International Journal of Botany

ISSN: 1811-9700

science alert

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International Journal of Botany 4 (3): 260-268, 2008
ISSN 1811-9700

Chemotaxonomy of Wild Diploid *Triticum* L. (Poaceae) Species in Iran

[1]Navaz Kharazian and [2]Mohammad Reza Rahiminejad
[1]Department of Botany, Faculty of Sciences, University of Shahrekord, Shahrekord, Iran
[2]Department of Botany, Faculty of Sciences, University of Isfahan, Isfahan, Iran

Abstract: This study evaluates the taxonomic status and the variation of wild diploid *Triticum* L. species using leaf flavonoid compounds in Iran. Two-dimensional maps of these species were provided using polyamide Thin Layer Chromatography. In order to show the taxonomic position of these species, the cluster analysis based on Euclidean Distance Coefficient and Ward Method and Factor analysis were applied (Principle Component Analysis). The flavnoid compounds purification of each accession and species was done. The results of cluster analysis showed that *T. boeoticum* subsp. *boeoticum* Boiss. and *T. boeoticum* subsp. *thaoudar* Reut. ex Boiss. are completely distinguished from each other. *T. boeoticum* subsp. *thaoudar* shows more similarity to *T. urartu* Tum. ex Gand., but *T. boeoticum* subsp. *boeoticum* displays affinity to *T. monococcum* L. The results of this study showed variability of flavnoid compounds at the diploid levels in *Triticum* species. Also flavnoid profiles can be mentioned as well marker to show the taxonomic position of these species.

Key words: Flavnoid, wild, *Triticum*, two dimensional map, Iran

INTRODUCTION

Triticum L. genus (Poaceae; Triticeae) has four wild diploid species (2n = 2x = 14; x = 7) growing in Iran (Bor, 1970, Rahiminejad and Kharazian, 2005). These species are as follow; *T. boeoticum* subsp. *boeoticum* Boiss., *T. boeoticum* subsp. *thaoudar* Reut. ex Boiss., *T. monococcum* L. and *T. urartu* Tum. ex Gand. (Bor, 1968, 1970).

There have always been debates concerning the taxonomy of the genus *Triticum* among the researchers. The complexes occurred among the species were due to the high similarity and the hybridization between the *Triticum* species which causes a high morphological similarity among these species (Lange and Jochemsen, 1992). These evidences have obscured the morphological limits of the species and caused taxonomic confusions in the number of species and nomenclatural debates in the genus *Aegilops* (Morrison, 1993). Also, high levels of variations have been observed in this genus (Waines and Barnhart, 1992).

Taxonomically, Dorofeev *et al*. (1979) reported that *T. urartu* is in Section *Urartu* Dorof. and Filatenko, while *T. monococcum* and *T. boeoticum* are grouped in Subgenus *Boeoticum* Migush. and Dorof., Section *Monococcon* Dum. Furthermore, Van Slageren (1994) showed that Section Monococca Flaksb. includes *T. monococcum* and *T. urartu*.

Morphologically, *T. urartu* is very similar to *T. boeoticum* (Yamagishi and Tanaka, 1978), while Kharazian *et al*. (2003) unfolded that *T. urartu* is different from the two other diploid species. Filatenko *et al*. (2001) reported that *T. boeoticum*, *T. monococcum* and *T. urartu* are considered as separate species. Controversially, Dhaliwal and Johnson (1976) showed *T. monococcum* is similar to *T. boeoticum*. In addition, these species have similar genome; AA, 2n = 2x = 14; x = 7 (Waines, 1995).

Chemotaxonomy is one of the important methods that display taxonomic position of taxa (Crowford, 1990). It is now possible to study phenolic profiles of high and low taxonomic levels, even of individual genotypes (Mika *et al*., 2005). The use of the distribution patterns of natural plant products-alkaloids, terpenes, phenolics, glucosinolites, terpenoids and carbohydrates is well-established as a major tool for investigating population structures, species, taxonomical problems and phyletic relationships of genera. Taxonomically, the most important phenolics are the flavnoids, which have a relatively common nucleus with great variety of types and patterns of side-groups that characterize the individual compounds. There is usually a considerable diversity of flavnoids in species (Nakipoklu, 2002). Also, extensive chemotaxonomic flavnoid research on the Poaceae detected the presence of flavone C-glycosides and tricin 5-glucoside (Bouaziz *et al*., 2001). Using thin layer chromatographic patterns, Dedio *et al*. (1969) presented the original taxonomic relationships in the genus

Corresponding Author: Navaz Kharazian, Department of Botany, Faculty of Sciences, University of Shahrekord, Shahrekord, Iran
Tel: +98-381-4424419 Fax: +98-381-4424419

Secale L. Thin-layer chromatography in these genus supported the general taxonomic relationships based on the morphological and cytological studies. The differences in chromatographic patterns were sufficient to determine the position of the Section of *Secale* genus. In addition, Bouaziz *et al.* (2001) showed the flavnoids of *Hyparrhenia hirta* Stapf (Poaceae) which grows in Tunisia. The most important compounds are 7-o-glucoside and vitexin. Also, Frey (1996) showed different phenolic profiles among *Trisetum* Pers.

