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Evaluation of agro-morphological traits related to grain yield of Iranian wheat genotypes in drought-stress and normal irrigation conditions

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Abstract

In order to evaluate several agro-morphological traits in 30 bread wheat genotypes, an experiment, based on randomized complete block design with three replications, was carried out under drought-stress and normal irrigation conditions in two locations. The traits, including grain yield, biological yield, harvest index, spike features, and peduncle characters were evaluated. The result of the combined ANOVA revealed that location and genotype effects were significant for all of the traits. Stress had a significant difference for all of the traits, except for spike density and spikelet per spike. The simple correlation results for each condition were significantly different, indicating that the relationships among traits were significantly influenced by drought stress and location. Factor analysis, based on principal component analysis and varimax rotation in the Shahed field under irrigation regimes showed that four significant factors accounted for about 78.2% and 77.7% of the total variation among characters for normal irrigation, and 84.8% for five factors under drought stress conditions. With respect to the achieved results, characters such as plant height, peduncle length, spike density, 1000-grain weight, harvest index, and biological yield had the highest communality and, consequently, provide a high relative contribution to wheat grain yield, and can be used as selective criteria in bread wheat breeding programs.

Keywords: Bread wheat, Drought stress, Factor analysis, Yield components.

Abbreviations: N_ normal irrigation; D_drought stress; GY_grain yield; BY_biological yield; HI_harvest index; TGW_1000-grain weight; SW_spike weight; SL_spike length; SPS_spikelet per spike; SD_spike density; TN_tiller number per plant; FTN_fertile tiller number per plant; PH_plant height; PL_peduncle length; PW_peduncle weight; PD_peduncle diagonal.

Introduction

Bread wheat (*Triticum aestivum* L.) which is one of the critical crops supports twenty percent of the total energy and protein in the human diet (FAO, 2016). Mostly, changing climate and increasing food demands necessitate wheat breeding plans that ensure high-quality and a stable yield potential, and to provide resistance to, or tolerance of, biotic and abiotic stresses (Crespo-Herrera et al., 2017). Lack of precipitation is one of the limiting factors in production of crops, such as wheat, in the world. In arid and semiarid regions, such as Iran, because of low precipitation rates and fluctuations in the distribution of rain, it is very hard to predict precipitation rates and distribution. Such conditions have led to significant grain

yield variations in consecutive years. Consequently, it is difficult to improve the yield of wheat-grain in such regions, through breeding, and producing drought-tolerant varieties. So, indirect selection, through traits related to grain yield, is one of the most important strategies in wheat breeding and, since wheat-grain yield results from the integration of many traits that affect plant growth, breeders are searching for optimal genotypes, regarding yield components (Golabadi et al., 2006). Morphological traits, with comparatively high inheritability, can be simply and accurately measured. Thus, thanks to their high correlation with yield, and being less affected by the environment, selection based on such traits could be a secure and rapid way for screening plant communities, and producing yield increases. So, environmental influences on yield improvement plans can be decreased through indirect selection for these traits (Dawari and Luthra, 1991). There are numerous approaches to investigate of morphological characters (for instance, plant height, peduncle characteristics, etc.) for the purpose of swelling yield under drought conditions (Bogale et al., 2011). As an example, peduncle length has been proposed as a valuable marker related to Product potential under drought conditions (Niari Khamssi and Najaphy, 2012).

Agronomic features could be helpful in wheat breeding programs based on statistical analysis. In this regard, studying the coefficients of correlation between different traits and yield is one approach, which can help to inform on the relative significance of such traits, and their values as selection criteria (Ebrahimnejad and Rameeh, 2016); however, it should be noted that, in different investigations, since there are negative, or insignificant, correlations between related traits and yield, or complex relationships between traits, so simple correlation coefficients alone are not the best way of making final judgments. Thus, it is necessary to utilize multi-variant statistical methods to provide a deeper understanding of the relationships between traits. Factor analysis is one of the powerful methods to manage and reduced data amount, and a noticeable conclusion may be accomplished from the data, which illustrate high between primary variables (Cooper, 1983). This technique is applied to conceive relationships between variables, structure of yield, and morphological traits of crops. Each factor is a linear combination of the original variables, and so it is partly possible to claim the meaning of what the components represent. The current study aims to determine the significance of traits related to yield, to evaluate the genetic diversity of bread-wheat from two different locations, and to clarify the association among some agronomic traits of bread-wheat, using correlation and factor analysis under drought stress conditions. This study may provide valuable information that can help to introduce superior Iranian wheat landrace genotypes with the desired agronomic traits for growth under drought stress conditions.

Results and discussion

Effect of genotype, experimental environments and their interactions

The results of the analysis of variance for each location separately revealed that there were significant differences between the studied genotypes for all measured traits in the NIGEB field (Fig 1.), while in the Shahed field, the effect of genotypes was significant for all the traits, except for FTN, PL, and PW (Fig 1.). The variance in normal irrigation and drought stress at the flowering stage was greater than half of the total variance for these traits, except for SL, SD, and SPS (in the NIGEB field), and PL, PD, SL, SD, and SPS (in the Shahed field). These results demonstrate that the studied genotypes reacted in a different way to the various environmental conditions, proposing the significance of the assessment of genotypes under different environmental situations, to be able to identify the best genetic makeup for a specific environment. The combined analysis of variance, as revealed by ANOVA, showed that mean squares, due to genotype and location, were significant (P<0.01) for all traits under both sets of stress conditions (data was not shown). A significant difference was observed between the two irrigation regimes in terms of all traits, except for SD and SPS. The insignificance difference of these traits is due to high inheritability of these traits, which are less affected by environment. The effects of stress × genotype, stress × location, location × genotype, and G × S × L were significant for most traits. Romagosa et al. (2009) suggested that parameters, such as geographic coordinates, environment temperature, soil features, and crop management, mostly caused difference in genotype reactions to environmental conditions at different locations. These results are in agreement with Asvari et al. (2012), Amiri et al. (2013) and Ebrahimnejad and Rameeh (2016) in showing strong variation for yield and yield components, which reveal the presence of genetic diversity for these attributes in the materials under both normal irrigation and drought stress conditions. Darzi Ramandi et al. (2016) evaluated 47 Iranian bread wheat genotypes (similar to some of our genotypes) under different water regimes; the mean comparison of drought tolerance indices and grain yield validated the significant influences of drought stress on yield, as well as significant differences among their genotypes.

