

Evaluation and Characterization of International Durum Wheat Nurseries under Rainfed Conditions in Iran

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ABSTRACT

Information on international nurseries for different plant attributes can be effective and useful in national breeding programs to improve crop productivity under rainfed conditions. An international durum wheat nursery consisting of 228 breeding lines and five check cultivars, received from the International Center for Agricultural Research in the Dry Areas (ICARDA), along with a local landrace were evaluated under rainfed conditions in the 2006-07 cropping season in the West of Iran. Several main traits i.e., days to heading, days to maturity, plant height, 1000-kernel weight and grain yield were recorded for preliminary evaluation of the germplasm. Several simple univariate methods and genotype-by-trait (GT) biplot analysis were used to examine the variation within the nursery and to provide information to enable better germplasm utilization in the national durum breeding program. Wide variation was observed for the genotypes based on the studied traits. It was found that the genotypes with the highest grain yield were tall and early in flowering and maturity, suggesting it is possible to find genotypes with good agronomic performance which warrant further evaluation to select elite lines for commercial release. The comparison of genotypes based on multiple traits confirmed the possibility of finding contrasting groups. The high heritability for the traits (except for 1000-kernel weight) is encouraging from a standpoint of increasing the selection efficiency. In conclusion, the GT-biplot offers a useful analytic tool for examining the variation among large sets of lines, for exploring multiple trait data and for aiding in multi-trait selection.

Keywords: durum wheat, genotype characterization, GT-biplot, international nursery, trait relations

INTRODUCTION

Durum wheat (*Triticum turgidum* L. var. durum) occupies small part of the wheat acreage, and accounts of 10% of total wheat production. World durum wheat production in recent years has been estimated to 30 million tons, with the European Union, Canada and the United States accounting for nearly 60% of total production. Durum wheat is one of the most important crops in the moderate rainfall areas of the Central and West Asia and North Africa (CWANA) region. This region produces about 13 million tons annually. Turkey, Syria, Morocco, Tunisia, Algeria and Iran account for 84% of that production (Bernnan *et al.* 2002). Durum wheat is produced predominantly under rain-fed conditions and it is generally grown under drier and more stressful conditions than bread wheat. Through regional and international collaborations, improved germplasms is regularly exchanged and tested by the national durum wheat research programs to identify adapted and high yielding genotypes (Sharma *et al.* 2008). Durum wheat in Iran is cultivated across diverse environments, ranging from warm lowlands to cold highlands. These environments are prone to severe drought every 5–7 years (Mohammadi *et al.* 2010, 2011), and rainfall and temperatures show large and unpredictable fluctuations within and over several cropping seasons. The Dryland Agricultural Research Institute (DARI) in Iran receives annually durum wheat germplasm nurseries from ICARDA, which are tested and compared to existing landraces and improved checks across diverse environments.

Numerous works have focused on the study of genetic diversity of durum wheat towards its efficient utilization in breeding (Aghaee *et al.* 2010; Melnikova *et al.* 2010).

International breeding programs aim to assist national programs to increase agricultural production by developing

superior cultivars. International nurseries, supplied upon request, provide useful germplasm for further selection and evaluation by national breeding programs to release improved varieties. The objective of durum wheat breeding undertaken at ICARDA is to assist CWANA countries to enhance durum wheat production by developing improved germplasm, improving crop management, upgrading manpower capabilities and developing efficient research methodologies (ICARDA 1988).

Three terms, passport, characterization and preliminary evaluation data, are used in genetic resources documentation (Anon 1985, 1991, 1995). Passport data is acquired at the time of collecting the sample and records among other things time and location of the collection and main descriptors of the accession. Characterization data consists of observations, which are highly heritable, easily observable and expressed in all environments. Normally these data are recorded during the first seed multiplication. Characterization data can be used as a management tool in future regenerations to allow the gene bank to validate the identity of an accession (DeLacy *et al.* 2000). Evaluation data is done by users to find the sources of sought traits. It is expected that the attributes measured for evaluation be selected by a consensus of users of the crop.

However, germplasm evaluation and variety selection must be based on multiple traits or breeding objectives (Yan and Rajcan 2002; Yan and Frégeau-Reid 2008). For most crops, although yield is the number one breeding objective, the other agronomic traits are also very important. A successful breeding program is the one having a pre-breeding activity to supply parental germplasm used in crosses and selection to develop promising lines for release to farmers. The requirement for a new variety is that it meets the minimum criterion for all essential breeding objectives while

having a superior package of traits, as measured by the selection index and failure to meet the minimum criterion for any breeding objective will lead to the failure of the variety. This is where independent culling and selection index must be applied. In contrast, the requirement for a parent is that it is outstanding in one or more of the breeding objectives; a higher selection index is desirable but not essential (Yan and Fréreau-Reid 2008).

