a durum wheat cultivar, and two bread wheat cultivars were also included in this study. Morphological diversity was analyzed using a set of twenty five qualitative and quantitative characters. Cluster analysis of qualitative traits of the 31 genotypes using the Dice coefficient followed by UPGMA algorithm revealed three major clusters having 11, 16 and 4 genotypes, respectively. Considerable variation was observed between species for qualitative characters and inter- and intraspecific variation for quantitative traits were significantly different.

Keywords: wild wheat; *Aegilops*; diversity; clusters; Iran

By 2020, the world demand for wheat will be 40% greater than it is today. There is growing concern among wheat breeders that the remaining variability in the bread wheat gene pool and the secondary gene pool of wheat is grossly inadequate for current and future breeding objectives (Rejesus *et al.* 1996; Braun *et al.* 1998). It is therefore necessary to broaden the genetic base of wheat. Germplasm accessions most distinct from modern cultivars are predicted to contain the highest number of unexploited potentially useful alleles (Vavilov 1940). The wild relatives of bread wheat, *Triticum aestivum* L., are considered as potential sources of useful alleles for bread-wheat improvement. The genus *Aegilops* L. and *Triticum* L. have contributed two (B and D) and one (A) of the three bread wheat genomes, respectively.

Modern bread wheat is a true breeding hybrid with its ancestry linked to three wild grass species still growing in the Middle East. Bread wheat first originated in the Fertile Crescent, an area in the Middle East, which stretches from Palestine and Lebanon into Syria, Turkey, Iraq and Iran. Diploid einkom types of wheat are the earliest and the most primitive, while the hexaploids including bread wheat, *Triticum aestivum,* constitute the most recent and latest step in the evolution of the wheat complex. Thousands of years ago, the first hybridization event is thought to have occurred when the wild grass *Aegilops speltoides* crossed with the wild diploid wheat, *Triticum monococcum.* The resultant hybrid was the tetraploid emmer wheat, *Triticum dicoccum.* Domestication of emmer wheat led to the evolution of the durum wheat. Hybridization of tetraploid durum wheat, *Triticum turgidum* var. *durum* (2*n* = 28, AABB) with the diploid wild goat grass, *Aegilops tauschii,* led to the origin and evolution of hexaploid wheat about 8000 years ago. Bread wheat is thus an allohexaploid, containing three distinct but genetically related (homoeologous) copies each of the three originally independent haploid genomes, the A, B and D (GILL & GILL 1994). With the evolution of wheat, civilizations thrived and spread from the Middle East to new continents, resulting in massive wheat production feeding the growing world population. The tribe *Triticeae* comprising of over 300 species including wheat, rye and barley is considered as germplasm source for wheat improvement by classical breeding approaches.

The pattern of genetic variation in farmers' wheat fields has undoubtedly changed over past 100 years with increasing cultivation of varieties released by plant breeding programs, but the implications of these changes for the security of useful genetic resources are significant. Amphiploids from interspecific crosses between tetraploid wheats and *Aegilops* species, as their close relatives, are useful bridging germplasm for introduction of desirable alien characters to bread wheats (MCINTOSH 1991; FRIEBE *et al.* 1996). Hence, there have been several collecting trips for these resources, e.g. KIHARA *et al.* (1965), HALLORAN (1968) and ZOHARY *et al.* (1969). Accessions of *Ae. squarrosa,* particularly those from Iran, have already proved a diverse genetic storehouse of potentially useful characteristics for incorporation into modern wheat cultivars (LAGUDAH *et al.* 1993). Likewise, THOMPSON and HAAK (1997) reported that 30 accessions from 39 accessions of *Ae. squarrosa* were observed to be resistant to root-lesion nematode (*Pratylenchus thornei*) originated from Iran. Two successful approaches were used to efficiently introgress desirable genes from *Ae. squarrosa* to bread wheat. These were direct crossing (LANGUDA *et al.* 1993) and via synthetic hexaploid wheat derived from *T. turgidum* × *Ae. squarrosa* (LAGUDAH *et al.* 1993).