Compare mean of yield and agro-morphological traits

R% is the percentage reduction of the mean of the traits under normal and drought conditions, in both the Shahed and NIGEB fields (Eq. 1). With respect to R%, it was clear that the reaction of characters to drought stress was different. The results reveal that drought stress decreased all of the traits, except for SD (Table 1 and 2). In the Shahed field, water deficiency had the highest effect on BY and GY, as it reduced the amount of factors to 32.31% and 46.61%, respectively (Table 1). It was observed, from the NIGEB field data (Table 2), that drought stress had the highest impact on GY (63.73%) and HI (51.77%).

Drought stress had a remarkable impact, not only on GY, but also on its components. Water scarcity at both sites decreases TGW. Results from this investigation are consistent with the findings of Mollasadeghi et al. (2013) and Kamrani (2015), who reported that drought stress decreased TGW, whereas irrigation increased TGW. In fact, irrigation at the time of grain filling led to increased photosynthetic products and their mobilization into the grain, and consequent grain-weight increase. In contrast, lack of sufficient humidity during this sensitive period caused a significant decrease in TGW. Plau-Butow et al. (2004) also concluded that water inefficiency during the flowering stage decreased grain formation, and its fertility, significantly, and if drought happened during the grain filling stage, it could significantly decrease the mobilization capacity of photosynthetic materials into the grain, and lead to shrinkage of the grain, and decreased TGW. Warrington et al. (1977) explained that drought stress at anthesis may lead to yield loss by reducing TGW and, if accompanied by high temperatures after anthesis, it may also accelerate wholeplant senescence, and reduce BY and HI. Mollasadeghi and Dadbakhsh (2011) also observed that GY, BY, HI, and TGW

reduced under stress conditions. They pointed out that stress causes sterile pollen, abnormal current photosynthesis, and also decreases transfer of material for grain storage, which can cause weight loss in grain genotypes. At both study locations, drought stress reduced the TN and FTN. Asvari et al. (2012) reported that GY, HI, PL, SL, and TN were reduced among the lines under drought stress conditions. Under stress conditions, PH decreased (5.53% in the Shahed field, and 7.71% in the NIGEB field). Sandhu and Hortpn (1977) reported that decreased PH under drought stress condition may be due to a low humidity reserve within the soil. Despite a relative increase in remobilization of reserves, Ercoli et al. (2008) also demonstrated a reduction in post-anthesis assimilation under drought conditions. Evaluation of the data of the present work shows that photosynthesis might be inhibited by drought imposed during the stem elongation stage, leading to a decline in SH and GY.

Drought stress caused a reduction in the characteristics of the peduncle in both locations. For instance PL decreased by 2.52% in the Shahed field, and 16.99% in the NIGEB field, compared to non-stress conditions. Mahpara et al. (2015) suggested that PL is a useful indicator of yield capacity in dry environments because the genotypes with longer peduncles have more stored carbohydrates for transferring to the seed. The high positive correlation between this trait and yield could confirm this idea. SL and SW were decreased under drought stress, but traits of SPS and SD showed the minimum response to stress. One of the most important yield components, SPS, is formed during the initial stage of stem elongation (Klerpper et al., 1998), and any unfavorable environmental factor during this period restricts the yield potential; however, in our study, these two traits (SD and SPS) not only had the lowest %R, but also the interactions are insignificant, so these traits could be useful under both normal and stress conditions. The results of Darzi Ramandi et al. (2016), using some of our genotypes, showed that, not only line numbers G41 and G11 presented superior performance under stressed and irrigated conditions, but also they were better for quantitative tolerance indices, in comparison to other genotypes. Additionally, genotypes G33, G37, G31, G32, and G23 were identified as drought susceptible.

Correlation between traits under stress and non-stress conditions

Correlation coefficients among studied traits, based on the data averages for drought stress and normal irrigation conditions in the two locations, are presented separately in Figure 2. Under non-stress condition in the Shahed location, GY had significant and positive correlation with SW (0.4*) and BY (0.55**) (Fig. 2a), while under drought stress condition, it had a positive and significant correlation with PL (0.37*), PW (0.37*), and HI (0.66**) (Fig. 2b). To assess the drought stress effect on wheat, Golabadi et al. (2006) reported positive and significant correlation between GY with PH, PL, awn length, number of grains per spike, and BY. Regarding the non-stress situation, they also claimed that, in a water deficit, GY had a positive and significant correlation with PL, SW, BY, and HI. Paknejad et al. (2009) also reported a significant positive

correlation between GY, and BY and HI under different regimes of water stress. Under non-stress condition, BY was significantly correlated with FTN (0.4*), PH (0.79**), PL (0.63**), PW (0.38*), and SL (0.4*) (Fig. 2a). Under drought stress condition, BY had a positive and significant correlation only with PH (0.67**) and PL (0.51**), and had a negative and significant correlation with SD (-0.39*) (Fig. 2b). Also, under both experimental conditions, BY indicated a negative correlation with HI (under stress, r = -0.66**, under non-stress r = -0.55**; Fig. 2a, b). Golparvar et al. (2006) investigated certain bread-wheat under both non-stress and drought stress conditions, and reported positive and significant correlations between BY and GY, SL, PH, and PL under both experimental conditions and, under drought stress conditions, in addition to these traits, BY had positive and significant correlation with TGW and ear weight. They also stated that, under non-stress condition, BY had a negative and significant correlation with HI. Under non-stress condition in the Shahed field, an increase in TGW and SD led to HI enhancement, and an increase in TN and FTN, PH, PL, SL, and BY resulted in a decrease in HI (Fig. 2a); however, under drought stress condition, HI only had a negative and significant correlation with PH and SL, and had a positive correlation with SD (Fig. 2b). With consideration to negative correlations between HI and BY under both irrigation regimes, the existence of a significant negative correlation between HI with PH and PL (as components of BY) seems to be normal. With respect to the SD correlation under both experimental conditions in the Shahed field, this trait can be used as an indirect selection criterion for improving GY.

In the NIGEB location, under drought stress and non-stress conditions, GY had a positive and significant correlation with PL, PW, BY, and HI (Fig. 2c), which is in conformity with the results of Bagrei and Bybordi (2015). Thus, it seems that these traits could be factors in yield augmentation, such that Taiz and Zeiger (2006) believed that measurement of biomass (BY), and BY components, are the best factors for determination of a plant's actual tolerance to drought stress. Additionally, GY showed positive and significant correlation with PH under nonstress condition (Fig. 2c), and with SW and SD under drought stress condition (Fig. 2d). Under both experimental conditions, BY had a positive and significant correlation with PH, PL, and PW. BY had a positive and negative correlation with SL and SD, respectively, under non-stress condition (Fig. 2c), and had a positive correlation with FTN, PD, SW, and SPS under drought stress condition (Fig. 2d). HI had a positive correlation with PH and PL under non-stress condition (Fig. 2c). Similar to results from the Shahed field, HI had a positive correlation with SD.