The main objectives of this study were to (i) examine the variation within the durum wheat international nursery received from ICARDA using the univariate and multivariate techniques, (ii) compare the introduced germplasm with the currently grown durum cultivars, (iii) identify introductions that warrant further evaluation, and (iv) to provide information for a reliable and efficient durum wheat improvement program for rainfed conditions of Iran.

MATERIALS AND METHODS

Plant material

International durum wheat nurseries are obtained annually from ICARDA for evaluation by the Dryland Agricultural Research Institute (DARI), Iran. In this study 228 durum wheat genotypes and five international durum checks, received from ICARDA, along with a local durum check (Zardak) were evaluated in one of the main research stations of DARI, Sararood research station, Kermanshah, Iran (34° 19' N; 47° 17' E, 1351 masl) during October to July in 2006-2007 cropping season. This site is representative of the areas with moderate cold winter and serves to breed durum wheat for both warm and cold areas of Iran (Mohammadi *et al.* 2010, 2011). The site is characterized by minimum and maximum temperature of -20 and 45°C, respectively, and 60-100 days of freezing temperatures annually. The average long-term annual precipitation is estimated to 455 mm, consisting of 90% rain and 10% snow. The soil at the site was clay loam. The plant materials were sown in 2 rows of 2.5 m long in a non-replicated trial. The lines were distributed in 12 blocks and the five checks and local landrace were repeated after every 20 experimental lines. Weeds were controlled manually. Fertilizer rates were 50 kg N ha⁻¹ and 50 kg P₂O₅ ha⁻¹ applied at planting. The main traits, which are more important for preliminary evaluation of germplasm under rainfed condition, were recorded for each entry. These traits included the days to heading (DH), days to maturity (DM), plant height (PH), thousand kernel weight (TKW) and grain yield (YLD). Days to heading was designated as the day until 50% of the plants in the plot had at least one open flower. Days to maturity were when 50% of the plants in the plot had yellow leaves. The PH was measured for each genotype at physiological maturity stage. The YLD after harvesting was measured for each genotype at each plot, and the TKW was weighing 1000 grains from each entry.

Statistical analysis

Several simple univariate statistics including minimum, maximum, range, mean and standard deviation (SD) were used to describe the variability among the genotypes, which were calculated for each trait based on the genotypes (Maggs-Kölling *et al.* 2000; Cicek *et al.* 2006; Prospero *et al.* 2006; Morris 2009). The data from the check cultivars were used for ANOVA and heritability analyses. Analysis of variance was conducted by the MSTAT software and Broad-sense heritability (H²b) was computed for each trait as: $H^2b = \sigma^2g / (\sigma^2g + \sigma^2e/r)$, where σ^2g and σ^2e are the components of variance for the genotypes and error effects respectively, which were calculated from the expected mean squares of the ANOVA (Nyquist 1991). Combination of the mean and SD for each attribute was also used to identify superior genotypes. In this case five categories of genotypes for each studied trait can be formed. In the case of YLD, TKW and PH, the genotypes with values > (mean + SD) and > (mean + 2SD) can be identified as desirable genotypes and those with values < (mean - SD) and < (mean - 2SD) can be identified as undesirable ones (Shakhatareh *et al.* 2010). In the case of the DH and DM, the genotypes with values less than mean, (mean-SD) and (mean-2SD) will be more desirable. The geno-

types with values between mean ± SD are average in their performance. This simple methodology can be useful for preliminary selection of desirable genotypes base on each attribute.

The GT-biplot, as described by Yan and Rajcan (2002), is constructed by plotting the first principal component (PC1) scores of the genotypes and the traits against their respective scores for the second principal component (PC2) that result from singular value decomposition (SVD) of traits-standardized data to study the genotype-by-trait (GT) interaction and to identify superior genotypes (Yan and Rajcan 2002). In the GT-biplot, a vector is drawn from the biplot origin to each marker of the traits to facilitate visualization of the relationships among the traits. The correlation coefficient between any two traits is approximated by the cosine of the angle between their vectors. Acute angles show a positive correlation, obtuse angles show a negative correlation and right angles no correlation. The length of the vector describes the discriminating ability of the trait (Yan and Rajcan 2002). A short vector may indicate that the trait is not related to other traits, that there is a lack of variation or that it is not suitable for genotype discrimination. All biplots presented in this study were generated using the GGE biplot software (Yan 2001). For details on theory and application of GT-biplot see Yan and Rajcan (2002).