Iran is located in an area, which is the center of origin for many crop plants. Furthermore, Iran is very rich in habitat diversity due to the diversity in its geomorphology, topography and climate. This has helped the survival of diverse plant species in the wild. Amongst the Iranian flora, there are some of the most important food crops such as wheat and its wild relatives. Wild relatives of common wheat, *Triticum aestivum* L., and durum wheat, *T. turgidum* L. var *durum*, are valuable sources of desirable characters for improving wheat cultivars. SKOVMAND *et al*. (2002) stated that although many landraces of wheats were collected in Iran and were available, wild wheat and *Aegilops* from Iran are still largely uncollected and unknown. One accession of *Triticum urartu*, the A-genome donor to durum and bread wheat, collected from the mountains near Isfahan and one collection from the mountains near Shiraz are maintained in USDA collection. According to SKOVEMAND *et al.* (2002) the mountainous area between Kermanshah, Isfahan and Shiraz needs to be collected for *Ae. speltoides*, *T. urartu*, *T. monococcum* ssp. *aegilopoides*, *T. turgidum* ssp. *dicoccoides* and *T. timopheevii* ssp. *armeniacum*, as well as other species of *Aegilops*. They also declared that how far wild wheats extend south of Shiraz is not known. In the Iranian desert, east of the Zagros Mountains, there are drought-tolerant and salt-tolerant goat grasses that have been little collected. Another promising area is the mountain chain that runs from Isfahan to Bam (SKOVMAND *et al*. 2002).

Identification and description of the genetic variability available in germplasm collections are the basis of improved plans designed to control genetic erosion; they are also a preliminary requirement for the exploitation of useful traits in plant breeding. This study was undertaken to evaluate the genetic diversity of 24 *Triticum* and *Aegilops* accessions collected from different regions in Iran.

MATERIALS AND METHODS

Diversity evaluation

A collection of twenty-five *Triticum* and *Aegilops* accessions belonging to four diploid (*T. monococcum, Ae. umbellulata, Ae. caudata* and *Ae. squarrosa*), five tetraploid (*T. dicoccoides, T. dicoccum, Ae. crassa* (4*x*), *Ae. cylindrica, Ae. triuncialis*) and two hexaploid (*T. compactum, Ae. crassa* (6*x*)) species and sampled from different eco-geographical regions of Iran was evaluated for morphological and agronomical characters (Table 1). Four synthetic hexaploid wheat lines provided by CIMMYT, a durum wheat cultivar and two bread wheat cultivars were also used in this study (Table 1). Morphological diversity was analyzed using a set of twenty five qualitative and quantitative characters, determined by preliminary visual

Table 1. Wild wheat relatives (*Triticum* and *Aegilops* accessions), synthetic wheat lines, durum and bread wheat cultivars used for diversity study

Species	Genome	Growing status	Location	Origin
T. monococcum var. *boeoticum*(1)	A	Wild	Semirom-Isfahan	Central Iran
T. monococcum var. *boeoticum* (2)	A	Wild	Kohkiloye-Boyerahmad	SW Iran
T. monococcum var. *boeoticum* (3)	A	Wild	Lorestan	West Iran
T. monococcum var. *boeoticum* (4)	A	Wild	Shirvancherdavel Ilam	West Iran
T. monococcum var. *boeoticum* (5)	A	Wild	Khoramabad Lorestan	West Iran
T. monococcum var. *boeoticum* (6)	A	Wild	Karaj Tehran	Iran
T. monococcum var. *boeoticum* (7)	A	Wild	Piranshahr Kordestan	West Iran
T. monococcum (1)	A	Wild	Shirvancherd-Ilam	West Iran
T. monococcum (2)	A	Wild	Shirvancherd-Ilam	West Iran
T. monococcum (3)	A	Wild	Lorestan	West Iran
T. monococcum (4)	A	Wild	Kermanshah	West Iran
T. dicoccoides	AB	Wild	Semirom-Isfahan	Central Iran
T. dicoccum	AB	Wild	West Azerbaijan	NW Iran
T. compactum	ABD	Wild	Maco-Azerbaijan	NW Iran
Ae. squarrosa	D	Wild	Ilam-Ilam	West Iran
Ae. crassa (6*x*)	DDM	Wild	Ilam-Ilam	West Iran
Ae. crassa (mixoploid, 4*x* & 6*x)*	DM-DDM	Wild	Ilam-Ilam	West Iran
Ae. crassa (4×)	DM	Wild	Ilam-Ilam	West Iran
Ae. glabra		Wild	Ilam-Ilam	West Iran
Ae. umbellulata	U	Wild	Ilam-Ilam	West Iran
Ae. caudata	C	Wild	Ilam-Ilam	West Iran
Ae. cylindrica	CD	Wild	Ilam-Ilam	West Iran
Ae. triuncialis (1)	UC	Wild	Ivan- Ilam	West Iran
Ae. triuncialis (2)	UC	Wild	Ilam-Ilam	West Iran
Altar84/*Ae. squarrosa* (219)	ABD	Syn.wheat	Genetic Resources	CIMMYT
Croc 1/*Ae. squarrosa* (879)	ABD	Syn.wheat	Genetic Resources	CIMMYT
Yar/*Ae. squarrosa* (783)	ABD	Syn.wheat	Genetic Resources	CIMMYT
Srn/*Ae. squarrosa* (358)	ABD	Syn.wheat	Genetic Resources	CIMMYT
T. durum cv. Langdon	AB	Durum wheat	Genetic Resources	CIMMYT
T. aestivum cv. Chinese spring	ABD	Bread wheat	Genetic Resource	CIMMYT
T. aestivum cv. Roshan	ABD	Bread wheat	Isfahan	Iran

