RESEARCH ARTICLE

Heritability, Expected Genetic Advance, and Genotype by Trait Analysis for Grain Yield and Agronomic Traits in Durum Wheat under Irrigated and Rainfed Conditions

KAMRANI MORTEZA[1*], ASGHAR EBADI[1], MANOOCHEHR SHIRI[1]

[1]Department of Plant Science, Moghan College of Agriculture and Natural Resources, University of Mohaghegh Ardabili, Ardabil, Iran.

Abstract

Assessment of genetic variability and relationships among traits are basic steps in crop improvement programs. The objectives of this research were to estimate genetic parameters in durum wheat genotypes and to investigate the interrelationships among agronomic traits using the genotype × trait biplot methodology. Fifty durum wheat (*Triticum turgidum* L.) genotypes were studied in a randomized complete block design with three replications under irrigated and rainfed conditions during 2013–2014 growing season. Significant (P > 0. 01) genetic variation for all traits was observed in both irrigated and rainfed conditions apart from total tiller per plant (TT) and fertile tiller per plant (FT), which were not significant in irrigated conditions. Biological yield (BY) showed the highest values of phenotypic and genotypic coefficients of variations and expected genetic advance under rainfed conditions. The highest heritability in a broad sense was observed for grain weight per spike (GWS) followed by stem weight under rainfed conditions. The biplot vector view indicate that there was a strong positive association between grain yield (GY) with BY and thousand kernel weight (TKW) in both conditions. According to polygon view genotypes G11 and G10 were the most favorable genotypes for GY, BY and TKW under irrigated and rainfed conditions, respectively.

Keywords: Durum wheat, expected genetic advance, genotype by trait biplot, heritability in a broad sense.

1. Introduction

Durum wheat (*Triticum turgidum* L.) is grown on 10% of the world's wheat area. In spite of its low acreage, durum wheat is an economically important crop because of its unique characteristics and end products [15]. Durum wheat is one of the most extensively cultivated crops under rainfed conditions in Mediterranean environments, where water stress and high temperature are the main constraints limiting productivity [2], although this condition offers an opportunity for the production of high-quality durum wheat [4].

Breeding programs depend on the knowledge of key traits, genetic systems controlling their inheritance and genetic and environmental factors that influence their expression. To plan an efficient developmental program, it is necessary to have an understanding of the breeding systems coupled with statistical analysis of inheritance data [25]. Analysis of variability among the traits and the association of a particular character in relation to other traits contributing to the yield of a crop would be of a great importance in planning a successful breeding program [14]. According to Raje and Rao (2000) genetic variability is essential in order to realize response to the selection [18]. The estimates of genetic parameters of variation are specific for a particular population and the phenotypic expression of the quantitative characters may be altered by environmental stresses that affect plant growth and development. Genetic advance is also of considerable importance because it indicates the magnitude of the expected genetic gain from one cycle of selection [7]. Heritability is a measure of the phenotypic variance attributable to genetic factors. The estimates of heritability alone give no indication of the associating genetic progress that would result from selecting the best plants. Heritability along with phenotypic variance and the selection intensity, however, promise the estimation of genetic advance or response to selection, which is more useful in the selection of promising lines [8, 9].

The GGE biplot methodology was developed originally for analyzing multi-environment trial data [29]. However, it can also be equally used for all types of 2-way data that assume an entry × tester structure [26]. The genotypes can be generalized as entries, and the multiple traits as testers [19]. The term GE interaction commonly refers to yield variation that cannot be explained by the genotype main effect (G), or the environment main effect (E). In addition, for genotype evaluation both G and GE must be considered simultaneously, and a similar GGE biplot can also be used to genotype evaluation across environments. Yan and Rajcan (2002) used a genotype by trait (GT) biplot, which is an application of the GGE biplot technique to study the GT data. A GT biplot is an effective tool for exploring multi-trait data [30]. It graphically displays the genotype by trait table, and allows the visualization of the associations among traits across the genotypes and of the traits profile of the genotypes [29]. Understanding the traits relationships also facilitates identification of traits that can be used in indirect selection for a target trait and those that may be redundantly measured.

The objectives of this study were: (i) to determine the levels of genetic variation and heritability in studied traits of durum wheat genotypes, (ii) to reveal the interrelationship among grain yield and related characteristics, and (iii) to identify traits that are suitable for indirect selection for improved grain yield in irrigated and rainfed conditions using GT biplot.

