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Agro-morphological characterization of durum wheat accessions using pattern analysis

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Abstract

Information on the variation available for different plant attributes has enabled germplasm collections to be effectively utilized in plant breeding. This investigation was carried out to characterize 85 durum wheat accessions based on 19 qualitative and quantitative agro-morphological attributes and to describe the genetic variation among the accessions as a subset of worldwide germplasm collection conserved in Iran under irrigated condition. The investigation was also aimed to study relationship among the traits and to find out adapted accessions that can be used in durum wheat breeding program. Univariate and Multivariate (clustering and ordination) techniques were used to investigate the diversity present among the accessions in the collection. Both cluster and ordination analyses suggested that eight groups of accessions existed. The comparison of accession groups based on traits verified that it is possible to find out contrasting group based on the traits for improving genetic materials in breeding programs. Applying accession-by-trait (AT) biplot analysis to the multiple trait data revealed that AT-biplot graphically displayed the interrelationships among traits and facilitated visual comparison of accessions and selection. The results also showed that, based on qualitative and quantitative measurements, the accessions in different groups were belonged to different countries which suggested that there was no clear relationship between accessions and geographical diversity. The information on diversity and relationships among the agro-morphological traits will be helpful to breeders in constructing their breeding populations and implementing selection strategies.

Keywords: Durum wheat accessions, genetic diversity, agro-morphological traits, multivariate analyses

Abbreviations: TKW: 1000- kernel weight; WSS: Weight of seeds per spike; NSS: Number of seeds per spike; NSPS: Number of spikelet per spike; SSPN: Sterile spikelet number; SL: Spike length; DH: Days to heading; NN: Number of nodes; ST: Stem thickness; PH: Plant height; PL: Peduncle length; NET: Number of effective tillers; Chl: Chlorophyll rate, YLD: Yield

Introduction

Genetic variability present in collection and preserved germplasms are important resource in generating new plant ideotypes having desired traits that help to increase crop production and thus improve the level of human nutrition (Singh, 1991). The germplasms of diverse plant species are maintained in gene banks around the world with collections holding anywhere from hundreds to thousands of accessions (IBPGR, 1992). Together with the important role of conserving genetic resources, gene banks also provide accessions for incorporation into plant breeding programs to develop new cultivars of crop and pasture species (Shands and Wiesner, 1992). In breeding programs, characterization of accessions based on multiple traits can be used as a management tool in regenerations to allow validating the identity of an accession. Evaluation data is used when searching the bank for useful or sets of useful germplasm (Delacy *et al.*, 2000). Studies of the variation present in germplasm collections have been carried out frequently using characterization of plant morphological attributes for white clover (Caradus *et al.*, 1990; Jahufer *et al.*, 1997; Rosso and Pagano, 2001), alfalfa (Rumbaugh *et al.*, 1988), wheat (Pecetti, 1992), white lupin (Rubio *et al.*, 2004), Fenugreek (McCormick *et al.*, 2009), apricot (Ruiz and Egea, 2008), watermelon (Szamosi *et al.*, 2009), sesame (Morris, 2009), safflower (Elfadl *et al.*, 2010) and vineyard peach (Nikolic *et al.*, 2010). Germplasm collections continue to play a vital role in providing the genetic resources needed for improving durum wheat. The ICARDA gene bank preserves more than 19600 accessions of durum wheat (including 15,020 accessions of landraces), 849 accessions of primitive wheats, 1585 accessions of wild Triticum and 301 accessions of *Aegilops* species with S genome (out of 1905 accessions of *Aegilops*). CIMMYT gene bank has also large number of accessions including 14,835 accessions (36% of which is breeding material of *T. durum* and accessions of *T. diccoccom* and *T. carthlicum*). Iran national gene bank holds a unique set of landraces of durum wheat (700 accessions) and wild relatives collected mainly within the country. International centers, annually collect, regenerate and conserve the genetic resources and they also evaluate and compare the morphological characteristics of accessions in a common environment. In fact, these aspects of breeding programs are conducted throughout the target region every year in which multiple traits are usually recorded. Effective interpretation and utilization of these breeding programs data is important at all stages of plant breeding, particularly when it is only possible to select on yield components. Numerous methods have been used to understand of the data patterns, although strategies may differ in overall appropriateness, different methods usually lead to the same or similar conclusions for a given dataset (Flores *et al.*, 1998; Rubio *et al.*, 2004). Different statistical procedures, ranging from simple univariate to the more complex multivariate techniques, have been used in the analysis of characterization data in the germplasm collection. Although statistics such as means, ranges and variances are helpful in providing information on the diversity of accessions in germplasm collections, they do not enable the simultaneous comparison of the accessions and the plant attributes (Harch *et al.*, 1995). Pattern analysis techniques such as clustering and ordination, have been used extensively to study the diversity among accessions for various plant species (Harch *et al.*, 1995; Harch *et al.*, 1996; Jahufer *et al.*, 1997; DeLacy *et al.*, 2000; Rosso and Pagano, 2001). In addition to clustering technique, the genotype-by-trait (GT) biplot has been applied to study relation among studied traits in a set of genotypes (Yan and Rajcan, 2002; Rubio *et al.*, 2004; Peterson *et al.*, 2005; Yan and Fregeau-Reid, 2008). It is an application of the GGE (genotype plus genotype-by-environment) biplot technique to study of the genotype-by-trait data, and to examine its usefulness in visualizing crop trait relationships, and its application in genotype evaluation comparison, and selection (Yan and Rajcan, 2002). However, little is known about the characterization of durum wheat accessions maintained in the gene bank of Iran based on a large number of qualitative and quantitative traits as well as the interrelationships among the traits which are more affect on genotype discrimination. More information, however, is needed to find out adapted accessions that are suitable for durum wheat breeding program in Iran. Therefore, the main objectives of this investigation were to (i) evaluate 85 durum wheat accessions on the basis of multiple agro-morphological traits which could be used to describe the genetic variation of a subset of accessions from several countries preserved in Iran's national gene bank and (ii) study the relationships among recorded traits using biplot analysis techniques.