In both experimental locations, and under both irrigation regimes, BY had a positive and significant correlation with PH, which is in accordance with the results of Ebrahimnejad and Rameeh (2016), suggesting greater BY for taller genotypes that could be related to a much higher stem, and possibility more remobilization of dry matter in the wheat. It suggests the effectiveness of this trait to select and identify desirable wheat lines for drought environments. Also, the HI had a positive correlation with GY and, since the HI represents the percentage of mobilization of organic material from source to sink, so genotypes with higher HI can transfer more carbohydrates from green shoots, and enhance yield, and

Table 1. Mean value of characteristics and grain yield of 30 bread wheat genotypes in the Shahed field.

~	TN		FTN		PH(cm)		PD(cm	ı)	PW(gr)	PL(cm)	0	SL(cm)		SW(gr)	SPS		SD		TGW(gr)	BM(gr/m ²))	YIELD(gr,	/m²)	н	
G	N	D	Ν	D	Ν	D	Ν	D	Ν	D	Ν	D	Ν	D	Ν	D	Ν	D	N	D	Ν	D	Ν	D	Ν	D	Ν	D
2	14.0	13.3	10.5	10.42	116.3	110.8	2.98	2.60	0.34	0.26	37.5	31.6	14.0	13.6	2.52	2.25	19.0	18.8	1.36	1.38	40.0	24.7	1841.9	1345.3	522.7	283.6	0.28	0.21
4	16.8	11.5	13.1	9.25	109.0	102.0	2.58	2.54	0.26	0.33	30.4	35.5	10.8	11.1	2.41	2.42	18.0	19.3	1.67	1.73	30.8	24.0	1861.9	1000.0	462.5	236.4	0.25	0.24
7	13.6	10.8	11.1	7.50	110.0	92.3	2.79	2.35	0.28	0.20	27.4	23.0	13.3	12.3	3.25	2.03	19.1	19.1	1.44	1.55	39.8	28.5	1659.9	1233.9	544.7	309.1	0.33	0.25
11	15.4	10.3	13.4	7.13	127.9	96.5	2.86	2.30	0.37	0.22	39.8	29.3	13.1	11.4	2.86	1.79	20.0	18.1	1.53	1.58	34.1	23.0	2146.9	945.0	737.3	484.8	0.34	0.51
13	9.1	7.3	5.9	6.00	90.5	108.8	3.39	3.05	0.39	0.38	27.7	33.8	11.2	10.3	3.12	2.35	17.4	19.3	1.55	1.88	42.0	33.7	1490.9	1439.9	530.9	400.0	0.36	0.28
15	10.8	10.3	8.9	6.75	129.0	99.8	2.58	2.22	0.33	0.16	37.7	26.3	12.1	10.3	3.28	1.69	20.3	17.8	1.68	1.73	35.1	23.8	2460.9	850.0	819.5	280.5	0.33	0.33
16	10.8	10.3	8.1	6.25	101.2	100.4	2.77	2.22	0.22	0.18	24.9	24.4	13.3	14.1	2.56	2.15	19.0	19.6	1.42	1.40	28.6	24.0	1344.6	1090.0	352.1	196.7	0.26	0.18
18	12.0	10.3	8.7	8.33	116.6	115.8	2.68	2.62	0.38	0.33	39.2	39.4	12.2	11.0	2.77	1.92	18.9	17.8	1.55	1.63	42.0	28.9	2004.6	1573.3	695.5	392.0	0.35	0.25
20	12.4	10.8	11.3	5.50	128.8	89.8	2.81	2.54	0.43	0.22	40.8	25.4	14.3	13.8	3.76	2.40	20.4	19.3	1.43	1.40	33.4	24.9	2721.9	840.0	770.0	208.2	0.28	0.25
23	18.0	9.9	14.0	6.38	105.4	89.9	2.37	1.95	0.22	0.14	28.1	23.3	11.2	10.1	2.19	1.43	16.9	16.5	1.51	1.64	45.8	29.8	1794.9	1068.0	497.8	300.0	0.28	0.28
27	11.6	9.8	8.9	7.88	111.8	105.6	2.43	2.27	0.26	0.25	29.9	29.6	12.3	11.4	3.10	2.17	18.2	17.3	1.48	1.51	48.9	40.1	1996.6	1211.0	640.7	497.3	0.32	0.41
30	14.9	12.3	11.3	8.50	107.4	104.0	2.12	2.13	0.18	0.22	30.2	32.5	11.1	10.3	1.64	1.41	15.9	16.0	1.43	1.56	38.8	30.3	1709.9	1010.0	524.1	333.6	0.31	0.33
31	11.1	10.6	9.3	8.25	119.5	106.8	2.52	2.69	0.35	0.23	35.6	29.5	13.9	12.9	3.08	2.25	19.4	19.5	1.40	1.51	29.6	25.3	1825.9	1232.6	467.3	270.7	0.26	0.22
32	11.9	8.8	10.8	5.50	126.0	98.1	2.59	2.35	0.26	0.18	31.8	23.8	12.4	12.0	2.23	1.91	19.8	20.1	1.60	1.68	28.2	31.2	2517.9	1015.0	733.5	198.6	0.29	0.20
33	11.5	9.1	9.4	7.50	122.3	119.1	2.61	2.39	0.31	0.25	35.4	33.5	13.1	11.3	3.27	1.96	18.8	16.1	1.43	1.42	45.4	29.0	2176.9	1809.9	632.7	128.2	0.29	0.07
36	10.4	11.5	8.0	9.75	111.4	110.1	2.76	2.55	0.27	0.22	28.0	28.4	12.9	13.9	3.01	2.05	17.8	18.9	1.38	1.36	31.8	25.1	1793.9	1521.9	525.8	309.1	0.29	0.20
37	11.4	8.9	9.0	7.13	104.9	110.3	2.70	2.77	0.27	0.27	27.6	32.3	13.2	13.1	3.14	2.16	17.9	19.1	1.36	1.46	38.0	25.9	1743.9	1429.9	716.2	372.7	0.41	0.26
40	13.0	11.8	10.4	9.08	107.3	109.5	2.41	2.27	0.25	0.25	30.9	32.1	12.0	11.3	2.68	2.20	17.5	16.8	1.46	1.48	39.6	24.5	1885.3	1686.6	623.9	342.7	0.33	0.20
41	14.0	7.9	11.4	6.38	108.8	106.1	2.70	2.64	0.37	0.38	36.3	39.9	10.6	10.7	2.92	2.45	16.8	18.2	1.59	1.70	44.3	31.6	1642.6	1085.0	707.8	370.9	0.43	0.34
43	13.4	13.5	10.0	12.00	115.1	114.3	2.62	2.80	0.31	0.35	29.9	34.4	12.0	12.9	3.20	2.77	18.4	20.8	1.53	1.61	44.7	30.0	1798.9	1339.9	695.5	372.9	0.39	0.28
44	11.3	14.5	8.8	11.75	107.0	112.8	2.69	2.33	0.30	0.23	28.9	37.1	12.6	13.0	3.37	1.64	21.8	17.5	1.72	1.35	39.2	26.9	2199.9	1120.0	660.9	315.1	0.30	0.28
45	12.8	10.6	8.5	8.75	87.8	111.4	1.99	2.43	0.13	0.28	18.8	32.2	11.1	12.4	2.13	1.98	18.3	18.6	1.64	1.50	46.5	24.6	824.0	1426.9	508.3	293.8	0.62	0.21
46	13.3	7.1	9.5	4.75	113.8	101.3	2.49	2.25	0.21	0.17	34.6	29.5	13.3	12.6	2.01	1.43	20.3	19.8	1.53	1.56	27.8	23.2	1899.9	1171.0	513.6	304.6	0.27	0.26
50	12.0	10.8	10.6	8.13	98.6	106.5	2.25	2.24	0.26	0.22	33.4	36.1	11.7	11.8	2.19	1.54	16.8	16.3	1.43	1.38	44.1	29.0	1409.9	1424.9	475.2	351.7	0.34	0.25
74	7.8	11.0	5.3	6.63	78.0	76.0	2.59	2.42	0.21	0.22	22.0	24.7	10.5	10.0	2.84	2.11	17.8	18.1	1.69	1.81	44.1	31.5	840.0	913.0	526.6	309.1	0.63	0.34
87	11.0	9.8	10.0	7.38	104.5	109.4	2.32	2.86	0.15	0.28	26.8	37.6	10.6	11.4	1.78	2.79	15.0	16.6	1.41	1.45	39.5	29.1	2319.9	1914.9	739.8	500.7	0.32	0.26
93	10.5	9.3	10.0	7.50	80.6	76.8	2.92	2.74	0.27	0.24	28.5	26.2	10.0	10.3	3.37	2.49	17.7	18.8	1.77	1.82	37.2	24.7	1485.3	751.3	734.7	332.9	0.49	0.44
105	8.0	10.4	7.1	8.00	82.5	83.6	2.74	2.98	0.31	0.27	30.5	28.5	9.0	10.6	2.94	2.89	17.9	18.8	1.98	1.76	39.7	28.0	1499.9	1304.9	696.0	413.9	0.46	0.32
111	10.8	9.0	8.0	7.63	85.6	86.4	2.96	2.71	0.35	0.32	33.1	34.9	11.9	10.6	2.98	2.08	17.9	17.5	1.50	1.66	39.1	26.8	1739.9	1187.0	756.2	396.0	0.43	0.33
127	9.8	8.8	9.8	6.25	118.0	94.4	2.99	2.53	0.44	0.24	40.8	27.6	9.8	9.5	2.91	1.83	14.3	14.8	1.46	1.56	51.1	34.7	1871.9	956.6	516.0	279.8	0.28	0.29
М	12.1	10.3	9.7	7.74	107.5	101.6	2.64	2.49	0.29	0.25	31.5	30.7	12.0	11.7	2.78	2.08	18.2	18.2	1.53	1.57	39.0	27.9	1817.0	1229.9	610.9	326.2	0.35	0.28
R%	14.7		20.1		5.50		5.64		13.7		2.52		2.60		25.1		0.30		-2.46		28.43		32.3		46.6		21.4	