RESULTS

Description of data

The data recorded on the 234 genotypes (228 experimental lines, five checks and Zardak landrace) and five traits are summarized in **Table 1**. For each trait, the overall means, maximum, minimum, range, and SD are given. For days to heading (DH), the values ranged from 181-189 days with a mean value of 184. The DH values for the international checks ranged from 182 to 186, while Zardak headed 186 days after emergence. This data showed the existence of 12 genotypes heading 5 days earlier than the local check. Based on DM, the experimental genotypes had a mean value equal to 215 days with a range from 212-221 days, with 209 of them earlier than the local check.

High variation was found among the genotypes for the

Table 1 Descriptive agronomic data of 234 genotypes from international durum wheat nursery (IDON) and five international and local checks evaluated under rainfed condition in 2006-07 cropping season, in Iran.

Statistics	Traits				
	DH	PH	DM	TKW	YLD
Mean	184	82	215	34	5180
Min	181	60	212	23	2660
Max	189	109	221	49	7420
Range	8	49	9	26	4760
SD	1.6	6.9	1.5	4.8	886.7

DH: days to heading; DM: days to maturity; PH: plant height; SD: standard deviation; TKW: thousand kernel weight; YLD: grain yield

Table 2 Grouping of durum wheat genotypes based on integrating mean values and SD for each studied traits.

Statistics groups	DH	PH	DM	TKW	YLD
Number of genotypes in each group					
>Mean	89	120	80	110	116
>Mean + SD	11	32	17	42	42
>Mean+2SD	2	4	6	4	4
<Mean	89	99	93	103	118
<Mean-SD	12	31	3	33	43
<Mean-2SD	0	2	0	2	4
Percentage (%) of the genotypes in each group					
>Mean	38	51	34	47	50
>Mean +SD	5	14	7	18	18
>Mean+2SD	1	2	3	2	2
<Mean	38	42	40	44	50
<Mean-SD	5	13	1	14	18
<Mean-2SD	0	1	0	1	2

DH: days to heading; DM: days to maturity; PH: plant height; SD: standard deviation;

TKW: thousand kernel weight; YLD: grain yield

Table 3 Analysis of variance, means comparison and heritability estimates for studied traits of durum wheat checks used

ANOVA Source	df	Traits				
		DH	PH	DM	TKW	YLD
Block	11	3.1	32.2	3.1	38.4	1197064
Genotype	5	33.3**	2137.1**	18.5**	23.8 ns	3922376**
Error	55	1.4	24.3	2.7	17.3	493347.3
Mean comparison for check cultivars						
Gidara (Check)		186 a	77 e	218 a	33 a	5003 b
Haurani (Check)		182 c	102 b	216 bc	33 a	4248 c
Korifla (Check)		185 b	82 d	215 c	36 a	4840 b
Omrabi (Check)		182 c	96 c	215 c	36 a	5610 a
Waha (Check)		185 ab	75 de	216 c	33 a	5760 ab
Zardak (Local check)		186 a	109 a	217 ab	31 a	4157 c
Broad-sense heritability (h^2b)		95.5	98.8	86.1	54.4	87.9

DH: days to heading; DM: days to maturity; PH: plant height; SD: standard deviation; TKW: thousand kernel weight; YLD: grain yield

Values followed by common letters are not significantly different at 5% level of probability

h^2b : broad sense heritability (%) estimated from ANOVA

plant height (PH). The values recorded for the PH varied from 60 - 109 cm with a mean of 82 cm and highest value recorded for the local check (Table 2).

TKW averaged 34 g with a range of 23 - 49 g. The international checks had lower TKW ranging from 33 to 36 g and local check had 31 g. Around 170 genotypes had TKW greater than local check and 110 genotypes had TKW greater than overall mean (34 g).

The grain yield (YLD) varied from 2660 to 7420 kg ha⁻¹ with a grand mean equal to 5180 kg ha⁻¹. Among the international checks, the YLD varied from 4248 to 5760 kg ha⁻¹, and 202 genotypes performed better than the local check and 116 experimental entries had yield performance greater than the mean, showing the potential to select higher yielding genotypes from the international durum wheat nursery.