Moreover, since Iran is one of the secondary centers of genetic diversity for diploid *Triticum* species, there is a need of using this genetic resource effectively in wheat improvement in this country. So far, the survey of flavnoid compounds in *Triticum* genus in Iran has not been studied, therefore the aims of this study are as follow:

- Detect the flavnoid compounds among the accessions
- Determine the taxonomic position via flavnoids
- Identify variability in accessions of wild diploid *Triticum* species in Iran

MATERIALS AND METHODS

Extraction, isolation and identification of flavnoids were based on the protocol of Markham (1982). Using leaf flavnoid chemistry from 14 accessions (Table 1) of wild *Triticum* species, the taxonomic status and the phytochemical variations of these species were studied. Two-dimensional maps (2DM) of these species were provided using methanol extracts on polyamide (MN-Polyamid-DC6) Thin Layer Chromatography (TLC). Moreover, Spots' detection in NP identifiers (Diphenylboric acid 2-Aminoethyle Ester) was performed under UV-254 nm and the presence/absence of spots was taken as a character state and it was applied in each accession of these species. In addition, R_f values (migration distance of the bands/distance of solvent front) in each accession were studied (Apaydin and Bilgener, 2000; Gulen and Eris, 2004). In order to show the taxonomic position of these species the Cluster analysis based on Euclidean Distance Coefficient, Ward Method as well as Factor analysis (Principle Component Analysis) via SPSS. V. 14 were applied; besides, the descriptive analysis was studied to estimate the Coefficient Variation (CV). The flavnoid compounds purification of each accession and species was carried out through a sephadex (LH20) column and one-dimensional maps (1 DM) on polyamide TLC plates. Identification of the purified compounds was performed based on their UV spectra (200-500 nm) and shift reagent, such as $AlCl_3$, $AlCl_3$/HCl, NaOAC, NaOAC/H_3BO_3 and Methanol (Markham, 1982).

Table 1: Locality of wild diploid *Triticum* species in natural habitat of Iran

Species	Locality	Height (m)
T. urartu		
46	Kurdestan-Asad abad	1977
2	Chahar mahal va Bakhtiyari-Shalamzar	1980
35	Kermanshah-Kamyaran	1240
T. boeoticum* subsp. *boeoticum		
36	Kurdestan-Janian	1770
39	Lurestan-Khoram abad	1820
60	Lurestan-Islam abad	1240
3	Lurestan-Sefid dasht	1800
T. boeoticum* subsp. *thaoudar		
37	Kurdestan-Janian	
25	Chaharmahal va Bakhtiari-Ardal	1820
54	Kurdestan-Kamyaran	1240
T. monococcum		
31	Lurestan-Islam abad	1250
32	Lurestan-Islam abad	1240
37	West of Azerbayjan-Zanjir boolagh, Ahar	1410
33	West of Azerbayjan-Ahar	1430

RESULTS

The two-dimensional flavnoid patterns of crude extracts of the taxa under study displayed the variability for each accession. Total number of spots were obtained in each species are presented as: (1) in *T. boeoticum* subsp. *boeoticum* 6-7 spots, (2) in *T. boeoticum* subsp. *thaoudar* 1-6 spots, (3) in *T. monococcum* 2-14 spots and (4) in *T. urartu* 2-4 spots. Dark yellow spots were common in *T. urartu*, *T. boeoticum* subsp. *boeoticum* and *T. monococcum*, blue spots were in *T. boeoticum* subsp. *boeoticum* and *T. monococcum*, orange spots were in *T. boeoticum* subsp. *thaoudar*, *boeoticum* and *T. monococcum* but violet spots were in *T. urartu*. Also, the presence and absence of flavnoid spots were surveyed in each accession (Table 2, Fig. 1, 2). Based on the color of each profile, the kind of flavnoid type is partially detected; *T. urartu* accessions have 3-OH flavonol, 5-OH flavonol or flavone, 4'-OH chalcone (Table 3, 4). In *T. boeoticum* subsp. *boeoticum* accessions observed Hydroflavone, flavonol, 5-o-glycosides, 3-o-flavonol, 5-OH flavone, dihydroflavonol, biflavonyl, 2'-OH chalcone, 6'-OH chalcone. *T. boeoticum* subsp. *thaoudar* have 2,4-OH chalcone. *T. monococcum* have flavone, flavonol, 3-OH flavonol, 5-OH falvonol, 2'-OH chalcone, 6'-OH chalcone.