grain yield :GY, biological yield: BY, harvest index :HI, 1000-grain weight: TGW, spike weight: SW, spike length: SL, spikelet per spike: SPS, spike density: SD, tiller number per plant: TN, fertile tiller number per plant: FTN, plant height: PH, peduncle length: PL, peduncle weight: PW, peduncle diagonal: PD. normal irrigation: N, drought stress: D, genotype: G, mean: M, Reduction percentage: R%



Fig 1. Variation in studied traits attributed to genetic and environmental factors in two fields. The different colors in the stacked bar diagram indicate the various factors that explain phenotypic variation. grain yield (GY), biological yield (BY), harvest index (HI), 1000-grain weight (TGW), spike weight (SW), spike length (SL), spikelet per spike (SPS), spike density (SD), tiller number per plant (TTN), fertile tiller number per plant (FTN), plant height (PH), peduncle length (PL), peduncle weight (PW), and peduncle diagonal (PD).

	TN		FTN		PH(cm)	PD(cm)	PW(gr)	PL(cm)	<u> </u>	SL(cm)		SW(gr)		SPS		SD		TGW(g	r)	BM(gr/m ²)	YIELD(gr	/m²)	HI	
G	Ν	D	Ν	D	N	D	N	D	N	D	N	D	N	D	N	D	Ν	D	Ν	D	Ν	D	N	D	N	D	Ν	D
2	9.52	6.28	6.05	4.30	63.9	70.1	1.89	1.8	0.07	0.11	13.7	16.3	10.4	11.4	1.38	0.82	13.5	15.0	1.3	1.32	33.2	18.0	1243.3	996.8	214.8	66.4	0.17	0.07
4	8.20	5.20	5.20	4.40	61.2	78.7	1.74	1.89	0.1	0.13	15.1	24.5	7.2	8.7	1.1	0.86	12.3	13.7	1.81	1.57	25.6	11.5	928.5	974.3	179.2	78.6	0.2	0.08
7	6.62	5.58	4.62	4.00	73.9	73.8	2.24	2.02	0.15	0.1	22.0	19.4	10.1	10.8	1.68	0.99	14.5	14.9	1.44	1.4	46.2	29.8	1446.7	1012.2	359.0	104.2	0.25	0.10
11	5.87	7.73	4.20	4.64	77.0	81.9	1.97	1.89	0.19	0.14	24.3	22.4	9.6	10.1	1.3	1.13	14.3	15.4	1.48	1.53	32.6	26.8	1380.1	1100.1	383.4	116.9	0.28	0.11
13	5.92	6.64	4.27	4.33	80.6	74.0	2.98	2.7	0.33	0.18	29.4	23.3	11.3	9.8	1.99	1.09	17.5	15.0	1.55	1.54	38.2	23.5	1324.1	1098.7	326.9	88.8	0.25	0.08
15	8.12	5.97	5.50	3.13	69.3	68.6	1.70	1.8	0.14	0.07	19.6	17.2	9.2	8.1	1.29	0.8	13.3	12.8	1.45	1.59	34.8	26.2	1275.9	1057.3	195.8	105.5	0.15	0.10
16	5.07	5.22	3.23	4.55	68.5	61.1	2.02	1.69	0.14	0.09	16.8	16.2	11.0	9.2	1.65	0.68	13.4	12.0	1.23	1.29	32.1	22.3	1299.9	1019.8	407.6	90.1	0.32	0.09
18	6.33	7.40	5.03	5.07	77.1	88.1	2.07	2.14	0.23	0.22	25.4	28.4	9.3	9.8	1.84	1.23	14.8	16.5	1.59	1.69	35.1	25.6	1207.9	1230.2	331.0	229.1	0.28	0.20
20	4.57	5.30	3.42	3.27	64.7	66.6	1.87	1.75	0.07	0.08	14.6	14.0	11.0	10.6	1.3	0.82	14.0	13.8	1.28	1.3	32.5	20.0	1034.0	969.1	174.9	82.4	0.17	0.09
23	8.20	5.33	6.67	4.20	77.4	76.4	1.90	1.83	0.13	0.13	22.7	23.7	9.5	9.9	1.51	0.94	14.3	14.1	1.51	1.43	79.7	28.1	1327.5	1048.0	295.6	119.7	0.22	0.11
27	6.29	4.43	4.04	3.08	79.3	74.6	1.93	1.72	0.12	0.09	19.7	17.6	11.2	9.7	1.6	1.00	15.2	14.2	1.37	1.46	36.1	22.4	1395.3	1058.4	313.2	90.1	0.21	0.09
30	9.07	7.17	6.93	3.67	85.4	59.5	1.70	1.51	0.13	0.08	28.4	17.3	8.4	8.4	1.07	0.45	9.9	11.1	1.18	1.33	40.8	23.5	1398.2	872.3	294.2	188.0	0.22	0.22