Materials and Methods

Plant Materials

Genetic materials consisted of 85 durum wheat accessions maintained at the national gene bank of SPII (Seed and Plant Improvement Institute), Karaj, Iran. The accessions studied were collections from 11 countries worldwide (Supplementary 1). Four out of 85 accessions were the check cultivars (Vee/Nac and Soissons as bread wheat checks, Dena and Zardak as durum wheat checks). The field experiment was carried out under irrigated conditions at the research station of SPII (ordination: latitude 35' 48^o N; longitude 51' 10^o E, altitude 1321 m) in north central Iran during the cropping season 2008-09. The plant materials were sown in 2 rows of 2.5 m long in a non-replicated trial. The checks were repeated every 10 genotypes, intervally. Weeds were controlled manually. Fertilizer application was 135 kg N ha^{-1} and 90 kg P_2O_5 ha^{-1} at planting.

The traits recorded

Durum wheat accessions were examined for (i) five qualitative traits, i.e., seed color (SC), glume color (GC), lodging (Lg), leaf type (LT) and shriveled seed (SS) (Supplementary 1) and (ii) fourteen quantitative traits, i.e., days to heading (DH), plant height (PH), 1000-kernel weight (TKW), weight of seeds per spike (WSS), number of seeds per spike (NSS), number of spikelet per spike (NSPS), sterile spiklet number (SSPN), spike length (SL), number of nodes (NN), stem thickness (ST), peduncle length (PL), number of effective tillers (NET), chlorophyll rate (Chl) and grain yield (YLD) per plot (Supplementary 2).

Statistical analysis

Several simple univariate statistics including minimum, maximum, means, ranges and standard deviation (SD) were used to describe the variability among the accessions, which were obtained for each trait based on the accessions (Maggs-Kölling et al., 2000; Prosperi et al., 2006; Morris, 2009). Coefficients of variation (CV %) (Francis and Kannenberg, 1978) was also calculated from the variance components and the overall means for all the investigated traits. Combination of the mean and SD for each attribute was also used to identify superior accessions. In this case five categorizes of accessions for each attribute can be characterized. The accessions with values > (mean + SD) and > (mean + 2SD) can be identified as desirable accessions for each attribute. The accessions with values between mean ± SD are average in their performance, and those with values < (mean – SD) and < (mean – 2SD) can be identified as undesirable ones (Shakhatreh et al., 2010). This simple methodology can be useful to preliminary selection of desirable accessions base on each attribute. Pattern analysis, defined by Williams (1976) as the joint use of classification and ordination methods, was applied to characterization of durum wheat accessions. This approach attempts to identify accessions that have similar performance for a set of traits, and the traits that have similar pattern for discriminating among genotypes. Clustering of accessions based on the morphological traits was carried out using an agglomerative hierarchical clustering procedure with squared Euclidean distance as a measure of dissimilarity and incremental sums of squares (Ward, 1963) as a grouping strategy. Dendrograms were constructed on the basis of fusion level to examine similarities in pattern of performance among accessions (in reaction to morphological attributes) and morphological attributes (in discriminating among accessions). Clustering summarizes data by grouping accessions with similar performance across morphological attributes and grouping those morphological attributes that produce similar discrimination among the performance of accessions. Thus, clustering summarizes complexity in the data with retention of the majority of the information by describing performance with relatively few accession groups or relatively few morphological attributes groups or both (Mungomery *et al.* 1974; Cooper and DeLacy, 1994; DeLacy *et al.* 1996). Accession-by-trait (AT) biplot was used to assess the patterns of relations among morphological attributes, genotypes and their interactions. Biplots were conducted in the dimension of first two principal components (PC1 and PC2), using a singular-value decomposition procedure (Gabriel, 1971; Kempton, 1984; Yan and Rajcan, 2002). Both the accession and attribute plotting points can be interpreted as vectors on the biplot, but as the accessions were investigated in terms of the attributes, attributes were represented as vectors and the accessions as points where the origin of biplot represents average values for all attributes (Delacy *et al.*, 2000). The attribute vectors are drawn in the positive direction, i.e. in the direction of increasing value for that attribute. The length of each vector is proportional to how well each attribute was modeled as each vector should be the same length if they were all equally well modeled. The angles of the vectors to each other in the biplot represent the phenotypic correlation between the attributes over all values of the accessions for each attribute (Delacy *et al.*, 2000). The cosine of angle between a pair of morphological attributes vectors approxi-

Table 1. Number of accessions with values greater than mean, (mean + SD) and (mean + 2SD)

Attributes	>Mean		> Mean + SD		> Mean + 2SD	
	Number	%	Number	%	Number	%
TKW[$]	42	49.4	14	16.5	1	1.2
WSS	43	50.6	16	18.8	5	5.9
NSS	37	43.5	12	14.1	4	4.7
NSPS	45	52.9	12	14.1	3	3.5
SSPN	47	55.3	15	17.6	1	1.2
SL	39	45.9	14	16.5	3	3.5
DH	47	55.3	8	9.4	3	3.5
NN	80	94.1	6	7.1	4	4.7
ST	45	52.9	11	12.9	4	4.7
PH	45	52.9	13	15.3	1	1.2
PL	47	55.3	11	12.9	1	1.2
NET	36	42.4	15	17.6	3	3.5
Chl	45	52.9	13	15.3	0	0.0
YLD	47	55.3	8	9.4	3	3.5
Mean	46.1	54.2	12.0	14.1	2.6	3.0