2. Material and Methods

2.1. Plant material and experimental conditions

Fifty durum wheat (*Triticum turgidum* L.) genotypes [10] from the wheat breeding project of International Maize and Wheat Improvement Center (CIMMYT) were evaluated during 2013–2014 growing season. The field experimental design was a randomized complete block design (RCBD) with three replications under two contrasting irrigation (irrigated and rainfed conditions) regimes conducted at the research farm of Mohaghegh Ardabili University located at Moghan, Iran (39° 39′ N, 48° 16′ E and 32 m above sea level). The soils at the experimental field are Typic Cambisols of the semiarid tropics with a Sandy-loam texture. Rainfall and mean temperature of the experimental site are shown in Figure 1. Seeds were planted on 1st Nov in the 2013–2014 growing season, in 1.2 m × 3 m plots, consisting of six rows 20 cm apart at 350 seeds m^{-2} for each condition. Based on a soil test before planting, 41 and 46 kg ha^{-1} of N and P_2O_5 were applied, respectively. The first irrigation was performed at the time of late tillering. The subsequent irrigations were applied every 14 days. Irrigated plants received irrigation water and rainfall water, while non-irrigated plants only received rainfall water during the growing season (November–Jun). Weed control in both growing seasons was conducted with an application of the herbicides Clodinafop-propargyl at 0.7 L ha^{-1} and Tribenuron-methyl at rate of 15 g ha^{-1}.
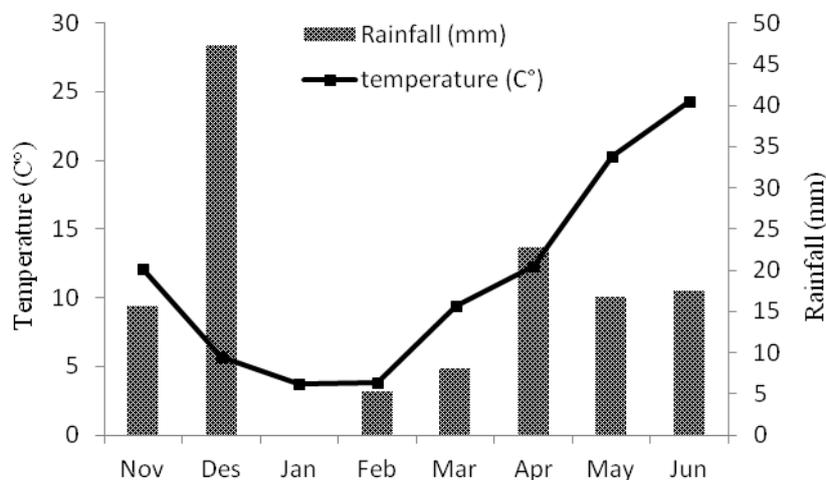

Figure 1. Rainfall and mean temperature for Moghan during 2013-14 cropping season

2.2. Agronomic traits

Grain yield (GY), biological yield (BY) and thousand kernel weight (TKW) were measured by harvesting 1 m^2 of the central part of each plot at maturity. Ten plants were randomly chosen from each plot to measure the number of grains per spike (GNS), grain weight per spike (GWS), spike weight (SPW), peduncle weight (PDW), stem weight (STW), total tiller per plant (TT), fertile tiller per plant (FT) and plant height (PH).

2.3. Data analysis

2.3.1. Estimation of genetic parameters

The genotypic coefficient of variation (GCV) and phenotypic coefficient of variation (PCV) were calculated for all quantitative traits, according to [24], using the equations:

$$GCV(\%) = \frac{\sqrt{\sigma_g^2}}{\bar{x}} \times 100$$

$$PCV(\%) = \frac{\sqrt{\sigma_p^2}}{\bar{x}} \times 100$$

Where σ_g^2 = genotypic variance, σ_p^2 = phenotypic variance and $\bar{x}$ = grand mean of the trait.

The heritability in a broad sense across years was calculated using the variance ratio as follows [17]:

$$h^2 = \frac{\sigma_g^2}{\frac{\sigma^2}{r} + \sigma_g^2}$$

Where σ_g^2 = genotypic variance, σ^2 = environmental variance, r = number of replications.

Expected genetic advance as percentage of the mean assuming selection of the superior 5% of the genotypes was also estimated following the procedure elaborated by [24]:

$$GA(\%) = k\, h^2\, \frac{\sqrt{\sigma_p^2}}{\bar{x}} \times 100$$

Where k = standardized selection differential constant (2.06) at 5% selection, σ_p^2 = phenotypic variance; h^2 = heritability in a broad sense.

2.3.2. Genotype by Trait (GT) biplot

The GT biplot approach [30] was used to display the genotype by trait data in a biplot and is based on the following formula:

$$\frac{\alpha_{ij} - \beta_j}{\sigma_j} = \sum_{n=1}^{z} \lambda_n \xi_{in} \eta_{jn} + \varepsilon_{ij} = \sum_{n=1}^{z} \xi_{in}^* \eta_{jn}^* + \varepsilon_{ij}$$

Where:

α_{ij} = The mean value of genotype i for trait j

β_j = The mean value of all genotypes for trait j

σ_j = The standard deviation of trait j among genotype means

λ_n = The singular value for Principal Component (PCn)

ξ_{in} = The PCn score for genotype i

η_{jn} = The PCn score for trait j

ε_{ij} = The residual associated with genotype i in trait j

To achieve trait-focused scaling between genotype and trait scores the singular value λ_n has to be absorbed by the singular vector for genotype ξ_{in} and for traits hjn.