31	6.55	5.67	5.52	2.92	82.9	55.3	2.27	1.85	0.15	0.07	23.9	11.1	11.4	9.5	1.78	1.03	14.8	12.7	1.29	1.33	31.5	18.4	1878.2	1006.2	426.2	108.3	0.22	0.11
32	6.91	7.47	5.69	3.00	77.7	65.9	1.99	1.43	0.18	0.09	23.5	15.0	11.1	9.9	1.67	0.77	15.1	14.7	1.36	1.48	33.4	27.3	2150.3	955.7	327.5	54.8	0.16	0.06
33	6.10	6.30	5.20	4.30	84.8	79.2	2.04	1.97	0.14	0.13	24.3	21.8	10.1	10.2	1.78	1.03	13.6	13.6	1.35	1.33	44.9	21.8	1358.4	1025.0	323.9	88.6	0.24	0.09
36	8.40	6.27	6.13	4.04	83.1	79.3	2.13	2.27	0.23	0.15	22.1	21.4	11.8	11.9	1./1	1.08	14.8	15.3	1.26	1.29	34.8	15.7	1504.8	1088.9	276.9	84.4	0.18	0.08
37	1.75	5.87	6.28	3.63	70.4	/3.1	2.02	2.00	0.12	0.1	19.9	1/./	11.8	11.0	1.69	0.96	15.2	14.0	1.29	1.27	36.3	36.7	1012.9	880.4	1/8.3	53.0	0.18	0.06
40	10.40	4.50	7.73	3.17	87.9	59.8 72 F	1.98	1.65	0.15	0.07	23.9	14.0	10.2	10.4	1.76	0.83	13.8	12.0	1.35	1.10	37.8	44.4	1542.3	926.5	502.4	40.0	0.36	0.04
41	7.23	6.05	5.0Z	4.60	04.2	73.5	2.33	2.15	0.34	0.17	33.2	24.0	9.5	9.4	1.70	1.12	14.0	14.9	1.0	1.56	39.5	20.4	1500 4	1124.6	401.5	1576	0.25	0.14
45	7.75 E 06	0.00 E 62	4.24	4.15	54.5 7E 1	72.1	1 00	1.92	0.22	0.11	27.1	10.1	10.0	0.1	1 25	0.04	14.7	12.0	1.35	1.35	40.9	20.5	1550.4	1021.2	276 1	11/ 7	0.32	0.14
44	7.60	5.02	4.24	1 22	20.2	22.0	2.07	2.10	0.15	0.15	27.1	22.0	9.4 10 E	3.1 11.2	1.23	1 26	14.2	12.0	1.20	1.4	43.0 25.6	22.7	13/4./	1021.3	370.1 200 E	14.7	0.24	0.11
45	9.48	6.42	6.99	3.42	75.6	65.7	1.87	1 72	0.10	0.10	20.8	17.1	10.5	10.4	1.02	0.73	14.5	14.2	13	1.41	28.7	12.2	1353 5	890.0	356.2	83.0	0.22	0.13
50	8 73	6.06	7 13	5.07	70.7	66.8	1.07	1 72	0.12	0.05	26.6	19.2	93	9.8	1.10	0.75	11.9	13.3	1.5	1 35	36.5	22.2	1546.4	1096 1	398.2	144 3	0.26	0.05
74	6 38	4 00	5.85	3 38	69.9	55.9	2 25	1 98	0.10	0.05	22.0	17.1	8.8	8.0	1.27	1.2	14.0	14.0	1.58	1.55	35.9	31.4	1171 2	986.4	236.2	148.1	0.20	0.15
87	8 58	5 73	6.67	3.62	74 5	69.7	1 41	2.50	0.18	0.12	25.9	22.0	9.1	11.2	1 14	1.05	13.1	15.1	1 42	1 35	37.4	21.0	1517.0	1105.0	369.0	136.3	0.24	0.12
93	5.15	2.80	4.42	2.20	58.4	67.5	2.2	2.09	0.11	0.12	19.0	22.5	8.9	8.4	1.58	1.58	15.5	13.8	1.75	1.64	26.0	28.2	976.8	1010.4	190.9	164.3	0.20	0.16
105	6.86	4.55	5.11	3.48	67.3	55.4	2.31	1.85	0.21	0.08	24.5	14.6	8.4	8.5	2.11	1.1	16.3	14.8	1.94	1.74	31.6	17.3	1160.1	949.7	254.4	96.4	0.20	0.10
111	5.57	3.96	4.63	3.09	59.3	56.6	2.12	2.15	0.19	0.11	22.1	19.4	8.6	9.4	1.51	1.15	14.1	15.1	1.63	1.61	27.8	22.2	1047.5	1015.7	109.9	128.6	0.11	0.13
127	5.85	5.87	4.07	4.09	74.8	66.9	2.28	2.09	0.15	0.18	26.6	23.1	8.1	7.7	1.41	0.84	11.1	10.5	1.37	1.37	40.8	26.9	1120.5	963.7	216.5	85.7	0.19	0.09
М	7.16	5.73	5.44	3.83	75.1	69.6	2.04	1.91	0.16	0.11	23.4	19.5	9.88	9.75	1.57	0.99	14.0	13.9	1.44	1.43	37.0	23.9	1360.8	1025.3	309.2	112.1	0.22	0.10
R%	20.0		29.5		7.37		6.22		29.4		17.0		1.32		37.0		0.26		-0.6		35.2		24.6		63.7		51.7	