[$] TKW: 1000- kernel weight; WSS: Weight of seeds per spike; NSS: Number of seeds per spike; NSPS: Number of spikelet per spike; SSPN: Sterile spikelet number; SL: Spike length; DH: Days to heading; NN: Number of nodes; ST: Stem thickness; PH: Plant height; PL: Peduncle length; NET: Number of effective tillers; Chl: Chlorophyll rate, YLD: Yield

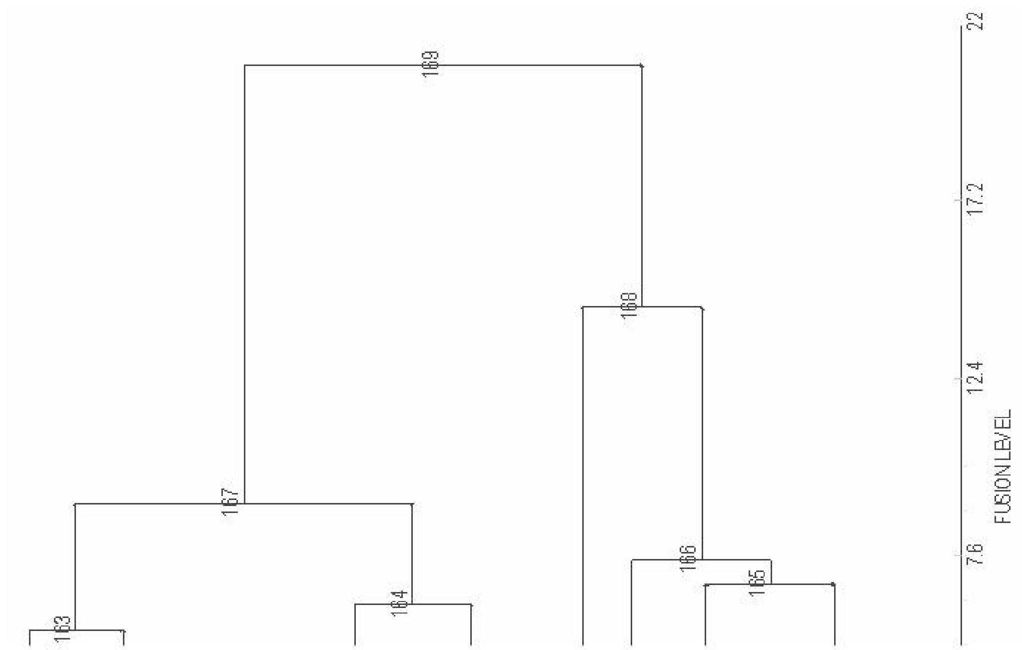
mates correlation between them (Yan and Rajcan, 2002; Yan and Kang, 2003). An acute angle (<90^o) indicate a positive correlation; an angle close to 90 degrees indicate the attributes are not correlated, whereas an obtuse angle close to 180 degrees represents a strong negative relationship (Alagarswamy and Chandra, 1998; Zhang *et al.*, 2006). The length on the attribute vector to the point where a perpendicular dropped from the genotype plotting point to the vector, is proportional to the modeled (predicted) value of that genotype for that attribute (Delacy *et al.*, 2000). The IRRISTAT statistical software (IRRI, 2005) was used to generate all analyses.

Results

The data recorded on the 85 durum wheat accessions for the qualitative and quantitative agronomical and morphological traits are given in Supplementaries 1 and 2. For each trait the overall mean, maximum, minimum, range, standard deviation (SD) and coefficient of variation (CV %) are also presented in Supplementary 2. The CV% is a parameter which is not related to unit of measured traits and will be effective in comparing of the studied traits. The CV% of the traits varied from 2.4 % (for DH) to 42.8 % (for SSPN). The lowest CV-values were observed for the traits DH followed by Chl, NN and NSPS indicating the least variation among the all accessions for these traits, while the highest values were found for the SSPN, YLD, NET and WSS. These results show that the traits with lowest CV were more repeatable than the other traits and can be reliable markers for the prediction of success in breeding programs. The superior accessions based on mean and SD can be identified for each trait. The groups included accessions based on (mean + SD) and (mean + 2SD) will give an indication of the superior accessions from the two groups for the character under consideration with high probability of success in selection in the case of sufficiently high heritability. Table 1 shows the number and percentage durum wheat accessions which had a better performance than mean, (mean + SD) and (mean + 2SD) based on each trait. The percentage of accessions with values higher than the mean across all traits varied from 42.4% (for NET) to 94.1% (for NN) (Table 1). In general, about 54% of the accessions had a better performance than the overall mean. On the other hands, 18.8% of accessions had WSS better than (mean +SD), while 17.6% of the accessions showed NSPS and NET higher value than the (mean + SD). The lowest percentage more than (mean + SD) were observed for the accessions based on the traits NN (7.1%), DH and YLD (9.4%). By appling this method, 14.1% of accessions in general were superior. The percentages of accessions with values better than (mean + 2SD) ranged from 0% (for Chl) to 5.9% (for WSS), using by this method only 3% of the accessions is selected based on over all traits (Table 1).