That is, $\xi_{in}^* = \xi_{in} \lambda_n^0 = \xi_{in}$ and $\eta_{jn}^* = \eta_{jn} \lambda_{jn}^1 = \eta_{jn} \lambda_n$.

Because n= 2 in a biplot, only PC1 and PC2 are retained in the model and such a model tends to be best for extracting patterns and rejecting noise from the data. A Genotype by Trait (GT) biplot is constructed by plotting PC1 scores against PC2 scores for each genotype and each trait [30].

All data were analyzed using the GGE biplot version 2.2.62 [26] and SAS 9.1 [22] statistical software.

3. Results and Discussion

3.1. Genetic variation

Influence of drought stress was significant on all studied traits, except total tiller per plant and fertile tiller per plant (Table 1). These results are in agreement with the findings of [1] and [12] who observed no significant differences between irrigation regimes for TT and FT in wheat. The mean squares for the genotypes were highly significant for grain yield, thousand-kernel weight, stem weight, peduncle weight, spike weight, grain weight per spike, number of grains per spike and plant height under irrigated conditions (Table 1). The effects of genotype was significant (P ≤ 0.01) for all studied traits except total tiller per plant and fertile tiller per plant (Table 1). These results indicate high genetic variability among genotypes that

enable us to select genotypes under irrigated and rainfed conditions.

3.2. Genetic parameters

Genotypic variance, phenotypic variance, genotypic coefficient of variation (GCV), phenotypic coefficient of variation (PCV), broad sense heritability and expected genetic advance expressed as percentage of mean for eight characters are presented in Table 2. The estimates of genotypic coefficient of variation and phenotypic coefficient of variation for all traits under

irrigated condition were lower than under rainfed condition, except number of grains per spike. Phenotypic coefficient of variation was highest in fertile tiller per plant (32.676%) and genotypic coefficient of variation was highest in grains weight per spike (20.536%) under irrigated conditions. For rainfed conditions, the highest GCV (33.185%) and PCV (37.766%) were in biological yield. Phenotypic coefficient of variation was higher than genotypic coefficient of variation for all traits which reflect the influence of environment on the expression of traits.

Table 1. Mean squares from analysis of variance of the traits of durum wheat genotype grown under irrigated (I) and rainfed (R) conditions.

Trait	Conditions	Mean Square			Mean	LSD$_{0.05}$
		Block	Genotype	Error		
Grain yield (t h^{-1})	I	0.226	0.405 **	0.092	2.44	0.22
	R	0.041	0.306 **	0.049	1.33	
Biological yield (t h^{-1})	I	1.073	2.451**	0.397	5.78	0.47
	R	0.141	1.741 **	0.255	2.80	
Thousand - kernel weight (gr)	I	81.000	19.489 **	5.674	43.60	4.01
	R	5.760	57.407 **	12.923	37.02	
Total tiller per plant	I	3.610	0.482 ns	0.304	1.96	0.84
	R	0.230	0.476 **	0.079	1.76	
Fertile tiller per plant	I	2.496	0.391 ns	0.278	1.77	0.73
	R	0.435	0.348 **	0.093	1.65	
Stem weight (gr)	I	0.037	0.125 **	0.013	1.31	0.08
	R	0.001	0.101 **	0.011	0.93	
Peduncle weight (gr)	I	0.001	0.014 **	0.002	0.49	0.04
	R	0.008	0.015 **	0.002	0.37	
Spike weight (gr)	I	0.041	0.485 **	0.113	2.69	0.16
	R	0.102	0.467 **	0.082	2.17	
Grain weight per spike (gr)	I	0.064	0.301 **	0.019	1.86	0.11
	R	0.008	0.1756 **	0.014	1.37	
Number of grains per spike	I	61.779	105.144 **	17.137	36.44	3.38
	R	0.144	76.654 **	8.589	31.71	
Plant height (cm)	I	52.562	77.065 **	14.348	75.44	3.15
	R	1.254	102.715 *	37.251	67.85	