Table 2. Mean value of characteristics and grain yield of 30 bread wheat genotypes in the NIGEB field.

grain yield :GY, biological yield: BY, harvest index :HI, 1000-grain weight: TGW, spike weight: SW, spike length: SL, spikelet per spike: SPS, spike density: SD, tiller number per plant: TN, fertile tiller number per plant: FTN, plant height: PH, peduncle length: PL, peduncle weight: PW, peduncle diagonal: PD. normal irrigation: N, drought stress: D, genotype: G, mean: M, Reduction percentage: R%

						Fact	tor pattern aft	er Varimax rota	ation
Trai	it			No	rmal			Dro	ought
		F1	F2	F3	F4	F1	F2	F3	F4
TN	0.66	-0.52	0.00	-0.14	-0.12	0.03	-0.19	0.90	
FTN	0.82	-0.38	-0.07	-0.02	0.17	0.26	-0.01	0.88	
PH	0.81	0.17	0.34	-0.19	0.04	0.86	-0.01	0.26	
PL	0.73	0.52	0.00	0.00	0.38	0.59	0.43	0.30	
PW	0.35	0.88	-0.07	0.03	0.81	0.29	0.34	0.07	
PD	-0.08	0.83	0.03	-0.06	0.92	0.08	0.03	-0.07	
SL	0.27	0.16	0.74	-0.46	0.03	0.31	-0.78	0.33	
SW	-0.05	0.79	0.21	0.22	0.86	-0.03	-0.13	0.04	
SPS	0.07	0.16	0.89	0.21	0.51	-0.22	-0.69	0.00	
SD	-0.32	-0.02	-0.04	0.81	0.4	-0.58	0.33	-0.38	
TGW	-0.10	0.10	-0.77	0.06	0.04	0.07	0.63	-0.23	
BM	0.78	0.26	0.34	0.14	0.22	0.85	0.09	0.04	
Yield	0.31	0.33	0.07	0.74	0.38	-0.12	0.64	0.26	
HI	-0.66	-0.08	-0.26	0.51	0.12	-0.73	0.51	0.19	
Eigen value	4.64	3.10	1.76	1.45	3.37	3.73	2.15	1.63	
Variability (%)	26.81	21.80	16.38	13.21	21.94	21.48	18.82	15.53	
Cumulative %	26.81	48 61	64 99	78 20	21 94	43 41	62 23	77 76	

 Table 3. Factor analysis for investigated traits of bread wheat genotypes in the Shahed field.



Fig 2. Pearson's correlations between the traits under stress and normal irrigation conditions in two locations. a) Normal irrigation in the Shahed field, b) Drought stress in the Shahed field, c) Normal irrigation in the NIGEB field, d) Drought stress in the NIGEB field. grain yield (GY), biological yield (BY), harvest index (HI), 1000-grain weight (TGW), spike weight (SW), spike length (SL), spikelet per spike (SPS), spike density (SD), tiller number per plant (TTN), fertile tiller number per plant (FTN), plant height (PH), peduncle length (PL), peduncle weight (PW), and peduncle diagonal (PD).

Table 4. Factor analysis for investigated traits of bread wheat genotypes in the NIGEB field.

						Factor	pattern after	Varimax rotati	ion	
Tra	it			Nor	mal			Drou	ght	
	F1	F2		F3	F4	F1	F2	F3	F4	F
TN	0.16	-0.21	0.92	0.04	0.17	0.07	0.82	0.14	-0.14	
FTN	0.25	-0.05	0.94	0.02	0.55	0.13	0.66	0.06	-0.10	
PH	0.80	0.21	0.29	0.25	0.70	0.01	0.38	0.38	0.02	
PL	0.80	0.28	0.2	-0.26	0.88	0.26	0.14	-0.03	-0.03	
PW	0.52	0.65	0.06	-0.27	0.93	0.17	0.12	0.04	-0.04	
PD	0.16	0.83	-0.26	-0.08	0.77	-0.01	-0.28	0.24	-0.03	
SL	0.06	0.36	0.01	0.92	0.00	-0.3	0.32	0.86	0.14	
SW	0.18	0.89	-0.04	0.07	0.50	0.3	-0.62	0.42	0.09	
SPS	-0.16	0.89	-0.07	0.19	0.39	0.13	-0.14	0.78	-0.29	
SD	-0.29	0.43	-0.06	-0.77	0.36	0.43	-0.54	-0.15	-0.42	
TGW	0.34	-0.07	0.19	0.03	0.00	0.00	-0.16	-0.06	0.92	
BM	0.64	0.05	0.16	0.39	0.60	0.44	0.11	0.39	-0.08	
Yield	0.91	0.06	0.06	0.21	0.23	0.96	0.01	0.01	-0.02	
HI	0.75	0.03	-0.02	0.03	0.07	0.96	0.00	-0.1	-0.02	
Eigen value	4.58	3.23	1.23	1.75	5.26	1.04	1.81	2.65	1.11	
Variability (%)	26.48	22.70	14.41	13.46	28.55	18.2	15.74	13.95	8.35	
Cumulative %	26.48	49 19	63.6	77.06	28 55	42 5	58 24	66 59	84 79	
74 91 50 1 2 -2 -2 -1 -0 F1 (26.8	4003 _{PN} 4003 _{PN} 46 87 4 30 23 1 1%)	2						B	3 0 TN 22 3 44 12 44 5 3 5 5 5 1 5 1 5 1 5 1 5 1 5 1 5 1	2
2 5 1 5 5 5 5 5 5 5 7 6 7 7 7 7 7 7 7 7 7 7 7	13 FBV pw 41 43 7 mmrield 7 mmrield 7 mmrield 7 mmrield 8 mm	_					1% (ar 34)	25 2 33 4 4 45 45 45 45	11 11 11 11 11 11 11 11 11 11	3
-2 -2 -1 0 F1 (26.4	- 30 1 8 %)	2					-	45 -2 -2	37 13 0.5 1.5 F1 (28.55 %)	5