Furthermore, R_f values of each accession were studied in aqueous and organic solvent system. Both maximum and minimum R_f in aqueous system were

observed in *T. boeoticum* subsp. *boeoticum* (1.76, 0.09, respectively), *T. monococcum* (1.72, 0.09, respectively). Also, maximum and minimum R_f in organic system were in *T. monococcum* (2.11, 0.14, respectively) (Table 5). In aqueous solvent systems, most of the stains have Hydroxyl groups with high polarity, but in organic solvent systems they have little polarity. In order to determine the flavnoid compounds, the fractions of each accession were surveyed. Absorption of UV spectrum via shift reagent such as $AlCl_3$, $AlCl_3$/HCl, NaOAc and NaOAC/H_3BO_3 were examined. Among *T. urartu* accessions, increased intensity (bathochromic shift) of Band I displays Hydroxylation at 2' and 4-positions and variability in B-ring *o*-Dihydroxylation. That is when Band II shows Oxygenation at 6 or 8-position. In *T. boeoticum* subsp. *boeoticum*, Band I shows Hydroxylation at 5 and 4-position and variability in B-ring *o*-Dihydroxylation and A-ring *o*-Dihydroxylation while Band II shows Hydroxylation at 7-position and Oxygenation at 6 or 8-position. In *T. boeoticum* subsp. *thaoudar* increased intensity demonstrates Hydroxylation at 7 and 2'-position and Oxygenation at 3'-position. Increased intensity of Band I in *T. monococcum* accessions indicates the variability of B-ring-*o*-Dihydroxylation and Hydroxylation at 4-position (Table 4).

Table 2: Presence and absence of each spot in each accession of *Triticum* accessions

Species/accessions	Pale yellow	Dark yellow	Blue	Orange	Violet
T. urartu					
40	+	+	-	-	-
35	+	-	-	-	-
2	+	-	-	-	+
T. boeoticum* subsp. *thaoudar					
37	+	-	-	+	-
54	+	-	-	-	-
25	+	-	-	+	-
T. boeoticum* subsp. *boeoticum					
36	+	+	-	-	-
3	+	-	+	+	-
39	+	-	+	+	-
60	+	-	+	+	-
T. monococcum					
37	+	-	-	+	-
31	+	-	+	+	-
33	+	-	+	+	-
32	+	+	+	-	-

+: Presence of especial spot, -: Absence of especial spot

Similar flavnoid compounds between *T. urartu* and *T. monococcum* are flavone, 4'-Hydroxychalcone,