** and * significant at 1 and 5% probability levels respectively; ns= not significant

The highest heritability in a broad sense was obtained for grain weight per spike (88.478%), stem weight (82.544%) and number of grains per spike (74.090%) in irrigated conditions (Table 2). This result for the traits with high heritability indicated that the selection for these traits will be effective because environment had little effect on them. Knowledge of heritability is essential since it helps breeders to determine the extent to which improvement is possible through selection [19]. However, high heritability alone does not generally guarantee a large enough gain to make

sufficient improvement through selection in advanced generations unless accompanied by a substantial amount of genetic advance [3]. Thus, genetic advance is another important selection parameter that aids breeders in a selection program [23]. According to Table 3, maximum genetic advance of 39.792% followed by 35.286% and 34.063% was recorded in grain weight per spike, stem weight and number of grains per spike, respectively in irrigated conditions. High heritability values followed by high genetic advance showed the presence of additive gene action

and selection could be effective in early segregating generations for these traits. Similar findings have been reported by [11] and [32]. High heritability for plant height coupled with low genetic advance indicates non-additive gene effects and improvement of the trait through selection may not be effective in this population. In the rainfed conditions, high heritability in a broad sense accompanied with high genetic advance was obtained for grain weight per spike (85.624%), stem weight (81.250%) and number of grains per spike (79.848%). In this environment a comparatively low value of heritability was observed for plant height (Table 2), indicating that selection for this character would not be effective due to predominant effects of non-additive gene in this population.

3.3. GT biplot analysis

The GT biplot for durum wheat dataset explained 56% and 64% of the total variation of the standardized data in the irrigated and rainfed conditions, respectively (Figure 2). In the irrigated conditions, the first two PCs (PC1 and PC2) explained 36% and 20%, respectively while in rainfed conditions, the first two PCs described 43% and 21%, respectively. A relatively low proportion of the total variation explained by the biplots indicates the complexity of the interrelationship among the traits [30].

Table 2. Genetic parameters for various characters in durum wheat under irrigated (I) and rainfed (R) conditions.

Trait	condition	σ_g^2	σ_p^2	GCV	PCV	H^2_B	GA
Grain yield (t h^{-1})	I	0.187	0.278	17.118	21.628	67.109	29.900
	R	0.151	0.200	29.169	33.600	75.363	52.163
Biological yield (t h^{-1})	I	1.126	1.523	18.363	21.357	73.928	32.526
	R	0.863	1.118	33.185	37.766	77.213	60.071
Thousand - kernel weight (gr)	I	6.908	12.582	6.028	8.135	54.907	9.202
	R	27.242	40.165	14.099	17.119	67.825	23.919
Total tiller per plant	I	0.089	0.393	15.238	31.989	22.691	14.953
	R	0.199	0.277	25.327	29.920	71.655	44.165
Fertile tiller per plant	I	0.057	0.335	13.477	32.676	17.010	11.450
	R	0.128	0.221	21.683	28.472	57.997	34.017
Stem weight (gr)	I	0.061	0.074	18.854	20.752	82.544	35.286
	R	0.049	0.061	23.899	26.514	81.250	44.377
Peduncle weight (gr)	I	0.007	0.009	16.454	19.145	73.864	29.130
	R	0.007	0.009	22.612	25.497	78.652	41.311
Spike weight (gr)	I	0.236	0.349	18.059	21.952	67.680	30.606
	R	0.223	0.304	21.757	25.425	73.226	38.353
Grain weight per spike (gr)	I	0.146	0.165	20.536	21.832	88.478	39.792
	R	0.081	0.095	20.774	22.450	85.624	39.599
Number of grains per spike	I	49.004	66.141	19.210	22.318	74.090	34.063
	R	34.033	42.622	18.397	20.588	79.848	33.865
Plant height (cm)	I	36.359	50.707	7.993	9.439	71.704	13.942
	R	32.732	69.984	8.432	12.330	46.771	11.879

σ_g^2 = Genotypic variance, σ_p^2 = phenotypic variance, GCV= genotypic coefficient of variation (%), PCV= phenotypic coefficient of variation (%), H^2_B= broad sense heritability (%), GA= genetic advance as a % mean.
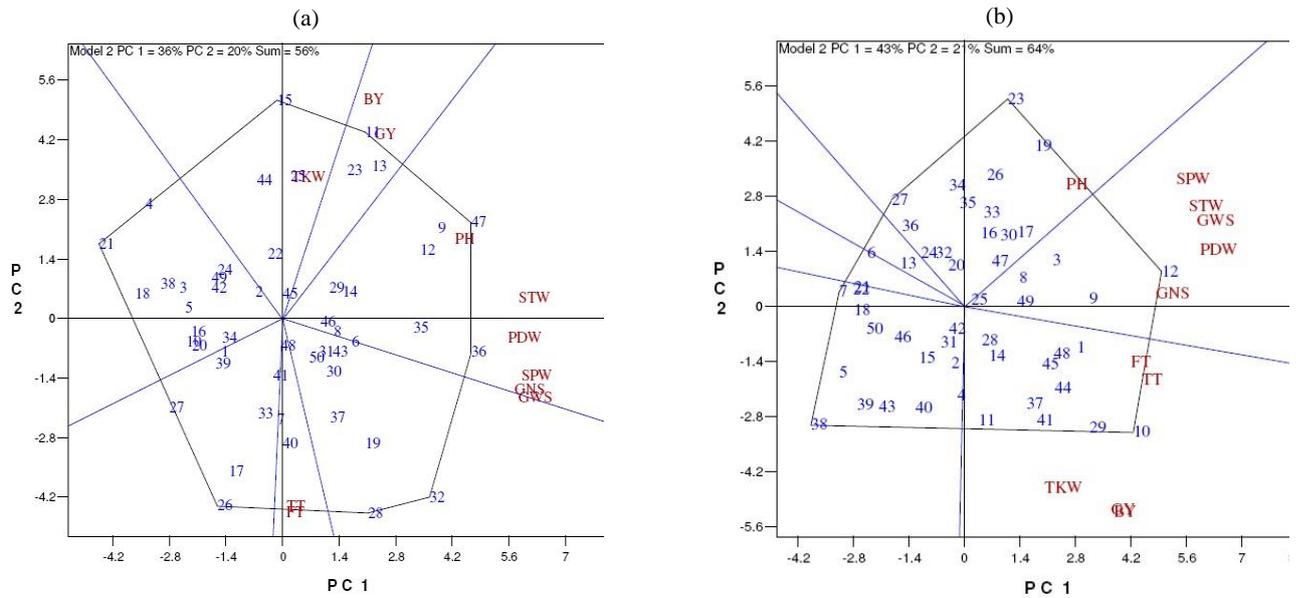
Figure 2. Polygon view of genotype × traits biplot of measured traits of 50 durum wheat genotypes under irrigated (a) and rainfed (b) conditions, showing which genotypes had the highest values for which traits.