The superior genotypes can be identified for each trait based on integrating of mean-value with SD. The groups including genotypes with a trait value of (mean + SD) and (mean + 2SD) will give an indication of the superior genotypes indicating high probability of success in selection in the case of sufficiently high heritability (Shakhatreh *et al.* 2010). Table 2 shows the number and percentage of durum wheat genotypes which had a better performance than mean, (mean + SD) and (mean + 2SD) based on each trait. The percentage of genotypes with values higher than the mean across all traits varied from 34% (for DM) to 51% (for PH) (Table 2). Around 50% of the genotypes had grain yield better than the mean, while 47% had TKW values higher than the mean and 51% had PH better than the mean. Based on these three agronomic traits, in general, about 50% of the genotypes had a better performance than the overall mean. In the case of days to heading, 38% of the genotypes had DH values less than the mean, while for DM, 40% of the genotypes had DM values less than the mean. In general about 40% of the genotypes tend to flower and mature before other genotypes. This set of genotypes will be suitable for improving the local check based on earliness. Around 19% of genotypes had YLD and TKW better than the (mean + SD), while 14% of the genotypes showed PH higher than the (mean + SD). In contrast, just 5 and 13% of the genotypes had DH and DM values less than the (mean - SD) (Table 2). The percentages of genotypes with values better than the (mean + 2SD) for YLD, TKW and PH were just 2%, while no genotype was found for the DH and DM with values less than the (mean - 2SD).

The results of ANOVA and mean comparison showed highly significant variation among the check cultivars for all the traits (except for TKW) (Table 3). Broad sense heritability estimates ranged from 54.4 g for TKW to 98.8 cm for PH. The other traits had high heritabilities (Table 3). The high heritability for most of the traits (except for TKW) is encouraging from the standpoint of breeding for high value of studied traits. The average heritability of TKW would indicate that selection for average TKW could be difficult unless sources of greater genetic variation were found.

Genotype by trait biplot analysis

Fig. 1 is a GT-biplot with a polygon view presenting the data of 234 genotypes and five major agronomic traits. The polygon view of a GT-biplot is the best way to visualize the interaction patterns between genotypes and traits and to effectively interpret the results of the biplot (Yan and Rajcan 2002). The biplot explained 62.2% of the total variation of the standardized data (Fig. 1). According to Fig. 1, the five traits fell into four groups, while the genotypes fell into 11 groups. The phenological traits (DH and DM) tend to be separated from each other with the genotype no. 149 as the latest in flowering and maturity. In addition, the entries 213, 227, 74, 215, 220, 68, 25, 62, 44, 229, 224, 206, 136, 71, 222, 75, 167, 1 and 169 tend also to flower and mature late.

The second group is based on YLD with genotype no. 182 as the best yielder, along with other high yielding lines 104, 33, 185, 190, 177, 196, 176, 78, 20, 28, 187, 81, 79, 174, 14, 81, 162, 180, 102, 189, 55, 28, 66, 36, 111, 98, 159, 84 and 208. The next group is based on TKW with genotype no. 41 having highest value and the lines 171, 192, 14 and 95 also showing high TKW. The PH made last group without any superior genotype. The vertex genotypes No. 78, 116, 103 and 151 without any trait in their sectors were not the best for any trait and indeed they were the poorest genotypes for most of the traits.

Relationships among traits

The first two PCs in the GT-biplot captured for 62.2% the total variation of the standardized data (Fig. 2). This relatively average proportion reflects the complexity of the relationships among the measured traits under rainfed conditions. Nevertheless, the fundamental patterns among the traits should be captured by the biplots (Kroonenberg 1995). In the GT-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. Provided that the biplot explained a sufficient amount of the total variation, the correlation coefficient between any two traits is approximated by the cosine of the angle between their vectors. A strong positive association was found between YLD and PH indicating they are similar in ranking of genotypes (Fig. 2). The DH and DM were positively correlated, showing the genotypes which tend to be early flowering are also early maturity. A strong negative correlation was found between the phenological traits (DH and DM) with the agronomic traits (YLD and PH) as indicated by the obtuse angles between their vectors, showing that the genotypes with good performance tend to earlier in flowering and maturity. The TKW was not associated with the YLD and PH as indicated by the right angle between their vectors, indicating they are independent in ranking of genotypes. The TKW was also independent from DM in ranking of genotypes and negatively associated with DH.

This study focused on the evaluations of 234 genotypes,

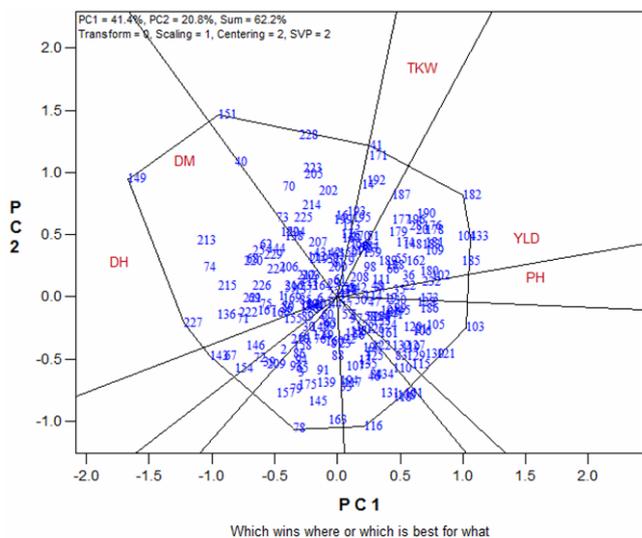


Fig. 1 Polygon view of "which-win-where" view of genotype by trait biplot for 234 durum wheat genotypes and five traits. DH: days to heading; PH: plant height; DM: days to maturity; TKW: thousand kernel weight; YLD: grain yield. The numbers are the genotype codes.

