



Modified Method for the Analysis of Genotype by Trait (Gt) Biplot as a Selection Criterion in Wheat under Water Stress Conditions

E.A.M. Abd-ElHamid⁽¹⁾, M.A. Aglan⁽¹⁾, Eman M.A. Hussein^{(2)#}

⁽¹⁾Wheat Research Section, Field Crop Research Institute, Agricultural Research Center (ARC), Giza, Egypt; ⁽²⁾Central Lab. For Design & Stat. Analysis Research, Agricultural Research Center (ARC), Giza, Egypt.



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IN Egypt, water deficits have dramatically increased in recent years due to over-exploitation of this resource and other challenges. That restricts reduce or decrease its ability to accomplish economic development goals. The present investigation was conducted at Sakha Agricultural Research Station to assess the genetic behavior of 18 bread wheat genotypes during the two growing seasons of 2015/2016 and 2016/2017 under normal and water stress conditions. The experimental design was a randomized complete block design with three replicates. Results showed large values of broad-sense heritability (h_b^2) which coupled with high values of genetic advance as a percentage of the mean (GA %) at 10% selection intensity for grain filling rate (93% and 19.91%) and chlorophyll b (82% and 22.22%) in the normal condition, respectively. Regarding the water stress condition, the grain yield (89% and 18.74%) and 1000-grain weight (87% and 17.62%) and proline (93% and 27.87%) recorded the highest values of h_b^2 and GA%, respectively. Genotypes G18, G17, G4, and G13 were the best tolerant under water stress condition and considered as promising genotype in breeding programs according to a genotype by yield*trait (GYT) biplot graph. On the other hand, G12, G8, and G16 were identified as sensitive genotypes. Undoubtedly, GY*T biplot graph is preferred because of it easy to interpret and more informative to identify more accurate selection criteria using grain yield and its attributes.

Keywords: Wheat, Water stress, Stress tolerance indices, Genetic parameters, GYT biplot graph.

Introduction

Egyptian government commenced the Sustainable Development Strategy 2030 in 2016; the strategy contains a set of economic, social, and environmental goals to be accomplished by the year 2030. However, accomplishing these development goals may be restricted in the coming years by the dilemma of water scarcity where Egypt suffers from limited water resources (Wahba et al., 2018).

Accordingly, deficiency of water in Egypt is the main challenge for agricultural horizontal expanding under current and future climate. Agriculture sector consumes 81.6% of the Egyptian annual water resources (CAPMAS,

2017). Significant changes in Egypt water intensive crops production and trade have been observed during the last 50 years. For example, 570% increase in wheat production during the period from 1961 to 2015 was observed and accompanied by 1456% increase in wheat net imports (FAO, 2017).

In Egypt, wheat (*Triticum aestivum* L.) is considered the first grain crop to feed for most social populations and the straw yield supports animals feeding. Wheat still on is the tops of list of cereal crops in terms of area and production. There is a huge gap between production and consumption in Egypt (Wuletaw et al., 2017). El-Gafy (2014) found that the water footprint of wheat production and consumption in Egypt

#Corresponding author email: mo_eman@hotmail.com

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fluctuate according to the changes in the crop production, foreign trade, per capita consumption, population, and climate effects. Accordingly, due to the serious current state of Egyptian water crisis, a more comprehensive perspective on the role of water in Egyptian trade and consumption is needed and implementing three different governmental water policies (reduce, reuse and recycle).

Accordingly, development of cultivars with high yield under limited water environments is a major goal of plant breeding (Cattivelli et al., 2008). Strenuous efforts have been made for a long time to develop such cultivars which could cope against biotic and abiotic stresses and give more production. Selection for yield under water deficit conditions is complicated by low heritability and large genotype environment interaction. The elite genotype for water stress conditions must combine a reasonably high yield potential with specific plant characters, which could compensate yield against moisture stress (Blum, 2005). Evaluation of yield performance of genotypes under both favorable and unfavorable conditions is vital for plant breeders to identify stress tolerant genotypes (Pirayvatlou, 2001). It is obvious that high-yielding genotypes under adequate conditions may be not stress tolerant (Mardeh et al., 2006); therefore, various studies favorite the selection under stress and non-stress environments (Rajaram & Van Ginkle, 2001).