Nevertheless, [13], [5], [29] and [20] represent that the fundamental patterns among the traits should be captured by the biplots. Among different ways to use a GT biplot, the polygon view helps identify genotypes with the highest values for one or more traits. It provides the best way to visualize the interaction patterns between genotypes and traits [30]. For this purpose, the genotypes that are connected with straight lines so that a polygon is formed with all other traits contained within the polygon.

According to polygon view of the dataset there are eight vertex genotypes in the irrigated conditions (Figure 2a) which are genotypes G28, G32, G36, G47, G11, G15, G21 and G26. These genotypes were the best or the poorest genotypes in some or all of the traits since they had the longest distance from the origin of the biplot. Therefore, it seems that G11 had the highest values for GY and BY. Genotypes G47 and G36 were the most favorable genotypes for PH, STW, PDW, SPW, GWS and GNS traits. Also, genotype G15 had highest value for TKW trait. On other hands, the vertex genotypes G28, G32 G21 and G26 were favorable in none of the measured traits in the irrigated conditions. Different vertex genotypes and their related genotypes which are located in different nine sections of biplot are good candidates for examination heterosis [31] for hybrid production in wheat using these genotypes or pure lines.

In the rainfed conditions, according to polygon view of the dataset there are six vertex genotypes (Figure 2b) which are G23, G12, G10, G38, G7 and G27. These genotypes are the best genotypes in some or all of the

traits in the saline conditions. The vertex genotypes G23 and G27 had the highest values for PH. The vertex genotype G12 and its relegated genotypes which are located in its sector had the highest values for SPW, STW, PDW, GWS and GNS traits. The vertex genotype G10 was the most favorable genotype for TT, FT, TKW, BY and GY traits. The vertex genotypes G38, and G7 were favorable in none of the measured traits (Figure 2b). Generally, it could be conclude that genotype G10 was the most favorable genotype in rainfed conditions. So, the genotype G10 can be recommended for cultivation in the rainfed environments.