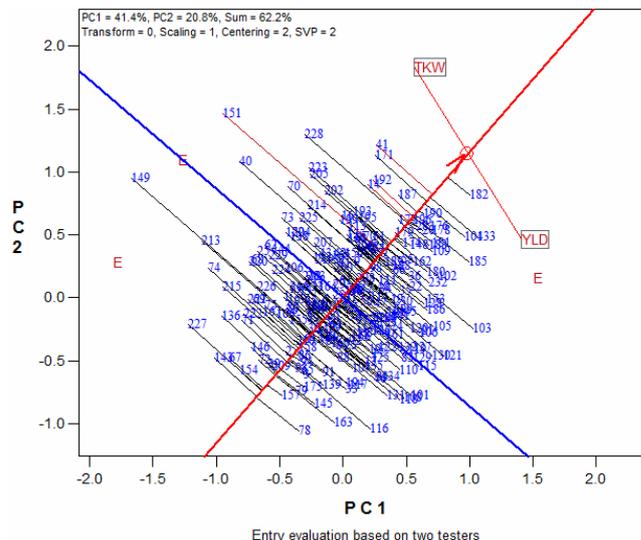


Fig 3 The GT-biplot which showing the performance of durum wheat genotypes based on thousand kernel weight (TKW) and grain yield (YLD) traits.

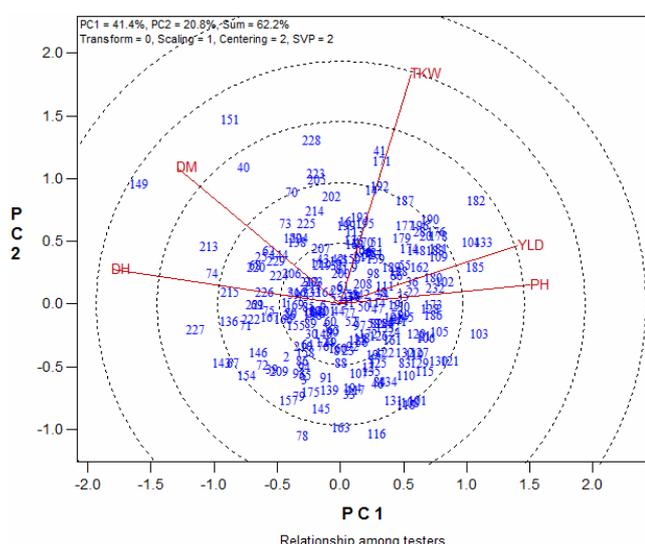


Fig 2 Polygon view of genotype by trait biplot which showing relationship among studied traits and the 234 durum wheat genotypes. DH: days to heading; PH: plant height; DM: days to maturity; TKW: thousand kernel weight; YLD: grain yield. The numbers are the genotype codes.

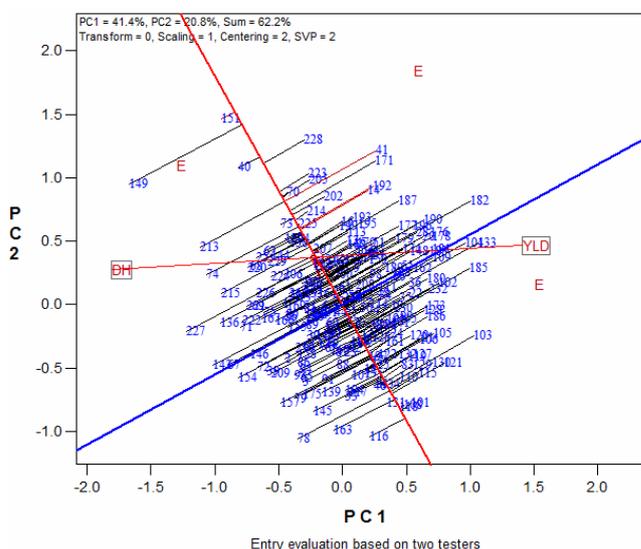


Fig. 4 The GT-biplot which showing the performance of durum wheat genotypes based on days to heading (DH) and grain yield (YLD) traits.