А

С

Fig 3. Biplot analysis graphs compromised from two first factors of 30 bread wheat genotypes. The numbers in the figure show the genotype position in the biplot. a) Normal irrigation in the Shahed field, b) Drought stress in the Shahed field, c) Normal irrigation in the NIGEB field, d) Drought stress in the NIGEB field. grain yield (GY), biological yield (BY), harvest index (HI), 1000-grain weight (TGW), spike weight (SW), spike length (SL), spikelet per spike (SPS), spike density (SD), tiller number per plant (TTN), fertile tiller number per plant (FTN), plant height (PH), peduncle length (PL), peduncle weight (PW), and peduncle diagonal (PD).

these facts could indicate the significance of this trait in breeding programs designed to develop higher-yielding genotypes for a target environment. Although TGW and FTN are the main components of yield, these showed no correlation with GY (as seen from Fig. 2). Emam et al. (2007), under conditions of both favorable moisture and drought stress, and also Bagrei and Bybordi (2015), under limited rainfall conditions, reported a lack of correlation between GY and TGW in bread-wheat.

Factor analysis

Because reports disagree about certain correlations, it is likely that determination of the GY component's role may depend on the evaluated cultivar, or line, and the environmental conditions. On the other hand, because of the complicated relationships between the majority of the traits with each other, and with yield, simple correlation coefficients may not present comprehensive information about the relationships between different traits, and it is vital to apply multivariate statistical methods, such as factor analysis, in order to better understand these relationships. It should be pointed out that, with regard to the use of varimax rotation in factor analysis, which leads to maximizing variance between factors, the factors that prove a higher percent of the variation between traits are more significant, and they should be used in breeding programs. In other words, using this technique, the traits affecting each factor are revealed, and the factor name is selected based on these characters and through related traits, genetic improvement of the factors will be possible (Tadesse and Bekele, 2001).

Under non-stress condition at the Shahed field, results obtained from factor analysis, using principal components, showed that four factors had Eigen values larger than 1, and these factors overall justified 78.20% of the variation in traits (Table 3). In order to name the factors, a loading value was used in each factor. Higher values suggest a greater effect on the respective factor. The first factor that made the largest contribution accounted for 26.81% of the total variation, and was composed of some of the components of TN, FTN, PH, PL, BM, and HI. Thus, this factor was named as yield components (Table 3, Fig. 3a). With respect to the results of the factor analysis, the first factor could be introduced as an effective factor in increasing yield. Selection of genotypes, based on first factor enhancement, could lead to an increase in yield components in the studied population, so superior genotypes for the first factor are 11, 20, and 23. Factor 2, which accounted for 21.80% of the total variation, was composed of PD, PW, and SW, and this factor was named peduncle character factor. The superior genotypes for this factor are 13, 18, 20, 33, 111, and 127 (Table 3, Fig. 3a). Our results indicated that a third factor accounted for about 16.38% of total variation, and it had positive coefficients for SL and SPS, and a negative coefficient for TGW (Table 3), and the genotypes 15, 16, 20, 31, 32, 44, 46 are superior for this factor. Factor 4 accounted for 13.21% of the variance, and consisted of SD and yield. On the other hand, SD correlated positively with HI. So it seems that increasing SD, especially in some genotypes,

including 15, 44, 93, and 105, could be the effective way of increasing GY and HI (Table 3).

In drought stress conditions, 14 initial variables were defined in four factors, and these independent factors accounted for 77.76% of the total variation (Table 3). The first factor that made the largest contribution, and possesses 21.94% of the total variation, was composed of PW, PD, and SW, and it was named as peduncle characters. The superior genotypes for this factor are 13, 41, 43, 87, and 105 (Table 3, Fig. 3b). The second factor, which accounted for 21.48% of the total variation, was composed of PH, PL, and BM (positive values), and SD and HI (negative values). Thus, this factor was called yield components. The superior genotypes for this factor are 18, 33, 40, and 87 (Table 3, Fig. 3b). Factor 3 accounted for 18.82 % of the total variation, and it played an important role in justifying character variation, such as TGW, yield, SL and SPS. This factor was named as yield factor. These values suggest that genotypes with high levels of TGW, especially 18, 27, 30, 41, 87, and 127, have higher yields (Table 3). It should be noted that the value of the trait of TGW is positive in this factor, but it is negative for SL and SPS. It is likely that increasing SL increases the space between spikes for more growth and development, but drought stress leads to a decrease of the GW, so the trait of TGW versus the trait of spike should be considered in wheat breeding programs. Factor 4, which accounted for 15.53% of the total variation, was composed of TN and FTN, and indicates the importance of tillering in relation to yield. Since tillering leads to an increased number of spikes per plant, and thus per surface unit, this factor is known as the factor affecting tillering. Nouri-Ganbalani et al. (2010) showed that, under different conditions, both TN and FTN per square meter were highly significant in explaining GY. The better genotypes, regarding this factor, are 2, 43, and 44 (Table 3).

In the NIGEB location, under non-stress conditions, factor analysis by means of major factors, and on the basis of specific numbers larger than 1, four factors were identified, and they together justify 77.06% of the variation among the characters (Table 4). Investigations suggest that the first factor described about 26.48% of the total primary variation, and coefficients of yield, PH, PL, TGW, BM, and HI had high loading values in this factor. These values indicate that genotypes with high levels of the first factor, including genotypes 11, 30, 41, 43, 44, and 50, have higher, and more optimal, yields (Table 4, Fig. 3c). Thus, the selection of genotypes based on increasing this first factor will lead to the increased performance of the genotypes under study. Considering values of the respective traits in this factor, it can be said that these traits are influenced by similar genes. It should be noted that traits in this factor that have high values are among the main elements of yield. Thus, the name of this factor was determined as the factor of yield and yield components. Moetamadipoor et al. (2015), in their study on wheat, using factor analysis, selected this name for the first factor. They reported that traits of yield and TGW in this factor have higher values. The second factor included about 22.7% of the total variation, and it had positive and large coefficients for the traits of SW, SPS, PD, and PW. This factor was called spike features. The superior genotypes for this factor are 13, 36, 41, 43, and 105 (Table 4, Fig. 3c). The third factor accounted for

14.41% of the total variation, and had large positive values for traits of TN and FTN, thus this factor can be called the factor affecting tillering. Genotypes 23, 30, 36, 37, 40, and 46 are more powerful in terms of this factor (Table 4). In the fourth factor, traits of SL and SD had the highest positive and negative values, respectively, and this factor accounts for about 13.46% of the total variation. Despite increasing SL, the space between spikes decreased, and this factor is named the factor affecting spike. The best genotypes in this factor include 2, 16, 20, 27, 31, 32, 36, and 37 (Table 4).