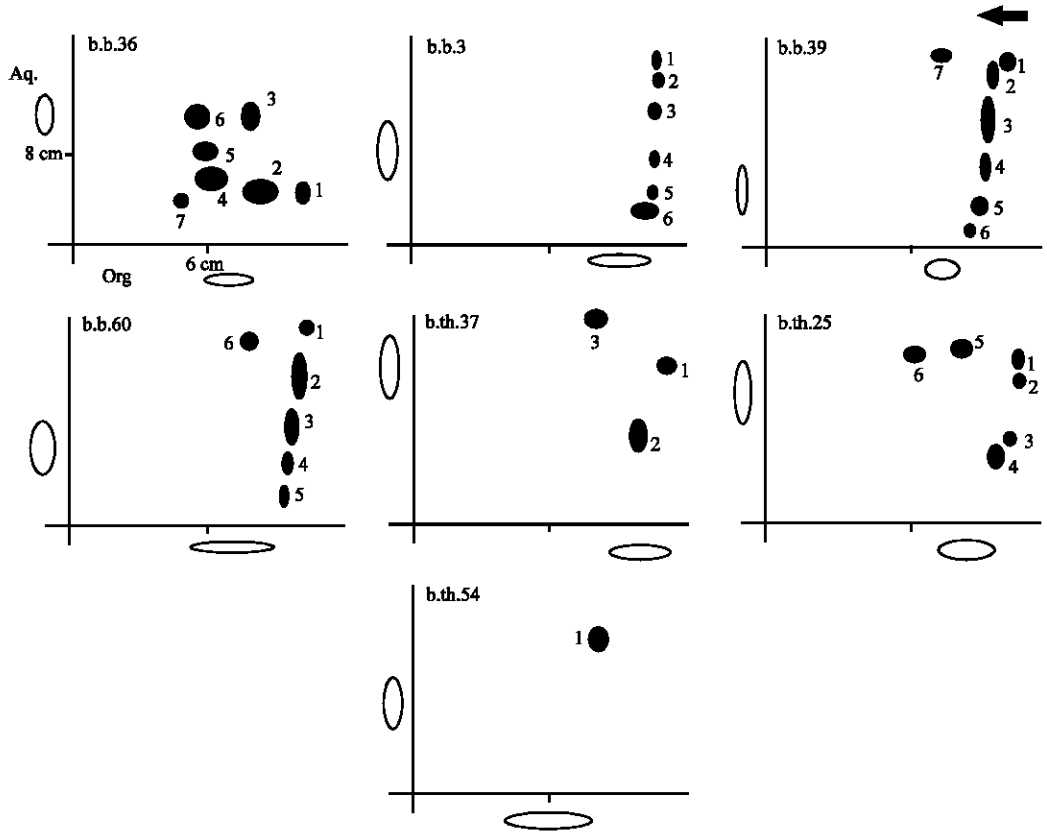

Fig. 1: Chromatogram of spots in *Triticum* species; b.b: *T. boeoticum* subsp. *boeoticum*, b.th: *T. boeoticum* subsp. *thaoudar*

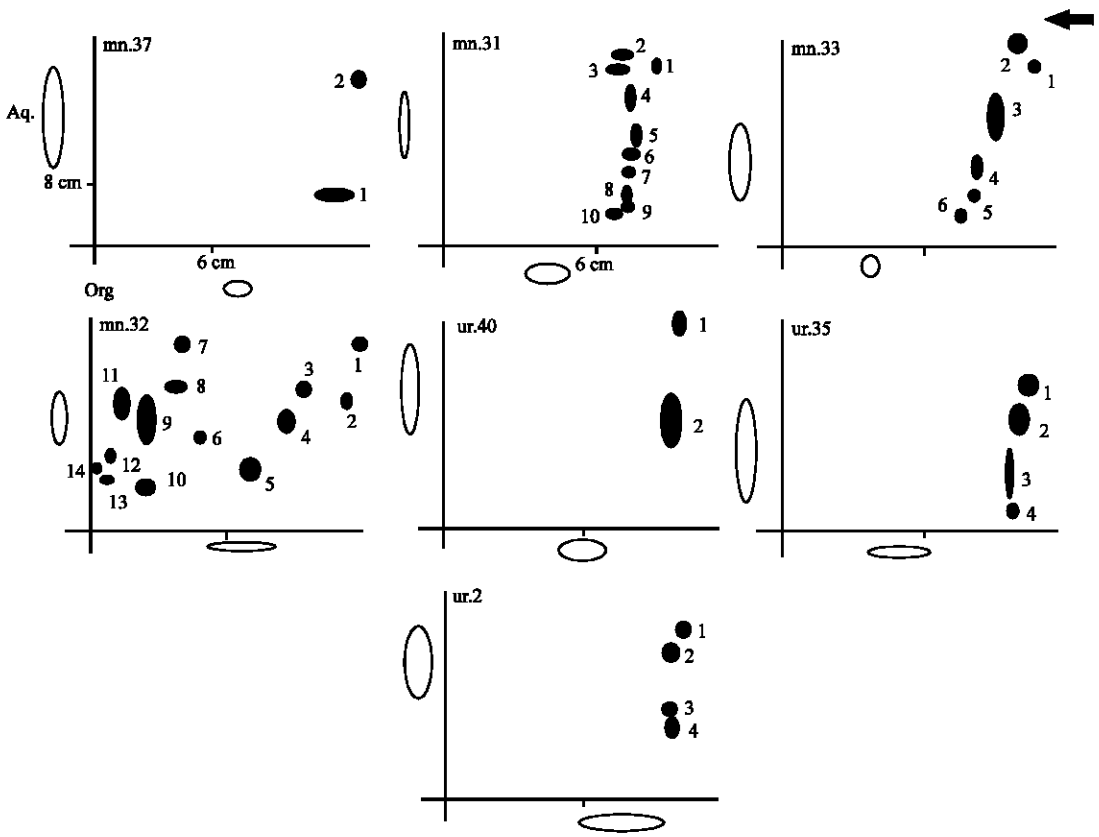

Fig. 2: Chromatogram of spots in *Triticum* species; m: *T. monococcum*, ur: *T. urartu*