Classification of accessions

The results of classification analysis for accessions are presented in Fig. 1. The numbers of accession groups were decided on the basis of the sums of squares (SS) retained in the reduced accession-by-trait matrix. Clustering of the 85 accessions, together with the four check cultivars, was truncated at the eight-group level which retained 68.2 % of the accession-by-trait SS. Differences among groups were determined by the agro-ecological differences in sites of collection and by the measured attributes. Group 8, the largest group contained 23 accessions, while groups 1, 2 and 4, the smallest groups, each consisted of 4 accessions. As indicated in the Fig. 1, the check cultivars, were separate in two groups, where Zardak separated in group 8 and Vee/Nac, Soissons and Dena, in group 4 (Fig. 1). For each attribute the individual groups showed different ranges of distribution. Accessions in group 1 had the highest peduncle length (PL) and sterile spikelet sumber (SSPN), while they had the lowest grain yield (YLD), days to heading (DH), number of seeds per spike (NSS) and weight of seed per spike (WSS) (Fig. 2). The highest thousand kernel weight (TKW), number of nodes (NN), stem thickness (ST) and chlorophyll rate (Chl) was found for accessions in group 2. The accessions included in group 3 had the highest DH and SSPN and the lowest ST and Chl. The yield performance in this group was about overall mean yield of accessions (218 gr/plot). The best performance was observed for the accessions in group 4. Three out of four checks were included in this group. The highest YLD, NSS, SL, WSS, NET and lowest lodging (Lg) was observed in this group. In this group the accessions had the lowest SSPN, PL and PH. The nine accessions included in group 5 had the maximum values for the NSPS, DH, SL, PL and PH, whereas these accessions were in minimum for the number of effective tillers (NET) (Fig. 2). The accessions in group 6



Group No	1	8	3	7	4	2	5	6
Checks		Zardak			Vee/Nac			
					Soissons			
					Dena			
Number of accessions in group	4	23	10	13	4	4	9	18

Fig 1. Dendrogram showing the clustering patterns of the 85 durum wheat accessions based on 15 agro-morphological attributes

were found to have the highest value of the TKW, WSS, SSPN and SL. The group 7 comprised 13 accessions with the highest ST and PL and with yield performance (253.7 gr/plot) greater than mean yield. Although group 8 contained the highest number of accessions (23), like group 1 the ranges of distribution this group across all 15 attributes was low. The highest NET was observed in this group followed by group 4. Mean yield of this group (191.0 gr/plot) was less than overall mean yield. The accessions in this group were also had the highest lodging and the lowest ST and Chl. In this group DH, SL, NSPS, SSPN, PH were also low.

Accession-by-trait biplot analysis

The accession-by-trait (AT) biplot analysis is shown in Fig. 3 which can be used to evaluate accessions based on multiple traits and to identify best accession groups for specific attribute groups. Figure 3 is an AT- biplot with a polygon view and it presents the data of 85 durum accessions with 15 attributes. In the biplot a vector is drawn from the biplot origin to each marker of the traits to facilitate visualization of the relationships between and among the traits. According to Kroonenberg (1995) the fundamental patterns among the traits should be captured by the biplots. The vertex accessions were the accession numbers 28, 61, 15, 8, 58, 16, 59, 84 and 82. These accessions were the best or the poorest accessions for some or all of the traits, because they had the longest distance from the origin of the biplot (Yan *et al.*, 2007). The vertex accessions for each sector are the one that gave the highest value for the traits that fall within that sector. Vertex accessions No. 82 and 84 without any trait in their sector were not the highest performance accessions for any trait and indeed they were the poorest accessions for most of the traits. The accessions and traits fell into eight sectors, which in each sector the best accession for each trait can be identified. Accordingly, the accession No. 28 had the highest NET, while the accession No. 61 had the highest PL and SSPN. The accession No. 15 was the best in PH, while the accession No. 8 was the best for TKW and DH. The accession No. 16 had the highest value for ST, SL, WSS and NSPS, while the accession No. 59 was winner for yield, NSS and non-lodging. The perpendicular lines to the polygon sides facilitate comparison between neighboring vertex accessions (Yan and Kang, 2003). Comparison between accession Nos. 61 and 28 indicates that accession No. 61 was better in PL and SSPN, while accession No. 28 was better in NET. Similarly, the accession No. 59 in comparison with accession No. 61 had greater value of YLD, NSS and resistant to lodging. The accession No. 8 was better than the accession No. 15 in TKW and DH. However, a biplot may not accurately reflect the means as it did not explain all variation of the data but it displays the most important patterns of the data (Yan and Rajcan, 2002). It can also be used to aid accession selection on the basis of multiple traits.

Relationships among agro-morphological attributes

The accession-by-trait biplot captured 36.2 % of the total variation of the standardized data. This low proportion reflects the complexity of the relationships among the measured traits (Yan and Rajcan, 2002). Nevertheless, the fundamental patterns among the traits should be captured by the biplots (Kroonenberg, 1995). In a biplot, a vector is drawn from the biplot origin to each marker of the traits to facilitate visualization of the relationships between and among the traits. Two traits are positively correlated if the angle between their vectors is <90°, negatively correlated if the angle is >90°, independent if the angle is 90°. Therefore, the

Table 2. Pearson's Correlation coefficients between agro-morphological traits calculated from 85 durum wheat accessions