Under drought stress conditions in the NIGEB field, five factors overall justified 84.8% of the variation in traits (Table 4), and each factor respectively accounted for about 28.55%, 18.22%, 15.74%, 13.95%, and 8.35% of the total primary variation. The first factor had positive and large coefficients for the traits of PH, PD, PL, PW, and BM. Thus, this factor can be called the factor affecting peduncle features. In regions with drought stress, it is better to use genotypes that have higher PH and peduncle features in order to speed up remobilization, prevent yield reduction, and increase plant tolerance. As a result, selected and modified genotypes, such as 4, 13, 18, 41, and 127, based on these traits, could increase PH and, thus, drought resistance (Table 4, Fig. 3d). In the second factor, yield and HI had the highest values. Thus, this factor was called the yield factor. There should be naturally high correlation between the yield and HI, which is well observed in the second factor. Genotypes 37 and 40 have been demonstrated as superior, regarding this factor (Table 4, Fig. 3d). The third factor had large positive values for traits of TN and FTN, and negative values for SW and SD, thus this factor can be called the factor affecting tiller and spike. It can be said that an increased number of spikes per plant and, in fact, surface unit, causes increasing competition among bushes for obtaining nutrition and light, and this competition leads to reduction of SW. Thus, the trait of FTN versus the trait of SW should be investigated in wheat breeding programs under drought stress conditions. Genotypes 30 and 50 are better for this factor. The fourth factor can be called the factor affecting spike, and it had the highest value for SL and SPS. Superiority in these traits of the following genotypes has been reported: 18, 30, 41, 43, 74, and 93. TGW is the trait that had the highest value in the fifth factor, thus this factor was named the factor affecting grain weight, and genotypes 2, 36, 45, and 87 are preferable for this factor (Table 4). Various research projects have employed factor analysis, and have considered different characters in wheat. Moetamadipoor et al. (2015) studied plant traits, and determined appropriate selection criteria to improve wheat yield in drought stress conditions, using factor analysis. He identified seven factors, including grain yield, characteristics of spike and peduncle, and grain characteristics. Zarei et al. (2013) studied 16 traits in durum wheat under rainfed conditions using factor analysis, and extracted four factors and the most important factor (first Factor) was strongly associated with the number of spikes per plant, the number of tillers per plant, biomass and grain yield. Similar results were obtained by Leilah and Al-Khateeb (2005) who stated that factor analysis had revealed the nine wheat traits into three main factors including yield components, spike characteristics and plant height.

Materials and methods

Experimental design and trial management

Thirty genotypes of bread-wheat, consisting of 24 bread-wheat lines and six wheat cultivars (selected from 180 local breadwheat genotypes, obtained from different wheat breeding programs of the Seed and Plant Improvement Institute of Iran), were assessed, using a randomized complete block design, with three replications, during 2014-2015, under two irrigation regimes (100% field capacity until harvest, and no irrigation after anthesis) in two locations: the research farm of Shahed University, located at Shahr-e-Rey, Tehran, Iran (15 km SW of Tehran, 35°34'N, 51°8'E, 1130 Meters above sea level), and the National Institute of Genetic Engineering and Biotechnology (NIGEB) research field, located at Vardavard (NW of Tehran, 35°44'N, 51°10'E, 1305 Meters above sea level). Minimum and maximum temperatures at the first location were -15°C and 41°C, respectively, and the climate is characterized by mean annual precipitation of 224 mm. At the second location, minimum and maximum temperatures were -20°C and 42°C, respectively, and the annual precipitation was 247.3 mm. In each field, sowing was done by hand, in plots with four rows, with 2 m long by 25 cm wide gaps between rows. Tillage of all plots was performed prior to sowing, and fertility was constrained by low organic matter and phosphorus content. Fertilizer application was performed before sowing; 50 kg ha⁻¹ of N and 50 kg ha⁻¹ of P_2O_5 were broadcast applied to the surface, and then tilled into the soil. Weeds were manually controlled during the growing season. After removing the borders, the plot grain-yields were calculated as productivity per m^2 . Five plants in each experimental unit were randomly selected, and the data associated with the five samples per plot were then averaged, and recorded for subsequent analysis. The following traits were evaluated: grain yield (GY), biological yield (BY), harvest index (HI), 1000-grain weight (TGW), spike weight (SW), spike length (SL), spikelet per spike (SPS), spike density (SD), tiller number per plant (TN), fertile tiller number per plant (FTN), plant height (PH), peduncle length (PL), peduncle weight (PW), and peduncle diagonal (PD).

Statistical analysis

 $R = (\mu_{NS} - \mu_{DS} / \mu_{NS}) \times 100$

All the statistical analyses were conducted using the SAS program (SAS Institute, 2009) and R package corrplot in Rstudio software. Analysis of variance, using the PROC GLM procedure, was applied to distinguish the effects of the field location, irrigation regimes, and genotypes on the analysis traits. The genotypic means of traits were compared using the LSD test at 5% probability levels. The reduction percentage in the mean value of each trait due to drought stress was calculated as follows:

Where; μ_{NS} and μ_{DS} are the means of the traits under normal and stress conditions, respectively.

Eq. 1

The correlation coefficients between the traits were estimated, and then factor analysis, on the basis of major factors, and varimax rotations, were performed on the data. Principal components analysis was used to extract the factorial load of the matrix, and also to estimate the number of factors (Cooper, 1983). Therefore, the factors that had a root larger than one were selected, and were used to form the factorial coefficients matrix. By means of varimax rotation, rotation was done on the major factorial loads matrix, and the matrix of rotated factorial loads was obtained. Also, we used a biplot of the two first factors to indicate the distribution pattern of the wheat genotypes in a graphical view.

Conclusion

The Inheritability of yield is low so selection for swelling yield could be done through yield components characters. Our results show that drought stress reduces grain yield and agronomic traits, except for SL, SD, SPS, and PL. Also, the information on genotypes, environment (including both irrigation regimes, at both locations), and their interactions, indicate differential responses of genotypes under irrigated and drought stress conditions, and provide considerable information for a suitable genetic resource for breeders. This study shows that evaluated traits, such as peduncle and spike features, could be important and helpful criteria for other breeders who seek to improve their germplasm. Factor analysis reveals that PH, PL, PD, SW, SD, and BM have the highest communality and, consequently, the highest relative contribution to wheat GY. Thus, selection for increasing such traits could be a reliable approach to increasing yield. In addition, the efficiency of selecting superior genotypes, such as 11, 18, 33, and 40, along with improving the mentioned traits, could be very significant.

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