Table 3: Flavnoid compounds among *Triticum* accessions in Iran

Flavnoid compounds	Urartu	Boeoticum	Thaoudar	Monococcum
Pseudobaptisin	+	-	-	+
2-Hydroxy-4'	+	-	+	-
Methoxy chalcone	+	+	+	+
Flavone				
4'-Hydroxy chalcone	+	+	+	+
3',4',7' Trihydroxy flavone	-	+	-	-
2-Hydroxy chalcone	-	+	+	-
2',4-Dihydroxy chalcone	-	+	+	-
2',3,'4'-Trihydroxy chalcone	-	+	-	-
Fustin 3-oglucoside	-	+	-	-
2'-Hydroxychalcone	-	-	+	-
2-2'-Dihydroxychalcone	-	-	+	-
3,4-Dihydroxy chalcone	-	-	+	-
Baptigenin	-	-	-	+
3,3',4'-Trihydroxyflavone	-	-	-	+
3',4',7-Trihydroxyflavone 7-o-rhamnoglucoside	-	-	-	+
3'-Hydroxy4'-Methoxyflavone	-	-	-	+
Sciadopitysin	-	-	-	+

+: Presence of especial flavnoid compound, -: Absence of especial flavnoid compound

Pseudobaptisin, *T. boeoticum* subsp. *boeoticum* and *T. monococcum* are flavone, 4'-Hydroxychalcone, 3',4',7' Trihydroxyflavone, between *T. urartu* and *T. boeoticum* subsp. *boeoticum* are flavone, 4'-Hydroxychalcone, between *T. boeoticum* subsp. *thaoudar* and *boeoticum* are 2-Hydroxychalcone, 4'-Hydroxychalcone, 2'-Hydroxy4'-Methoxychalcone, 2',4- Dihydroxychalcone, between *T. monococcum* and *T. boeoticum* subsp. *thaoudar* are 2'-Hydroxychalcone, 2'-Hydroxy4'-Methoxychalcone, 4'-Hydroxychalcone and between *T. urartu* and *T. boeoticum* subsp. *thaoudar* is 4'-Hydroxychalcone. Therefore 4'-Hydroxychalcone one of the flavnoid compounds which is common among these species (Table 3).

Table 4: Summary of the main flavnoid variation features among diploid *Triticum* species

Flavnoid compounds	Urartu	Boeoticum	Thaoudar	Monococcum
2'-Hydroxylation	+	-	+	-
4-Hydroxylation	+	+	-	+
5-Hydroxylation	-	+	-	-
7-Hydroxylation	-	+	+	-
B-ring *o*-dihydroxylation	+	+	-	+
A-ring *o*-dihydroxylation	-	+	-	-
6-Oxygenation	+	+	-	+
8-Oxygenation	+	+	-	+
3'-Oxygenation	-	-	+	-

+: Presence of flavnoid variation features, -: Absence of flavnoid variation features

