

Morphological Characterization of Accessions of *Aegilops tauschii*

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ABSTRACT

In this study, 55 accessions of *Aegilops tauschii* were evaluated to determine phenotypic diversity among them. The accessions were subdivided into 7 gene pools according to their country of origin. Data were collected on spikelet number, peduncle length, stem length, spikelet weight, seed weight, spike length, number of fertile stem, days to 50% flowering and days to 50% maturity. First three principal components with eigenvalues more than 1 contributed 67.77% of the variability amongst accessions, whereas PC₃ to PC₉ were less than unity. The first two principal components suggested that evaluated characters are useful for distinguishing the two subspecies of *Aegilops tauschii*. The accessions of subsp. *strangulata* showed the larger dispersion than the accessions of subsp. *tauschii*. The distribution of *Ae. tauschii* accessions provided useful information for the future collection and for the genetic resource management in these regions.

Key Words: *Aegilops tauschii*; Phenotypic diversity; PCA; Gene pool; Origin sites

INTRODUCTION

Cultivated bread and durum wheat descend from hybridized wild grasses. There is extensive genetic evidence that *Aegilops tauschii* Coss. (syn. *Ae. squarrosa* L., syn. *Triticum tauschii* (Coss.) Schmal. 2n = 14, DD) is the D genome progenitor of common bread wheat (*T. aestivum* L. em. Thell., 2n = 6x = 42, AABBDD) (Kihara, 1944; McFadden & Sears, 1946).

The genus *Aegilops* contains 22 species comprising both diploids and polyploids that originated from the center of origin, in the Middle East (Van Slageren, 1994). Gene pool of *Ae. tauschii* is currently considered the most important gene resource for wheat improvement. Study of molecular variation provided evidence that all forms of hexaploid wheat share a single D-genome genepool (Dvorak *et al.*, 1998). Eig (1929) divided the *Ae. tauschii* into two subspecies named *tauschii* and *strangulata*. The D genome of *T. aestivum* was shown to be genetically most closely affiliated with the *Ae. tauschii* subsp. *strangulata* gene pool in Transcaucasia, Armenia in particular, and southwestern shore of Caspian Sea, Iran, and this geographic area is the most likely birthplace of *T. aestivum* (Dvorak *et al.*, 1998). Accessions of *Ae. tauschii* subsp. *strangulata* from Armenia and Western Caspian Iran are genetically very similar to the D genome of wheat and are structurally identical with it (Dvorak *et al.*, 1998). Lagudah and Halloran (1988) found that subsp. *strangulata* occurring only along the Caspian Sea, Iran.

The genus *Aegilops* has an important potential utilization in wheat improvement because of its resistance to different biotic and abiotic stresses and close relation with the cultivated wheat. Therefore, a better knowledge of the

eco-geographical distribution of *Aegilops* species and their collection and conservation are required (Zaharieva *et al.*, 2004). Phenotypic characters can be used to estimate the variation within and between origin sites. Hammer (1980) and Knaggs *et al.* (2000) have been studied the germplasm of *Ae. tauschii* species using morphological characters. The objectives of this research were to characterize phenotypic variation in the collection of *Ae. tauschii* and to investigate the phenotypic relationships among different origins (countries).

MATERIALS AND METHODS

Fifty five accessions of *Aegilops tauschii* were provided by the gene bank of the Agricultural college at the University of Tehran, Iran. Eighteen accessions were of the subspecies *strangulata* and 37 accessions were of the subspecies *tauschii*. The accessions evaluated were from Iran, Turkey, Azerbaijan, Tadjikistan, Turkmenistan, Afghanistan and Armenia and the origin (country) of 18 accessions is unknown (Table I). Each accession was planted in 1 m long rows with 0.5 m row spacing in experimental station of Agriculture College at the University of Tehran, Iran, during 2004. For characterization and evaluation, data were recorded following descriptors established for *Aegilops* (IBPGR, 1981) with some modifications.

Data on days to 50% flowering (days from sowing to appearance of 50% flowers), days to 50% maturity (days from sowing to appearance of first maturity) were recorded by a single value for each row. Spikelet number, peduncle length (cm), stem length (cm), spikelet weight (g), seed weight (g), spike length (cm) and number of fertile stem

Table II. Mean and standard deviation of accessions over characters

Country	Spikelet number	Peduncle length	Stem length	Spikelet weight	Seed weight	Spike length	Number of fertile stem	Days to 50% flowering	Days to 50% maturity
Iran	7.75±1.26	19.86±2.59	39.84±4.33	6.88±1.54	1.35±0.24	7.17±1.17	24.17±5.51	186.85±5.66	223.2±6.11
Turkey	7.18±0.26	18.81±0.26	36.00±2.12	6.53±1.10	1.28±0.02	6.81±0.61	21.83±0.70	180.5±0.70	213.5±0.70
Azerbaijan	6.78±0.47	21.18±1.43	43.53±3.81	7.75±2.05	1.49±0.28	6.21±0.31	20.75±8.86	190.25±2.50	227.5±5.74
Tadjikistan	7.08±0.28	22.22±6.63	43.54±4.56	8.31±3.27	1.38±0.34	6.52±0.64	27.27±3.67	189.66±3.78	227.33±5.50
Turkmenistan	6.31±0.44	24.21±1.37	43.68±4.33	8.30±1.41	1.48±0.05	5.59±0.92	23.41±0.59	190.5±0.70	231±1.41
Armenia	6.87±0.18	23.34±2.25	46.81±2.56	7.94±3.62	1.58±0.14	6.68±0.26	25.58±12.84	189.5±0.70	224.5±9.19
Afghanistan	7.00 ± 0.71	19.37 ± 6.72	41.21± 8.49	6.92± 0.86	1.45±0.10	6.26±0.94	25.54±8.36	187.7±5.12	226±7.52

Table III. Principal components (PCs) for characters in 55 accessions of *Ae. tauschii*

	PC1	PC2	PC3
Eigenvalue	2.925	1.886	1.285
Proportion of σ^2	32.49	21.00	14.28
Cumulative σ^2	32.49	53.49	67.77
Character	Eigenvector		
Spikelet number	-0.743	0.257	0.020
Peduncle length	-0.090	0.772	-0.129
Stem length	0.481	0.675	-0.020
Spikelet weight	0.701	0.208	0.451
Seed weight	0.721	0.060	0.442
Spike length	-0.657	0.521	0.178
Number of fertile stem	0.168	-0.673	-0.010
Days to 50% flowering	-0.08	-0.020	0.817
Days to 50% maturity	0.351	-0.146	0.820

been reported by Dvorak *et al.* (1998). As the unknown accessions have been dispersed in all sites, it was difficult to find their origins.

In general we found that although two subspecies of *Ae. tauschii* separated using principal component analysis, but this method couldn't group accessions according to origin sites. Differences among country gene pools as well as among entries were wide, suggesting that further selection for relevant characters could be possible.

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