The vector view is one of the applications of the GT biplot to study the relationships between and among traits. In the vector view of 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 selected traits. The correlation coefficient between any two traits is approximated by the cosine of the angle between their vectors [29]. The most prominent relations by vector-view biplot in the irrigated conditions (Figure 3a) are: a strong positive association between GY with TKW and BY; between STW and PDW; among SPW, GWS and GNS; and between TT and FT; as indicated by the small obtuse angles between their vectors (r=cos 0=+1). There was a near zero correlation between GY and BY with SPW, GWS and GNS, between TKW and PDW as indicated by the near perpendicular vectors (r=cos90=0). There was a negative correlation between GY, BY and TKW with TT and FT as indicated by the near an angle of
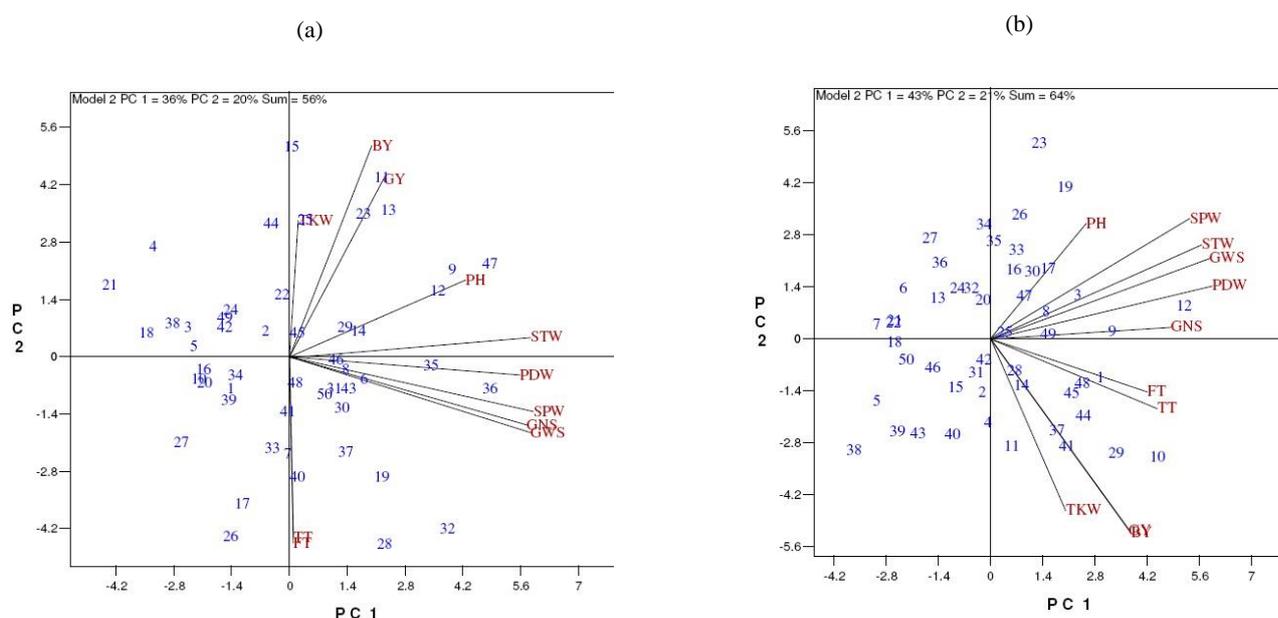
approximately 180 degrees (r=cos180=−1).

Figure 3. Vector view of genotype × traits biplot of measured traits of 50 durum wheat genotypes under irrigated (a) and rainfed (b) conditions, showing interrelationships among traits.

The most prominent relations in the rainfed conditions (Figure 3b) are: a strong positive association among GY, BY and TKW; between TT and FT; among SPW, STW, GWS and PDW as indicated by the small obtuse angles between their vectors (r=cos 0=+1). There was a near zero correlation between GY, BY and TKW with SPW, STW and GWS; as indicated by the near perpendicular vectors (r=cos90=0). There was a negative correlation between PH with GY, BY and TKW as indicated by the near an angle of approximately 180 degrees (r=cos180=−1). The statistical properties of this technique have been described in detail by [28] and [30]. Mohammadi and Amri (2011) found that biological yield and thousand kernel weight were correlated with grain yield in durum wheat and that visual selection would be valid [16]. Similarly, Gholizadeh and Dehghani (2016) reported that biological yield and thousand kernel weight were significantly correlated with grain yield in durum wheat [6].

Figure 4 shows a polygon view of the durum wheat dataset in eleven traits averaged across two environments and the following information can be understood: the vertex genotypes in this study are G12, G37, G15, G38, G5, G27 and G19. Genotype G12 had the highest values for all of the measured traits except GY, BY and TKW. This genotype (G12) and the other genotypes of this sector had good amounts of PH, SPW, STW, GWS, GNS, PDW, TT and FT. The vertex

genotype G37 and its related genotypes which fall in its sector were good for GY, BY and TKW traits. The other vertex genotypes (G15, G38, G5, G27 and G19) and related sectors were not suitable performance for the measured traits averaged across two environments (Figure 4). The vector view of GT biplot across two environments (Figure 5) showed there were high positive correlations between GY with BY, TKW, TT and FT. Also, Figure 5 shows that there were positive correlations among PH, SPW, STW, GWS, GNS, and PDW. There was an approximately zero correlations between GY with PH, SPW, STW and GWS.

Knowledge of the interrelationships between grain yield and its components will improve the efficiency of breeding programs especially under drought stress conditions through appropriate selection criteria. A better understanding of relationships between traits can be obtained by using biplot method. It is clear that the biplot methodology is an excellent tool for visual data analysis. The biplot approach has some advantages compared with conventional methods of data analysis [27, 31]. The first advantage of the biplot is graphical display of data, which largely enhances our ability to understand the patterns of the data. The second is that it is more interpretative and facilitates pair-wise genotype comparisons and effectively reveals the interrelationships among traits. Based on different trait relationships, selection for grain yield or any target trait is not only the simplest, but also the most effective

strategy in durum wheat breeding. The third advantage of the GT biplot method is that it facilitates