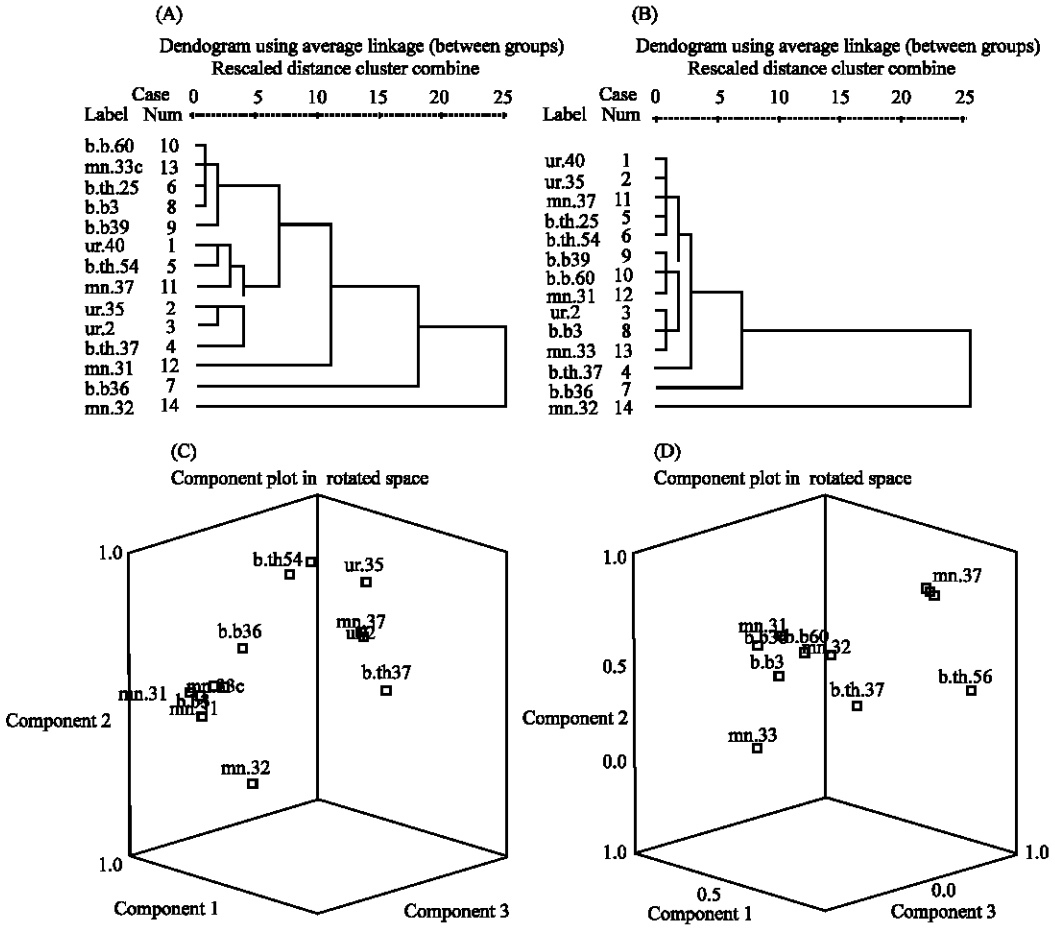

Fig. 3: Cluster and Factor analysis among *Triticum* accessions in aqueous and organic system; A and C in aqueous system, B and D in organic system, b.b: *T. boeoticum* subsp. *boeoticum*, b.th: *T. boeoticum* subsp. *thaoudar*, mn: *T. monococcum* and ur: *T. urartu*

Relationships between these species based on the R_f data are shown graphically in Fig. 1 and 2. Maximum CV in aqueous solvent system is related to subsp. *thaoudar* (75.3) and *boeoticum* (64.6) and in organic solvent system it is in *T. boeoticum* subsp. *thaoudar* (64.2) and *T. monococcum* (67.8), while minimum C.V. in both systems were in *T. urartu* (34.7 aqueous, 15.27 organic) (Table 6). The statistical analyses such as Cluster analysis were investigated in both aqueous and organic solvent systems. In aqueous system, two groups were comprised. (1) *T. monococcum*, *T. boeoticum* subsp. *boeoticum*, *T. boeoticum* subsp. *thaoudar*; *T. boeoticum* subsp. *thaoudar*, *T. urartu*, *T. monococcum*; *T. urartu*, *T. boeoticum* subsp. *thaoudar*, (2) *T. monococcum*, *T. boeoticum* subsp. *boeoticum*. In most of the clusters *T. urartu* and *T. boeoticum* subsp. *thaoudar* grouped together, also *T. monococcum* and *T. boeoticum* subsp. *boeoticum* were close together. Two subspecies of *T. boeoticum* were discrete from each other and *T. monococcum* clustered with two subspecies of *boeoticum* (Fig. 3). Using Factor analysis for aqueous system, it was observed that two groups in two components were comprised; (1) *T. urartu*, *T. boeoticum* subsp. *thaoudar*, *T. monococcum* (2) *T. monococcum*, *T. boeoticum* subsp. *boeoticum*, *T. boeoticum* subsp. *thaoudar*. In this analysis, two subspecies are exactly separated (Fig. 3). The results of clustering in organic solvent system proved three distinct groups, (1) *T. urartu*, *T. boeoticum* subsp. *thaoudar*, *T. monococcum*, *T. monococcum*, *T. boeoticum* subsp. *boeoticum*, *T. urartu*, *T. boeoticum* subsp. *thaoudar* (2) *T. monococcum*, *T. boeoticum* subsp. *boeoticum*. In this system, two subspecies of *T. boeoticum* were distincted. Using Factor analysis for organic data presented two comprised groups and therefore, affirmed the Factor analysis performed for aqueous solvent system (Fig. 3).

Based on these results, aqueous solvent system is more appropriate for determining taxonomic position than organic system.

DISCUSSION

Little information is available about the variation extension among the wild progenitors of *Triticum* species (Hedge *et al*., 2000). There are conflicting reports on the amount of diversity in diploid wheat populations, specifically in chemotaxonomy. Based on the results of this study, *T. urartu* accessions with B-ring *o*-Dihydroxylation, Oxygenation at positions 6 and 8 and 4-Hydroxylation are common in *T. monococcum* and *T. boeoticum* subsp. *boeoticum* (Table 5), which is in accordance with Hammer *et al*. (2000) using micro satellites. Van Slageren (1994) and Dubcovsky and Dvorak (1995) reported that *T. monococcum* and *T. urartu* were related in phylogenetic trees. Using flavnoid chemistry, it was observed that *T. monococcum* and *T. urartu* were related, noticeably *T. urartu* having 2'- Hydroxylation is similar to *T. boeoticum* subsp. *thaoudar* (Table 5). In this study two subspecies of *T. boeoticum* were distincted in flavnoid variation, whereas these are exclusively similar in 7-Hydroxylation.