	TKW	WSS	NSS	NSPS	SSPN	SL	DH	NN	ST	Lg	PH	PL	NET	Chl
TKW[$]	1													
WSS	0.67**	1												
NSS	-0.06	0.68**	1											
NSPS	0.19	0.51**	0.54**	1										
SSPN	0.03	-0.34**	-0.46**	0.08	1									
SL	0.16	0.26*	0.26*	0.50**	-0.01	1								
DH	0.30**	0.19	-0.01	0.22*	0.17	0.14	1							
NN	0.15	0.05	-0.08	-0.05	-0.02	0.10	0.00	1						
ST	0.03	0.22*	0.23*	0.39**	-0.14	0.10	0.07	0.00	1					
Lg	-0.10	0.17	0.33**	0.25*	-0.19	0.30**	0.22*	0.06	0.31**	1				
PH	0.32**	0.06	-0.24*	0.20	0.29**	0.11	0.52**	0.08	0.13	-0.03	1			
PL	-0.09	-0.12	-0.14	-0.07	0.05	-0.22*	-0.17	-0.05	0.14	-0.21*	0.32**	1		
NET	-0.11	-0.15	-0.08	-0.10	0.03	0.08	-0.23*	0.00	-0.17	-0.10	-0.29**	0.00	1	
Chl	0.11	0.01	-0.06	0.07	0.14	-0.06	-0.08	0.12	-0.02	-0.02	-0.06	-0.12	0.11	1
YLD	0.06	0.27*	0.32**	0.09	-0.07	0.09	0.05	-0.01	0.06	0.43**	-0.20	-0.17	-0.03	0.01

[$] TKW: 1000- kernel weight; WSS: Weight of seeds per spike; NSS: Number of seeds per spike; NSPS: Number of spikelet per spike; SSPN: Sterile spikelet number; SL: Spike length; DH: Days to heading; NN: Number of nodes; ST: Stem thickness; PH: Plant height; PL: Peduncle length; NET: Number of effective tillers; Chl: Chlorophyll rate, YLD: Yield

*, ** significant at 5% and 1% level of probability

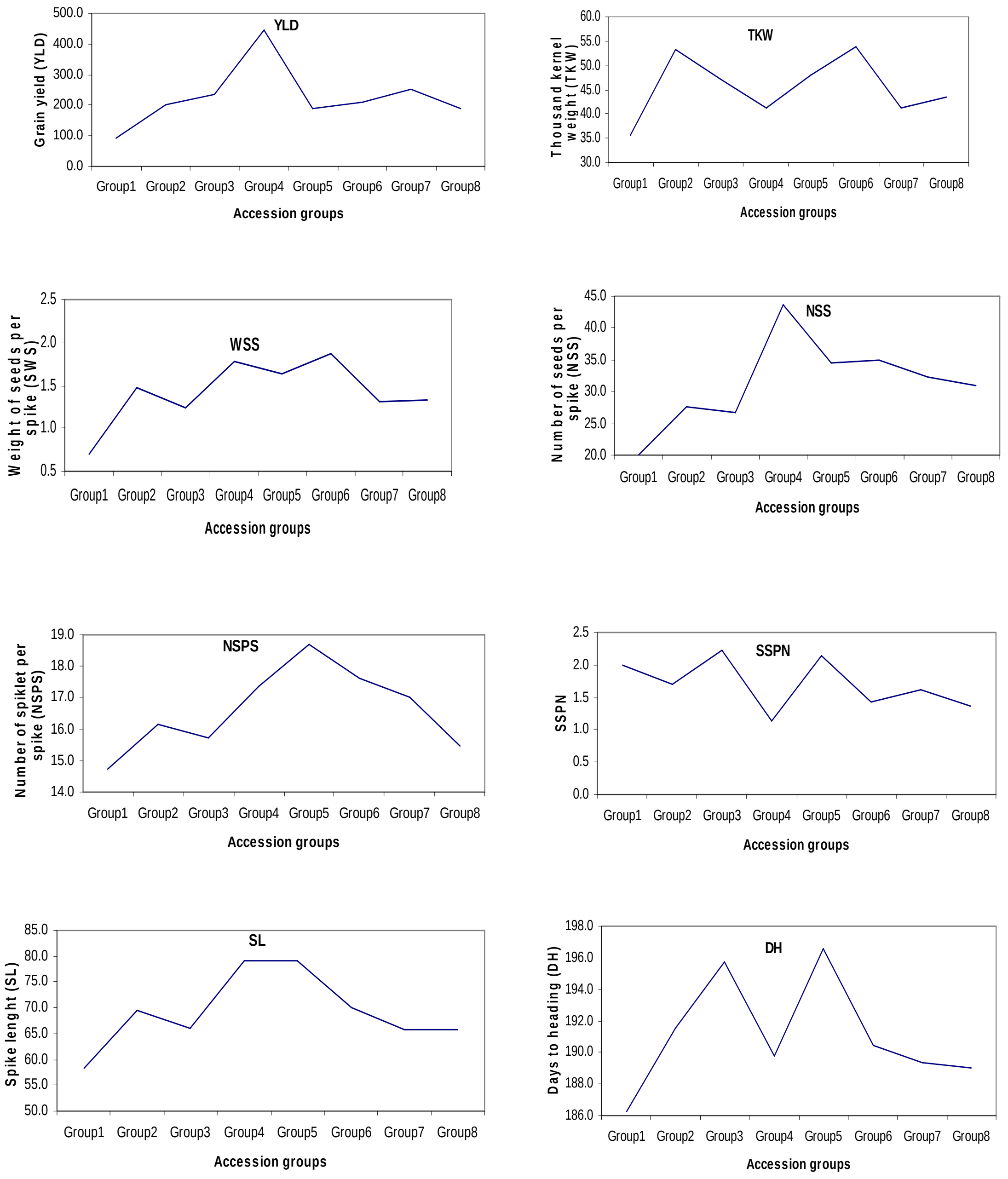


Fig 2. Performance plots of eight durum wheat accession groups identified by cluster analysis for each trait .