examination of the collections. They were easy to score, appeared to vary between the accessions and made an obvious contribution to the plant phenotype. These comprised hairy leaf, hairy node, leaf color, leaf waxiness, leaf tip necrosis, leaf base color, pubescence, culm color, hairy flag leaf, glume shape (elongated), glume color, hairy glume, hairy peduncle, branched spike, hairy spike neck, anther color, grain color, awn color, hairy awn, plant height, days to jointing, days to heading, glume length, awn length, flag leaf length.

Numerical analysis

The binary data from qualitative traits were used. The data matrix was analyzed with NTSYS computer package (version 1.50) (Rohlf 1989). The Dice

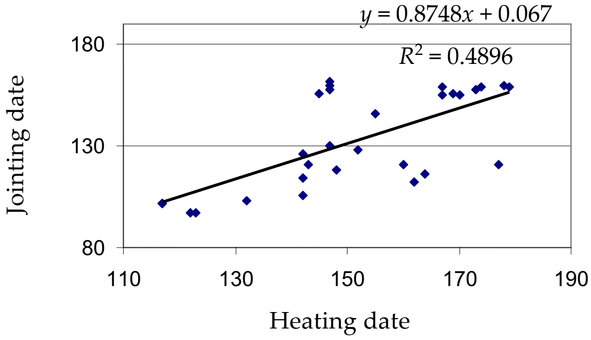

Figure 1. Relationship between heading date and jointing date measured on 31 used wheat genotypes

similarity index (Nei & Li 1979) and the unweighted pair group method (UPGMA) (Sneath & Snokal 1973) were combined to construct a dendogram for qualitative traits.

Cluster analysis was also used to classify 31 wheat genotypes of wheat based on Jaccard's similarity coefficient (Jaccard 1908) and Ward's clustering method (Ward 1963) for quantitative traits.

RESULTS AND DISCUSSION

Accessions belonging to both *Triticum* and *Aegilops* species proved to be highly variable for many characters. Considerable variation was observed between species for qualitative characters including hairy leaf, hairy node, leaf color, leaf waxiness, leaf tip necrosis, leaf base color, stem color, culm color, hairy flag leaf, glume (elongated), glume color, hairy glume, hairy peduncle, branched spike, hairy spike neck, anther color, grain color, awn color, hairy awn. However, all accessions had green leaf base color with the exception of *Ae. cylindrica* which had a purple color of leaf base. Comparison of phenological stages of the studied species indicated that *Ae. crassa* is early-jointing and early-heading type while *T. monococcum* is late-jointing and late heading type. Earliness could represent an important trait of adaptation, supporting plant survival and reproduction under drought and heat stress. Inter-and intraspecific variations for leaf color were observed. Leaf color has been invoked as an important trait in heat avoidance. It was postulated that pale leaf color is likely to be a passive adaptation to high light intensities (Aase 1971). Low chlorophyll content would limit the heating effects of storing light by decreasing the light absorptance of the leaf. *Triticum dicoccum* possessed the highest flag leaf length and *Ae. glabra* and *Ae. umbellulata* had the lowest flag leaf lengths among the studied wild wheat species.