In cluster and Factor analysis *T. urartu* and *T. boeoticum* subsp. *thaoudar* were approximately grouped together. Morphologically, *T. urartu* is very similar to *T. boeoticum* (Yamagishi and Tanaka, 1978). *T. monococcum* and *T. boeoticum* subsp. *boeoticum* also grouped together and displayed affinity between them, which in accordance with Dorofeev *et al*. (1979) and Jaaska (1993, 1997). In addition, Dhaliwal and Johnson (1976) and Waines and Barnhart (1992) proved that *T. monococcum* is similar to *T. boeoticum*. Furthermore, using meiotic paring behavior and analysis

Table 5: R_f values of *Triticum* accessions in aquatic and organic phase

Taxa	R_f organic	R_f aqueous	Spots	Taxa	R_f organic	R_f aqueous	Spots
T. boeoticum subsp. *boeoticum* 36	0.23	1.50	Spot 1	*T. urartu* 40	0.47	0.44	Spot 1
	0.75	1.63	Spot 2		0.55	1.11	Spot 2
	0.78	0.83	Spot 3	*T. urartu* 35	0.44	0.60	Spot 1
	1.07	1.76	Spot 4		0.49	0.79	Spot 2
	1.10	1.24	Spot 5		0.49	1.16	Spot 3
	1.30	0.92	Spot 6		0.48	1.26	Spot 4
	1.15	1.92	Spot 7	*T. urartu* 2	0.28	0.63	Spot 1
T. boeoticum subsp. *boeoticum* 3	0.24	0.09	Spot 1		0.48	0.75	Spot 2
	0.26	0.21	Spot 2		0.43	1.23	Spot 3
	0.31	0.50	Spot 3		0.50	1.32	Spot 4
	0.26	0.78	Spot 4	*T. monococcum* 37	0.75	0.20	Spot 1
	0.31	1.17	Spot 5		0.83	0.19	Spot 2
	0.40	1.32	Spot 6	*T. monococcum* 31	0.37	0.15	Spot 1
T. boeoticum subsp. *boeoticum* 39	0.29	0.20	Spot 1		0.60	0.09	Spot 2
	0.38	0.27	Spot 2		0.62	0.19	Spot 3
	0.36	0.49	Spot 3		0.40	0.57	Spot 4
	0.32	0.73	Spot 4		0.43	0.84	Spot 5
	0.41	0.93	Spot 5		0.50	0.97	Spot 6
	0.50	1.02	Spot 6		0.51	1.07	Spot 7
	1.00	0.08	Spot 7		0.56	1.19	Spot 8
T. boeoticum subsp. *boeoticum* 60	0.41	0.17	Spot 1		0.66	1.23	Spot 9
	0.33	0.61	Spot 2		0.73	1.28	Spot 10
	0.36	0.77	Spot 3	*T. monococcum* 33	0.22	0.14	Spot 1
	0.38	1.03	Spot 4		0.33	0.10	Spot 2
	0.48	1.18	Spot 5		0.32	0.62	Spot 3
	1.05	0.22	Spot 6		0.37	0.83	Spot 4
T. boeoticum subsp. *thaoudar* 37	0.20	0.56	Spot 1		0.57	1.03	Spot 5
	0.62	1.60	Spot 2		0.60	1.09	Spot 6
	1.20	0.20	Spot 3	*T. monococcum* 32	0.14	0.15	Spot 1
T. boeoticum subsp. *thaoudar* 25	0.20	0.45	Spot 1		0.34	0.64	Sport 2
	0.23	0.57	Spot 2		0.74	0.61	Sport 3
	0.40	1.20	Spot 3		0.87	0.94	Spot 4
	0.44	1.43	Spot 4		1.14	1.51	Spot 5
	0.84	0.19	Spot 5		1.48	0.89	Spot 6
	1.09	0.20	Spot 6		1.54	0.25	Spot 7
T. boeoticum subsp. *thaoudar* 54	0.43	0.55	Spot 1		1.60	0.54	Spot 8
					1.68	0.84	Spot 9
					1.68	1.70	Spot 10
					1.80	0.76	Spot 11
					1.87	1.50	Spot 12
					1.88	1.72	Spot 13
					2.11	1.48	Spot 14

of the polymorphisms of repeated nucleotide sequences *T. urartu* was found to be as a donor of A and B genome in polyploid wheat (Dhaliwal and Johnson, 1976, Dvorak *et al*., 1993; Hammer *et al*., 2000). Controversially, Filatenko *et al*. (2001) reported that *T. boeoticum*, *T. monococcum* and *T. urartu* are considered as separate species. Also, Dorofeev *et al*. (1979) and Kharazian *et al*. (2003) evolved that *T. urartu* is different from the two other diploid species. Using isoenzyme markers, Jaaska (1993) reported that *T. boeoticum* and *T. urartu* were found to differ with regard to acid phosphatase, esterase and superoxide dismutase, showing distinctly different gene pools.