selected from ICARDA, on the basis of multiple traits under rainfed conditions in Iran. Results showed high level of variation among the genotypes, traits and their interactions and verified that the genotypes can be characterized based on multiple traits. The GT-biplot also can be used to discriminate genotypes based on each trait (Yan and Rajcan 2002). The best genotypes based on YLD and PH were genotypes no. 185, 133, 104, 182 and 102, while the genotypes no. 14, 171, 192, 14 and 187 were the best based on the TKW (Fig. 2). The genotypes no. 149, 213, 151, 74, 215, 227, 40, 151, 220 and 68 characterized by phenological traits (DH and DM) as genotypes with late flowering and maturity and with lowest grain yield and plant height. In contrast, the genotypes characterized by high YLD and PH tend to flower and mature before other genotypes. The genotypes near to origin of biplot had average performance on the basis of multiple traits. However, the negative strong correlation between the phenological traits (DH and DM) and yield indicates that it should be possible to select genotypes that are high in yield and earlier in DH and DM.

Evaluation of genotypes based on two traits

Fig. 3 compares the relative performance of genotypes based on YLD and TKW traits. The performance of genotypes can be easily compared using GT-biplot. To compare the genotypes based on YLD and TKW, their markers should first be connected by a straight line; and then a perpendicular line that passes through the plot origin will be drawn. This perpendicular line divides the genotypes into two groups, each of these two traits having some genotypes on its side of the perpendicular, and vice versa. Accordingly the genotypes which are placed on the side of YLD can be separated from those are placed on the side of TKW. According to Fig. 3, if the objective is to separate the most favorable genotypes based on YLD and in contrast the genotype nos. 41, 171, 187, 192, 14, 228, 151, 223, 203, 202, 70, 214, 40, 195, 193 based on TKW. This indicates the genotypes can be easily grouped based on traits with GT-biplot analysis. Similarly Fig. 4 compares the performance of genotypes based on YLD and DH. The two traits have the biggest difference from each other, showing they tend to discriminate

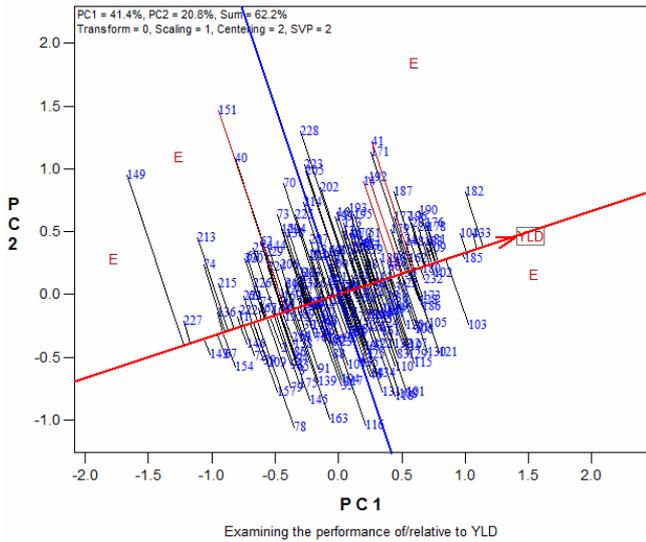


Fig. 5 The GT-biplot which showing the ranking of durum wheat genotypes based on grain yield (YLD).

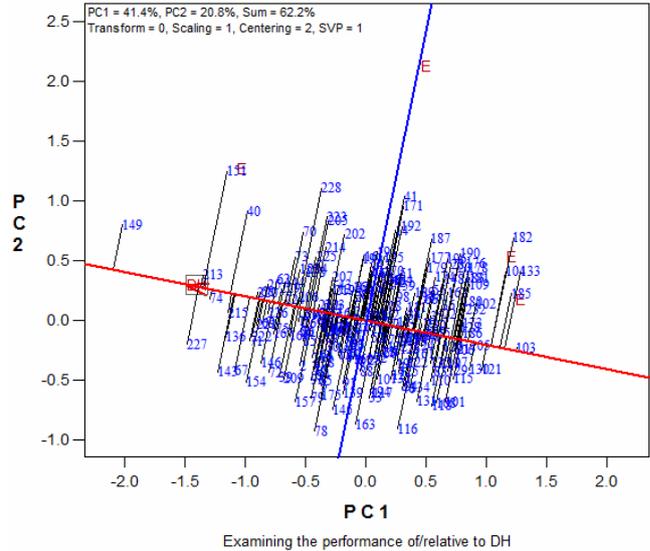


Fig. 7 The GT-biplot which showing the ranking of durum wheat genotypes based on days to heading (DH).