The relationship between jointing date and heading date was assessed using data from all wheat genotypes and presented in Figure 1. Positive relationship with highly significant correlation ($r = 0.70$) was observed between jointing date and heading date in this study. Positive relationship with relatively small correlation ($r = 0.34$) was observed between flag leaf length and awn length (Figure 2).

The highest awn length belonged to *T. dicoccoides* and the lowest one belonged to both *Ae. glabra* and *Ae. umbellulata*. One accession (accession 2) of *Ae. triuncialis* had the longest spike length while its lowest value belonged to both *Ae. glabra* and *Ae. umbellulata*. Accession 3 of *T. monococcum* var. *boeoticum* possessed the highest glume length while *Ae. glabra* and *Ae. umbellulata* had the lowest length among the wild wheat species.

Cluster analysis of wheat genotypes based on qualitative traits using the Dice coefficient fol-

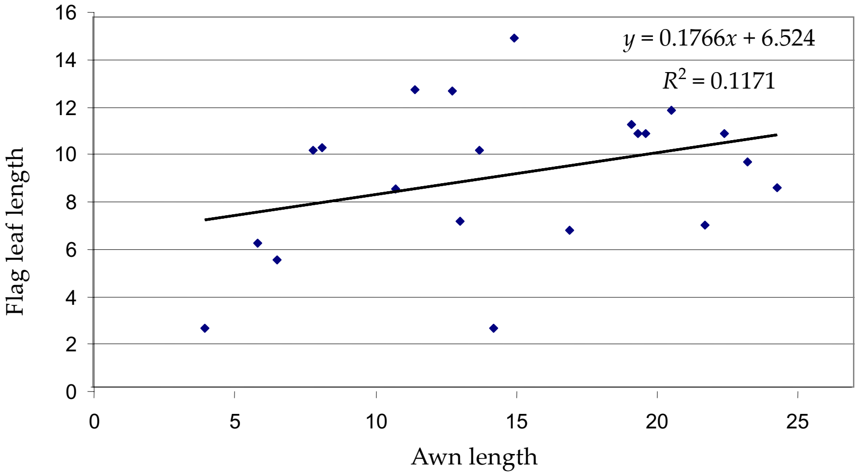

Figure 2. Relationship between flag leaf length and awn length using most of the wheat genotypes