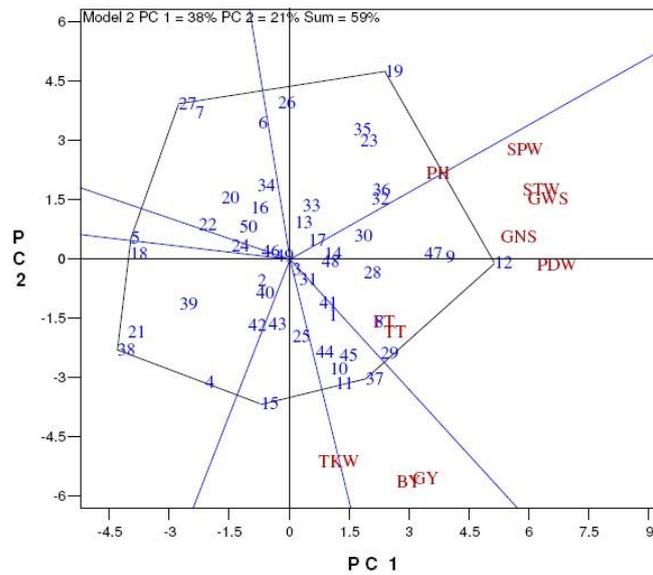identification of possible which-won-where patterns or which-lost-where patterns [21, 6].

Figure 4. Polygon view of genotype × traits biplot of measured traits of 50 durum wheat genotypes across environments, showing which genotypes had the highest values for which traits.
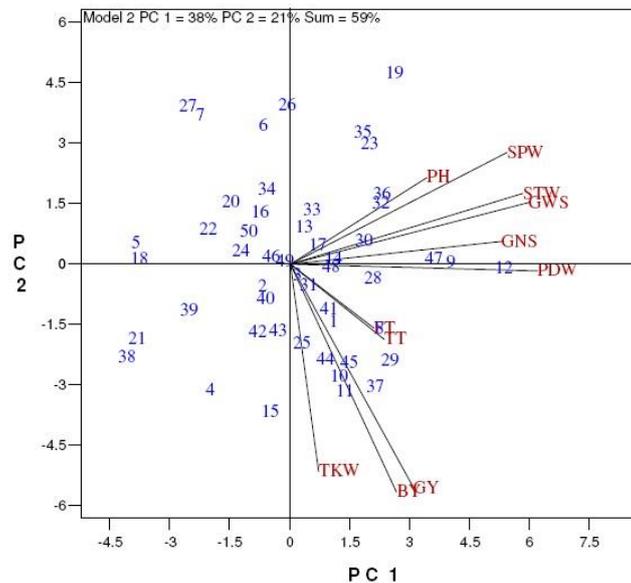

Figure 5. Vector view of genotype × traits biplot of measured traits of 50 durum wheat genotypes across environments, showing interrelationships among traits.

4. Conclusions

The present study revealed high genetic variability among durum wheat genotypes for all traits tested which gives an opportunity to plant breeders for the improvement of these traits. Grain yield was highly heritable in both conditions, with moderate genetic advance as a percentage mean in irrigated and high in rainfed conditions indicating that yield performance

could be improved to exceed the best commercial cultivars. The high heritability estimate of grain yield indicated that genetic variation was higher than the environmental variation in this study. The vector view of the GT-biplot indicated that BY and TKW traits are positively correlated with grain yield and can be considered as suitable selection criteria for the development of high yielding durum wheat varieties.

Among 50 studied genotypes, genotype G10 was the most drought-tolerant genotype and is suggested as a suitable genotype for rainfed conditions.

5. Acknowledgments

6. References

1. Akram M: **Growth and yield components of wheat under water stress of different growth stages.** Bangladesh Journal of Agricultural Research 2011, 36(3):455-468.

2. Araus JL, Slafer MP, Reynolds MP, Royo C: **Plant breeding and drought in C3 cereals: what should we breed for?** Annals of Botany 2002, 89: 925-940.

3. Bhargava A, Shukla S, Katiyar RS, Ohri D: **Selection parameters for genetic improvement in Chenopodium grain on sodic soil.** Journal of Applied Horticulture 2003, 5: 45-48.

4. Borghi B, Corbellini M, Minoia C, Palumbo M, Fonzo ND, Perenzin M: **Effects of Mediterranean climate on wheat bread-making quality.** European Journal of Agronomy 1997, 6:145-154.

5. Flores F, Moreno MT, Cubero JI: **A comparison of univariate and multivariate methods to analyze G × E interaction.** Field Crops Research 1998, 56: 271-286.

6. Gholizadeh A, Dehghani H: **Graphic analysis of trait relations of Iranian bread wheat germplasm under non-saline and saline conditions using the biplot method.** Genetika 2016, 48(2): 473 -486.

7. Hamdi A, Ghareib EI, Shafey AA, Ibrahim SA: **Genetic variability, heritability and expected genetic advance for earliness and seed yield from selection in lentil.** Egypt Journal Agricultural Research 2003, 81: 125-137.