correlation coefficient between any two traits in Fig. 4 can be approximated by the cosine of the angle between the vectors. The most prominent positive associations are: a strong positive association between PH, NN, DH and TKW; between SSPN and PL; between NSPS, ST, SL and WSS; and between YLD, NSS and Lg as indicated by the small acute angles between their vectors. Fig. 4 also shows a negative association between YLD with PL and NSPS as indicated by the large obtuse angles between their vectors (angles near to 180 degrees). Such negative relationships were also found between NET with TKW and DH, between NSS with PL and SSPN, and between Lg with PL and SSPN. There was an approximately zero correlations between PH with attributes YLD, NSS and Lg, and between DH with YLD, NSS and Lg, between TKW with YLD and Lg. No association was also observed between NSPS and SSPN. Correlation coefficients among the attributes (Table 2) can further verify these results and indicate the biplot correctly displays relationships among the traits. However, exact match is not to be expected, because the biplot describes the interrelationships among all traits on the basis of overall pattern of the data, whereas correlation coefficients only describe the relationship between two traits (Yan and Rajcan, 2002). The traits with strong positive associations are tending to discriminate accessions in similar fashions and those with negative associations tend to discriminate accessions in opposite direction. For instant, the accessions discriminated by the YLD are differ from those discriminated by PL and SSPN. Similarly the accessions discriminated based on TKW and DH are differ from those selected by NET (Fig. 4). This indicates the biplot is a power tool in grouping of traits and their ability in discriminating of accessions. The length of the attribute vector also is a good marker to show ability of traits in discriminating accessions; the traits with longer vector will

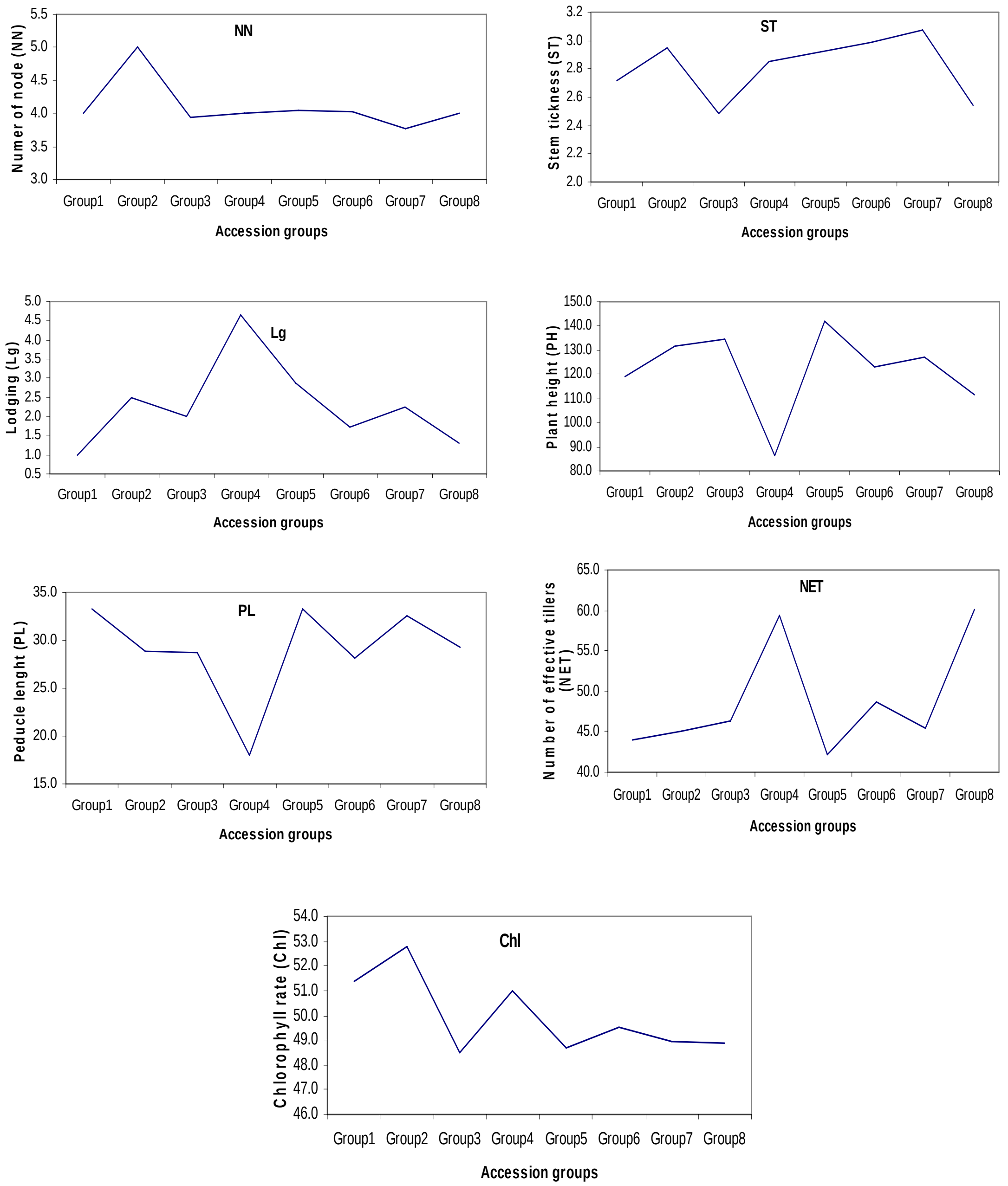


Fig 2. (Continued)

be more success in discriminating accessions. In this case most of the traits had good ability for discriminating accessions. The Chl and NN had the least discriminating ability while the PH, SNS, SWS, SPNS, DH and TKW had the highest discriminating ability.