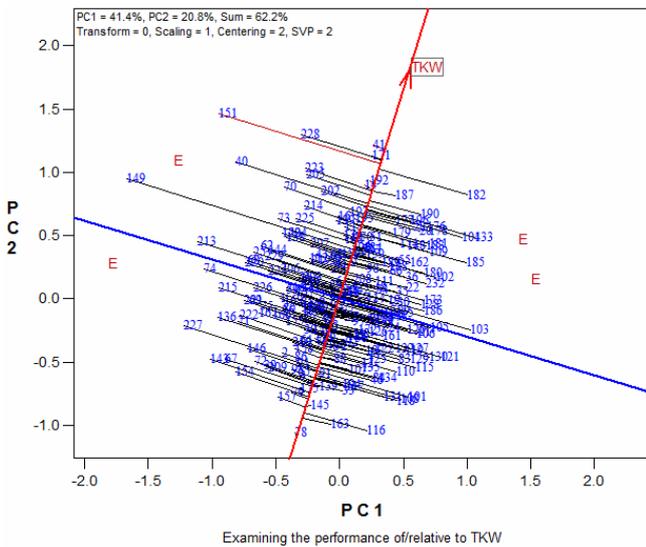


Fig. 6 The GT-biplot which showing the ranking of durum wheat genotypes based on thousand kernel weight (TKW).

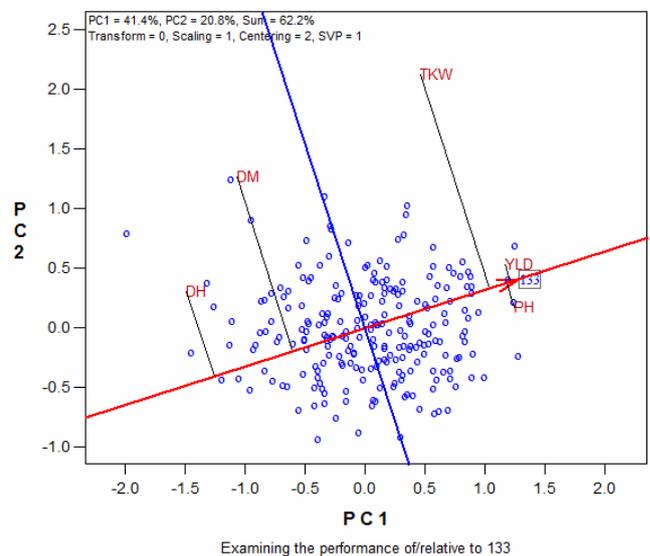


Fig. 8 Ranking of traits based on the highest yielding durum wheat genotype. DH: days to heading; PH: plant height; DM: days to maturity; TKW: thousand kernel weight; YLD: grain yield.

the genotypes in opposite directions. The genotypes can be separated into two groups: those placed on the side of YLD which have high yield and tend to flower before the other genotypes which are placed on the side of DH. This indicates that GT-biplot is an excellent tool for visualizing genotype-by-trait data, genotype characterization and for revealing the interrelationships among crop traits (Yan and Kang 2003; Peterson *et al.* 2005; Egesi *et al.* 2007; Fernandez-Aparicio *et al.* 2009).

Evaluation of genotypes based on specific traits

Fig. 5 illustrates the graphic comparison of the relative performance of all genotypes based on YLD which is the most important trait under rainfed conditions. A line was drawn that passed through the biplot's origin and the YLD marker to make an YLD-axis, and then a line was perpendicularly drawn from each genotype toward the YLD-axis. The genotypes were ranked on the basis of their projections onto the YLD-axis, with rank increasing in the direction toward the positive end (Yan *et al.* 2000; Yan and Hunt 2002). Based on YLD, genotype nos. 182 followed by 133, 104, 185, 103, 109, 78, 76 and 190 had the highest yield performance, while the genotype nos. 149 followed by 227, 143, 67, 154, 213, 74, 215 and 136 were found to be the

most undesirable genotypes. The rest genotypes ranked between these two groups of genotypes.

Fig. 6 also shows the ranking of genotypes based on TKW. The superior genotypes based on the TKW were genotypes no. 41, 171, 228, 151, 182, 192, 14, 187, 205, 223, 190, 40 and 202, while the genotype nos. 78, 163, 116, 157, 145, 79, 154, 67, 147, 75, 139, 55, 209, 72, 39 and 13 can be identified as undesirable ones. Similarly, **Fig. 7** shows the ranking of genotypes based on DH, where the genotype nos. 149, 227, 213, 151, 40, 215, 136, 143, 67, 222 and 154 had the highest number of days to heading (DH) while, in contrast, the genotype nos. 103, 185, 133, 104, 182, 130, 121, 105 and 86 with the lowest values of DH, tend to flower earlier than the other tested genotypes.