So far, the researches did not have any supporting evidence which could clearly separate the wild diploid species (Morrison, 1993) and subspecies. In this study two subspecies of *T. boeoticum*; *thaoudar* and *boeoticum* were separated exactly (Fig. 3). Using microsatellites, Hammer *et al*. (2000) reported that two subspecies of *T. boeoticum* have different genomes. Based on flavnoid compounds these four species seem to have genomic relationships because of similarity in B-ring *o*-Dihydroxylation and 4-Hydroxylation, flavone and 4'-Hydroxychalcone which can provide the gene flow among diploid species. This similarity confuses the limits of diploid species. Noticeably, *T. monococcum* accessions display oxidation patterns of flavones which can be observed in Sciadopitysin, 3',4',7'-Trihydroxyflavone 7-*o*-rhamnoglucoside and 3,3',4'-Trihydroxyflavone. Both *T. uraartu* and *T. monococcum* have Oxidation flavnoids patterns which are related to Pseudobaptisin (Table 4). Therefore, these evidences show that *T. urartu* can be mentioned as one of the diploid ancestors to other diploid *Triticum* species. Nevertheless, these four wild diploid species are different from each other (Dhaliwal, 1977).

Little information is available on the extent of genetic variation in the wild *Triticum* species (Hedge *et al*., 2000, Moghaddam *et al*., 2000). Hedge *et al*. (2000) reported that *T. monococcum* and *T. urartu* accessions have polymorphic loci, but the low heterozygosity is indirectly resulting in high hybridization among the accessions. The flavnoid profiles among *T. monococcum* accessions present high variability in their flavnoid patterns which confirm these results (Fig. 2). Noticeably, they reported that *T. urartu* has the highest genetic diversity, which is not in accordance with present results (Table 6), *T. urartu* accessions have the least variability in their profile (Fig. 2). Intraspecific alloenzymic variability was found to be low in this species (Jaaska, 1993). Diversity and polymorphism of flavnoid compounds in accessions of *T. monococcum* and *T. boeoticum* subsp. *thaoudar* and *boeoticum* are more than *T. urartu* (Table 5, 6 and Fig. 1, 2) which are in agreement with Hedge *et al*. (2000) results, therefore maximum CV in aqueous solvent system is related to subsp. *thaoudar* and *boeoticum* and in organic solvent system it is in *T. boeoticum* subsp. *thaoudar* and *T. monococcum*, while minimum CV in both systems were in *T. urartu* (Table 6). Yaghoobi Saray (1979) and Hedge *et al*. (2000) reported higher levels of alloenzyme diversity in *T. monococcum* and *T. urartu*. Genetic variability which was approximately identical for diploid species may be brought about by similar kinds of evolutionary forces for which all the species might have had identical response. Phenolic profiles specifically demonstrate genetic affinity and significant polymorphism among species (Mika *et al*., 2005). These polymorphisms of flavnoid profiles have been showed in Fig. 1 and 2.

Table 6: Variability of flavnoid compounds among *Triticum* accessions in Iran

Species	R_f aqueous	R_f organic
T. urartu		
Mean	0.92	0.46
SD*	0.32	0.07
CV**	34.70	15.20
T. monococcum		
Mean	0.79	0.87
SD	0.50	0.59
CV	63.20	67.80
T. boeoticum* subsp. *thaoudar		
Mean	0.69	0.56
SD	0.52	0.36
CV	75.30	64.20
T. boeoticum* subsp. *boeoticum		
Mean	0.82	0.54
SD	0.53	0.33
CV	64.60	61.10

*Standard Deviation, **Coefficient of Variation

CONCLUSION

The widespread occurrence of flavnoid compounds in *Triticum* genus makes them useful markers for taxonomy and evolutionary relationships (Mika *et al*., 2005). To use flavnoid compounds more widely as genetic markers, these would have to be not only universal and abundant, but also environmentally stable and convenient for identifying taxonomic position (Fairbbothers *et al*., 1975). In addition, such studies should be performed at the population level as well.

ACKNOWLEDGMENTS

Authors are thankful to the University of Isfahan and Shahrekord to grant the research project No. 28. This research was performed at Department of Botany, Faculty of Sciences, University of Isfahan, Isfahan, Iran, on October 2003.

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