Discussion

This study focused on the characterization of 85 durum wheat accessions collected from several countries using different agro-morphological attributes under irrigated condition in Iran. Results showed high level and significant variation among the accessions, traits and their interactions and verified the accession groups can be separated based on studied traits. High variation in agro-morphological traits among durum wheat accessions was reflected by wide ranges for most of the characteristics (Supplementary 2). Phenotypic variation for the durum accessions can be also explained on the basis of the diverse geographic origins of these accessions. Since most of studied traits (see Supplementary 2) are quantitative, the extensive variability among accessions is probably attributed to genetic differences as well as the environment in which they were regenerated (Moriss, 2009). The multivariate analyses helped in finding contrasting durum accession groups for future breeding programs. Crossing of group 4 accessions, characterized by highest yielding potential, number of seed per spike (NSS), number of effective tillers (NET) and resist to lodging, with groups 2 and 6, characterized by 1000-kernel weight (TKW) and stem thickness (ST), can be used to produce breeding populations to be used in recurrent selection for improved and combining yield with TKW and ST. These populations could contain new recombinant genotypes with the intermediate to high combination of YLD, TKW and ST that will be valuable in developing durum wheat cultivars for the irrigated condition of Iran. The results also showed the accessions in group 4 had the least PH, which indicates positive response to N fertilizer to reach to their potential.

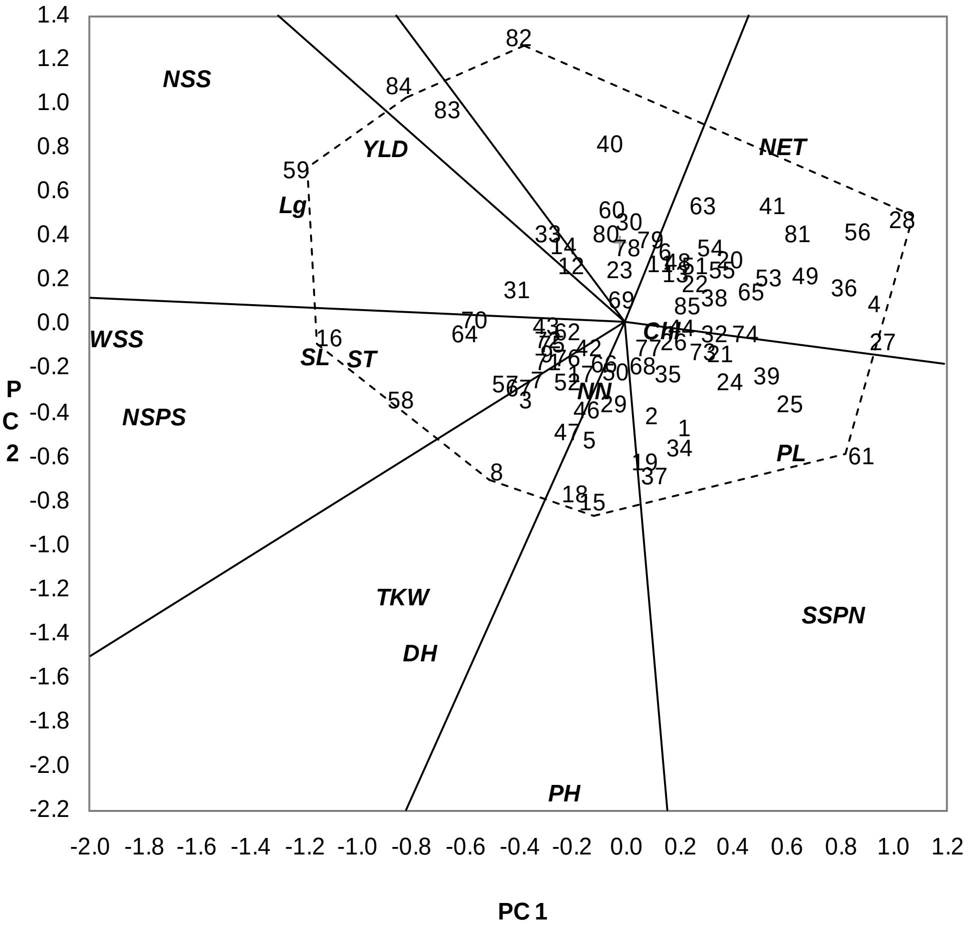


Fig 3. biplot showing the accession-by-trait data analysis of 85 accessions and 15 agro-morphological attributes. TKW: 1000- kernel weight; WSS: Weight of seeds per spike; NSS: Number of seeds per spike; NSPS: Number of spikelet per spike; SSPN: Sterile spikelet number; SL: Spike length; DH: Days to heading; NN: Number of nodes; ST: Stem thickness; PH: Plant height; PL: Peduncle length; NET: Number of effective tillers; Chl: Chlorophyll rate, YLD: Yield