Evaluation of a specific genotype based on multiple traits

Fig. 8 compares the relative performance of genotype no. 133 as specific genotype (with the highest yield) on the based of multiple traits. This is done by first drawing a straight line passing through the biplot origin and the marker of genotype 133, then drawing perpendiculars to this

straight line from the trait markers. The genotype 133 was closed to YLD and PH, followed by TKW, DM and DH. The line that is perpendicular to the 133 vector and passing through the biplot's origin separates the traits for which genotype no. 133 performed well. For example, the genotype no. 133 was best for YLD, PH and TKW, while due to its long distance from DH and DM, it was also a top genotype with early flowering and maturity.

DISCUSSION

ICARDA makes contributions in a wide range of areas, including a number of collaborative research projects with Iran, and will have some critical contributions that are not all captured in this study. In particular, ICARDA has the unique role of collecting, evaluating and distributing germplasm to breeding programs for its mandate crops around the world. While the analysis in this report does not identify the value of those activities, it is acknowledged that ICARDA plays a critical role as a source of germplasm for the Iranian breeding programs.

To improve productivity of crops particularly durum wheat, Iran has developed collaboration with ICARDA over more than two decades. The success of durum wheat in Iran, as a food security crop, is largely due to its good ability and capacity to yield well under drought-prone areas. However, large differential genotypic responses occur under varying environmental conditions (Bokanga *et al.* 1994; Mkumbira *et al.* 2003). Iran has been regularly testing germplasm obtained from ICARDA and processed all the way to release some as new varieties in Iran. Fortunately, the results of two decades of breeding efforts jointly between ICARDA and DARI, led to the release of stable durum genotypes with high-yielding ability and adapted to harsh conditions of the rainfed mild cold winter areas of Iran (Mohammadi and Amri 2009).

Phenotypic variation in international nurseries has been studied extensively concentrated on the traits that could benefit modern cultivars (Rubio *et al.* 2004; Vanhala *et al.* 2004; Morris 2009; Shakhatareh *et al.* 2010). The current study focused on the evaluation of variation among the durum wheat international nursery received from ICARDA, under rainfed conditions, for several major agronomical and phenological traits. Results showed high and significant variation among genotypes compared with local check for the traits examined. This was shown using both univariate and multivariate statistical methods. It is well documented that in a breeding program, the first priority trait is yield (García del Moral *et al.* 2003; Peterson *et al.* 2005; Cicek *et al.* 2006). Any cultivar with good agronomic traits will not be successful if it has low yield potential. The positive correlation between yield and PH would be useful if we are selecting for high levels of both traits. However, the strong negative correlation between yield and phenological traits (DH and DM) under rainfed conditions would be helpful when selecting for high yield and earliness. As result of this study, the genotypes with the highest yields were tallest and early flowering and maturity under rainfed conditions. The grain weight (TKW) was not associated with both contrasting traits [(yield + PH) vs. (DH + DM)]. However, the results showed that germplasm can be considered as an important source of genes for earliness, for yield performance, and for improving some yield components such as grain weight which is an important trait under rainfed conditions in the regions where terminal drought stress is common.

According to Yan and Rajcan (2002) we have used the GT-biplot, as already applied by others (Rubio *et al.* 2004; Peterson *et al.* 2005; Gonzalez *et al.* 2006; Yan *et al.* 2007; Yan and Frégeau-Reid 2008), to compare genotypes on the basis of multiple traits and to identify genotypes or groups of genotypes that are particularly good in certain aspects and therefore can be candidates as parents in national durum wheat breeding program. The GT-biplots clearly show which genotype(s) are better for what trait(s), and what traits are similar in characterizing genotypes. Thus, the

genotypes characterized based on YLD and PH are completely different from those characterized using phenological traits (DH and DM). This study demonstrated that the GT-biplot is an excellent tool for visualizing genotype by trait data. By applying this technique to our data, interrelationships among the studied traits were clearly shown, providing more information on these relationships and on characterization of genotypes based on the traits. This approach can be used to select parental material to be used in durum wheat breeding program and to identify promising lines for further evaluation and potential release to farmers in the mild winter cold rainfed areas of Iran. The studied germplasm showed its potential for the genetic improvement of most characteristics using GT biplots. Therefore, it was easy to identify some genotypes with characteristics different from other genotypes for earliness, grain weight and yield performance.

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