8. Igbal S, Mahmood T, Tahira ALI, Anwar M, Sarwar M: **Path coefficient analysis in different genotypes of soybean (*Glycine max L.*).** Pakistan Journal of Biological Science 2003, 6: 1085-1087.

9. Johnson HW, Robinson HF, Comstock RE: **Estimates of genetic and environmental variability in soybeans.** Agronomy Journal 1955, 47: 314-318.

10. Kamrani M, Hoseine Y, Ebadollahi A: **Evaluation for heat stress tolerance in durum wheat genotypes using stress tolerance indices.** Archives of Agronomy and Soil Science 2018, 64(1): 38-45.

11. Kashif M, Khaliq I: **Heritability, Correlation and Path Coefficient Analysis for Some Metric Traits in Wheat.** International Journal of Agriculture and Biology 2004, 6(1): 138-142.

12. Khayatneghad, M., Zaefizadeh, M., Gholamin, R. and Jamaati-e-Somarein, S.H. 2010. Study of genetic diversity and path analysis for yield in durum wheat genotypes under water and dry conditions. World Applied Sciences Journal 9(6):655-665.

13. Kroonenberg PM: **Introduction to biplots for G × E tables.** Research Report 51. Centre for Statistics, University of Queensland, Brisbane, Australia; 1995.

14. Mary SS, Goplan A: **Dissection of genetic attributes yield traits of folder cowpea in F3 and F4.** Journal of Applied Science 2006, 2: 805-808.

15. Mohammadi M, Karimizadeh R, Shefazadeh MK, Sadeghzadeh B: **Statistical analysis of durum wheat yield under semi-warm dryland condition.** Australian Journal of Crop Science 2011, 5(10):1292-1297.

16. Mohammadi R, Amri A: **Graphic analysis of trait relations and genotype evaluation in durum wheat.** Journal of Crop Improvement 2011, 25: 680-696.

17. Nyquist WE: **Estimation of heritability and prediction of selection response in plant populations.** Critical Reviews in Plant Sciences 1991, 10: 253-322.

18. Raje RS, Rao SK: **Genetic parameters of variation for yield and its components in mungbean (*Vigna radiate* (L) Wilc.) over enviroments.** Legume Research 2000, 23: 211-216.

19. Robinson HF, Comstock RE, Harvey PH: **Estimates of heritability and the degree of dominance in corn.** Agronomy Journal 1949, 41: 353-359.

20. Rubio J, Cubero JI, Martin LM, Suso MJ, Flores F: **Biplot analysis of trait relations of**

white lupin in Spain. Euphytica 2004, 135:217-224.

21. Sabaghnia N, Mohebodini M, Janmohammadi M: **Biplot analysis of trait relations of spinach (*Spinacia oleracea* L.) landraces.** Genetika 2016, 48(2): 675-690.

22. SAS Institute Inc.: **SAS/STAT user's guide.** Version 9.1. SAS Institute Inc., Cary NC, USA; 2004.

23. Shukla S, Bhargava A, Chatterjee A, Singh SP: **Estimates of genetic parameters to determine variability for foliage yield and its different quantitative and qualitative traits in vegetable amaranth (*A. tricolor*).** Journal of Genetics and Breeding 2004, 58: 169-176.

24. Singh RK, Chaudhary BD: **Biometrical methods in quantitative genetic analysis.** Kalayani Publishers, Ludhiana, India; 2004.

25. Srivastava JP, Dhamania AB: **Use of collections in cereal improvement in semi-arid areas.** Cambridge University, Cambridge. 1989.

26. Yan W: **GGE biplot – A Windows application for graphical analysis of multi-environment trial data and other types of**

two-way data. Agronomy Journal 2001, 93:1111-1118.

27. Yan W, Hunt LA: **Biplot analysis of diallel data.** Crop Science 2002, 42(1): 21-30.

28. Yan W, Hunt LA, Sheng Q, Szlavnics Z: **Cultivar evaluation and mega environment investigation based on the GGE biplot.** Crop Science 2000, 40:597-605.

29. Yan W, Kang MS: **GGE Biplot Analysis: A Graphical Tool for Breeders, Geneticists and Agronomists.** CRC Press LLC., Boca Roton, Florida; 2003.

30. Yan W, Rajcan I: **Biplot analysis of test sites and trait relations of soybean in Ontario.** Crop Science 2002, 42: 11-20.

31. Yan W, Kang MS, Ma S, Woods S, Cornelius PL: **GGE biplot vs. AMMI analysis of genotype-by-environment data.** Crop Science 2007, 47:596-605.

32. Yousaf A, Atta BM, Akhter J, Monneveux P, Lateef Z: **Genetic variability, association and diversity studies in wheat (*Triticum aestivum* L.) germplasm.** Pakistan Journal of Botany 2008, 40(5): 2087-2097.