Groups 1 and 8 with the least DH and the highest lodging had the lowest yielding performance (Fig. 2). These two groups showed more earliness and were susceptible to irrigation (with the highest lodging). Therefore they may be more suitable for rainfed conditions. The biplot technique was used as an useful statistical tool for visualizing accession-by-trait data and helped correctly in showing interrelationships among the traits. It provided a tool for visual comparison among accessions on the basis of multiple traits. The biplot also can be used in independent culling based on multiple traits and in comparing selection strategies (Yan and Rajcan, 2002). The vertex accessions in biplot can be characterized for specific attributes, while those are near to origin of biplot can be considered as accessions with characterized for a wide range of attributes. Based on the trait relationships, different group of traits with different responses in discrimination of accessions were identified. The accessions Nos. 59, 84, 83 had good potential based on the attributes of grain yield (YLD), number of seeds per spike (NSPS) and non-lodging (Lg) (Fig. 4). The responses of these accessions were poor for the attributes PL and SSPN. The accession Nos. 61, 25, 1, 24, 25, 36, 34 had the best response for PL and SSPN. The accession Nos. 8, 18, 15, 47 and 5 were the best for the attributes TKW, DH and PH. Two attributes (Chl and NN) were poor in discriminating accessions due to their short vectors. The attributes WSS, NSPS, SL were tended to discriminate in the same fashion and were associated with yield performance. These traits were able to discriminate the accession Nos. 16, 58, 64 and 70. Appling biplot technique to discriminate of accessions based on traits already used in different crops. For instance, this methodology is applied in white clover (Jahufer *et al.*, 1997), wheat (Delacy *et al.*, 2000), soybean (Yan and Rajcan, 2002; Cicek *et al.*, 2006), white lupin (Rubio *et al.*, 2004) and oat (Peterson *et al.*, 2005; Yan and Frégeau-Reid, 2008). This study also compared the agro-morphological attributes of durum wheat from Iran and 10 other countries under irrigated condition. The data obtained show that both Iranian and non-Iranian germplasm resources represent a wide range of diversity for agro-morphological traits. The investigations were also very useful in choosing the precious accessions for further breeding programs. Results of accession classification revealed that accessions within each cluster belonged to different countries which suggested that there was no clear relationship between accessions and geographical diversity. Therefore, more emphasis has to be directed to accessions level rather than geographical level as a source of diversity in this germplasm. Such results have been reported in different crops by several studies on white clover (Jahufer et. Al., 1997), durum wheat (Annicchiarico *et al.*, 2000), safflower (Jaradat and Shahid, 2006; Khan *et al.* 2009) and watermelon (Szamosi *et al.*, 2009). These results could be attributed to free exchange of materials that may have overlapped the previous diversity distribution pattern of the domesticated

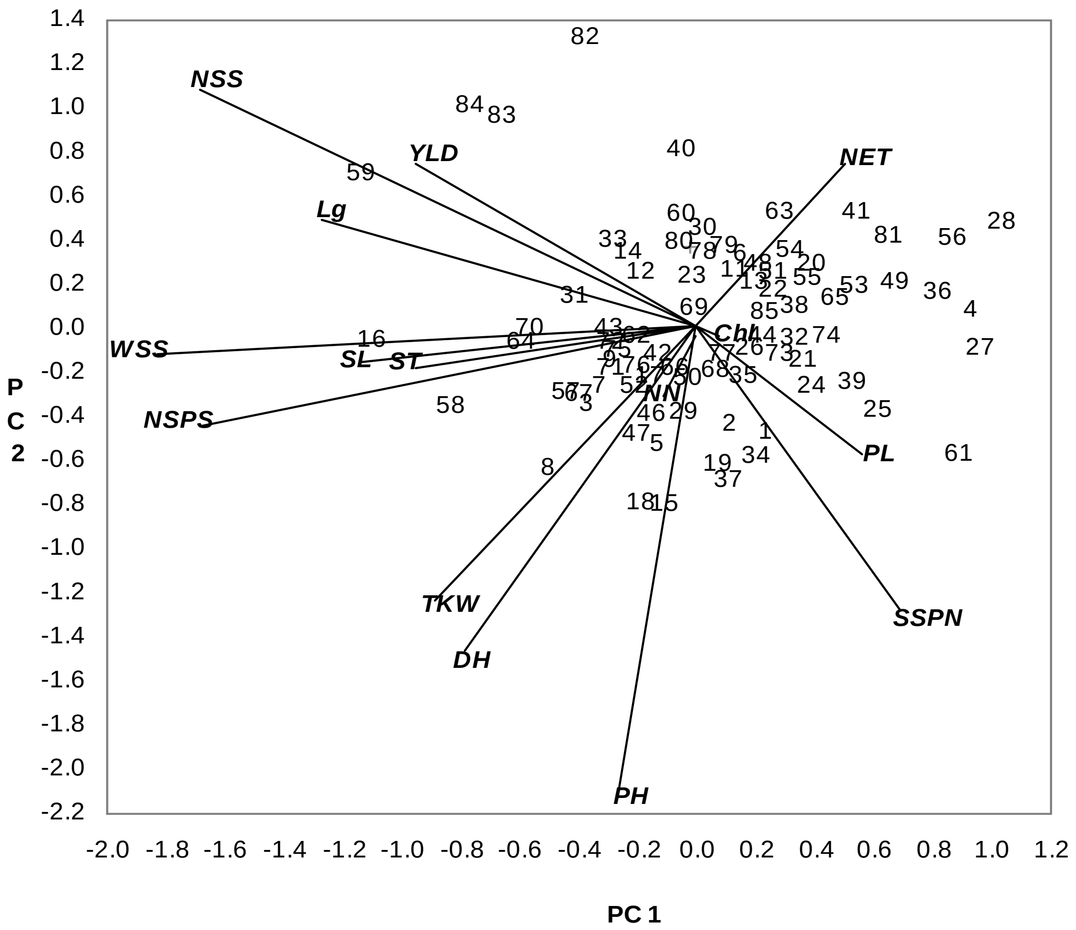


Fig 4. The biplot showing the interrelationship among all measured traits for 85 durum wheat accessions. The numbers are ccessions and the vectors are traits. TKW: 1000- kernel weight; WSS: Weight of seeds per spike; NSS: Number of seeds per spike; NSPS: Number of spikelet per spike; SSPN: Sterile spikelet number; SL: Spike length; DH: Days to heading; NN: Number of nodes; ST: Stem thickness; PH: Plant height; PL: Peduncle length; NET: Number of effective tillers; Chl: Chlorophyll rate, YLD: Yield

species (Jaradat and Shahid 2006). However these results supported that based on both qualitative and quantitative measurements, Iranian and non-Iranian accessions show many similarities, therefore cannot be separated clearly. However, phenotypic evaluation is influenced by environment and might not distinguish between closely related accessions. Therefore further and molecular investigations are needed to verify this statement.

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