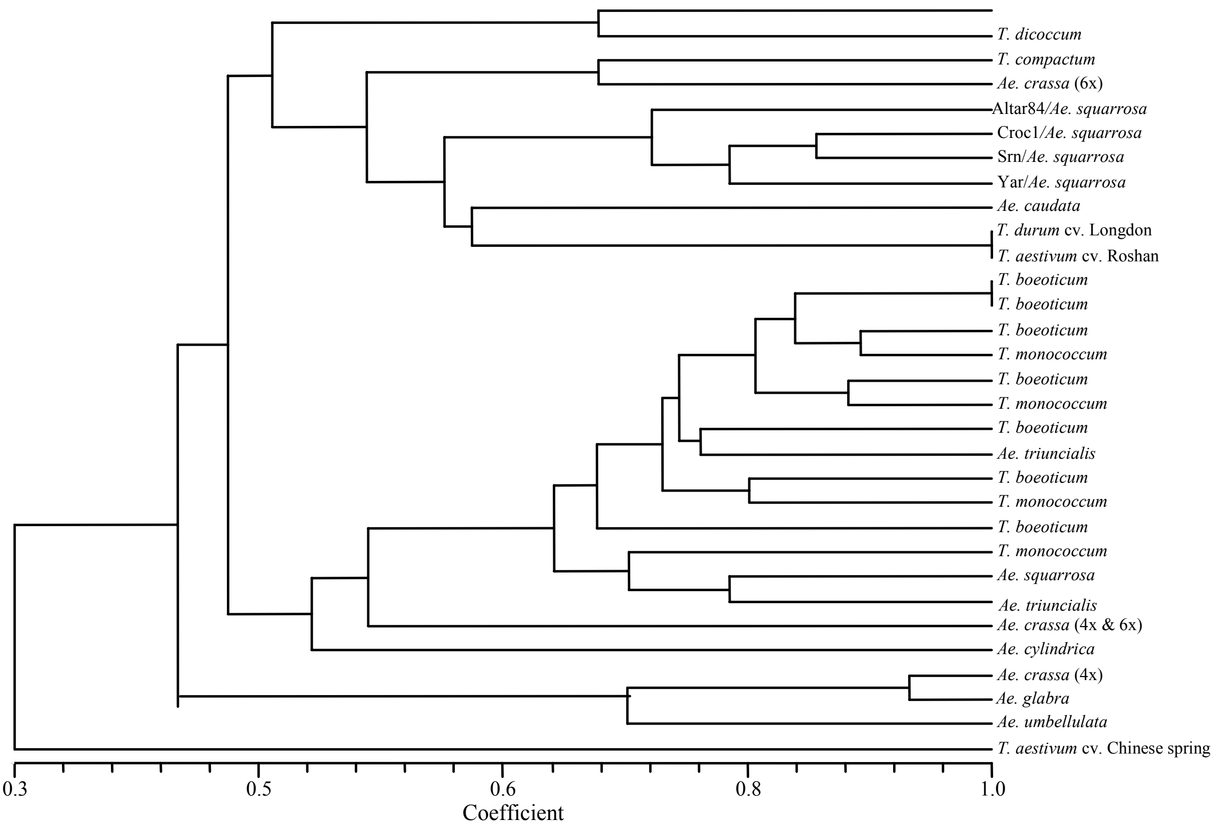

Figure 3. Dendrogram of 31 wheat genotypes (wild accessions, synthetic and cultivated wheats) constructed for 19 qualitative traits using UPGMA clustering based on Dice's similarity coefficients

lowed by UPGMA algorithm revealed three major clusters having 11, 16 and 4 genotypes, respectively (Figure 3). The first cluster comprised *T. dicoccoides, T. dicoccum, T. compactum, Ae. crassa* (6*x*), *Ae. caudate,* four synthetic wheats, *T. durum* cv. Longdon and *T. aestivum* cv. Roshan. Seven *T. monococcum* var. *boeoticum* accessions, four *T. monococcum* accessions, two accessions of *Ae. triuncialis, Ae. cylindrica, Ae. squarrosa, Ae. crassa* (4*x* & 6*x*) belonged to second cluster. The third cluster comprised the four remaining genotypes which included *Ae. crassa* (4*x*), *Ae. glabra, Ae. umbellulata* and *T. aestivum* cv. Chinese spring.

The Ward's Dendrogram obtained from quantitative data failed to discriminate among wheat accessions (data not shown). This may be due to using relatively small number of the quantitative traits in this study.

Wild relatives of common wheat, *Triticum aestivum* L., and durum wheat, *T. turgidum* L. var *durum,* are the valuable sources of desirable characters for improving wheat cultivars. Since the genus *Aegilops* L. bears a close and important relationship with durum and bread wheat, more detailed study of them should also be beneficial in understanding these polyploid wheats. Interspecific hybridization between durum wheat landraces and *Aegilops* accessions indicated that *Aegilops* parents exhibited great influence ($P < 0.001$) on crossability. Among the *Aegilops* parents both accessions of *Ae. crassa* gave the highest proportion of regenerated plants (42.1% and 37.8% embryo culturability), which were significantly superior than the others. The remaining species of *Aegilops* did not differ significantly for the regenerated plant possessing a range 14.7% to 19%. The highest direct seed set was observed in F_1 hybrids of *T. turgidum* × *Ae. crassa* (4*x*) with 97 surviving seedlings (Arzani *et al.* 2000).

In conclusion, morphological genetic diversity observed in twenty-four accessions of wild relatives of wheats, which collected from different parts of Iran, revealed that they are rich in unexploited potentially useful alleles. This concluded remark is in agreement with those of Lagudah *et al.* (1993) and Thompson and Haak (1997) who found accessions of *Ae. squarrosa* particularly those from Iran as a diverse genetic storehouse of potentially useful characteristics for incorporation into modern wheat cultivars.

Acknowledgment. This research was supported in part by Interuniversity Research Funds of Isfahan University of Technology and Shahrekord University.

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