Stress tolerance indices (STI) widely used as simple mathematical equations that quantify and compare the grain yields under stressed and non-stressed conditions to differentiate the tolerant/sensitive genotypes (Mitra, 2001). There are various stress tolerance indices such as mean productivity (MP) (Rosielle & Hamblin, 1981), geometric mean productivity (GMP) and stress tolerance index (STI).

Knowledge on heritability and genetic advance is a basic step to identify the characters amenable to genetic improvement through selection. The heritability values without considering genetic advance would be impractically useful in breeding program depending on visual selection. Plant breeders have become increasingly able to use directly yield components as selection criteria to achieve results more quickly and efficiently than selecting for yield performance itself.

A genotype by yield*trait (GY*T) biplot is a novel approach was proposed by Yan & Frégeau-Reid (2018) to tackle the problem of genotype evaluation on multiple traits. It is based on the following conceptualizations: 1) Yield is the most important trait and all other target traits are important only when combined with high yield, 2) The superiority of a genotype should be judged by its weight based on combining yield with other target traits, rather than the individual traits. In Egypt, on wheat crop, no references have been found about the use of yield*trait (GY*T) biplot graph in making selection criteria of grain yield and its components. Accordingly, the main goals of this investigation were to: (1) Evaluate the response of early and grain yield characters of 18 bread wheat genotypes under normal and water stress conditions, (2) Identify the water deficit tolerant wheat genotypes based on stress tolerance indices (STI) and (3) Using new approach of genotype by yield*trait (GYT) biplot, as a selection criterion to evaluate 18 bread wheat under water stress conditions.

Materials and Methods

This study was conducted at the Experimental Farm of Sakha Agricultural Research Station, Kafr El-Sheikh, Egypt, during 2015/2016 and 2016/2017 seasons. Eighteen bread wheat (*Triticum aestivum* L.) genotypes were used and grown on mid-November in the two seasons. The tested wheat genotypes contained 14 lines that were selected as promising lines from the local breeding program in addition to four cultivars used as checks, i.e., Giza 171, Shandweel 1, Gemmeiza 11 and Sids 12. The name and pedigree of the studied genotypes are listed in Table 1. In each season, the entries were evaluated in two experiments represented two different irrigation conditions. The first was irrigated four times after planting irrigation (normal irrigation) while the second one was to give one surface-irrigation during the tillering stage after planting irrigation by (25 days). The experimental design was randomized complete block design with three replicates for each irrigation condition. Before cultivation, soil samples at 0-30 cm depth and from 30-60cm were collected during the two of season's study. Details of soil properties of the research site seasons are in Table 2. The meteorological data were recorded for the two winter growing seasons from Sakha meteorological station as shown in Table 3.

TABLE 1. Name and pedigree of the studied wheat genotypes.

Genotype	Pedigree
Line 1	ATTILA*2 / PBW65 /4/ CHEN / AEGILOPS SQUARROSA (TAUS) // BCN /3/ 2*KAUZ
Line 2	VEE / KOEL // 2* SKAUZ /3/ KAUZ // BOW / NKT
Line 3	PFAU / MILAN /5/ WEAVER /4/ NAC / TH.AC // 3* PVN /3/ MIRLO / BUC
Giza 171	SAKHA 93 / GEMMEIZA 9
Line 5	OASIS / SKAUZ // 4* BCN /6/ CNDO / R143 // ENTE / MEXI 2 /3/ AEGILOPS .SQUARROSA (TAUS) /4/ WEVER /5/ 2*TAUZ
Line 6	SERI*3 // RL6010 / 4*YR /3/ PASTOR /4/ BAV92 /5/ KAUZ // BOW / NKT
Gemmiza 11	BOW**S**KVZ**S**//7C/SER182/3 /GIZA168/SAKHA 61
Line 8	VEE/PJN//2*TUI/3/GALVEZ/WEAVER /7/ BUC // 7C / ALD /5/ MAYA74 / ON // 1160.147 /3/ BB / GLL /4/CHAH**S** /6/ MAYA / VUL // CMH74A.630 /4*SX
Sids 12	BUC//7C/ALD/5/MAYA74/ON//1160.147/3/BB/GLL/4/CHAT**S**/6/MAYA/VUL//CMH74 A.630/4*SX
Line 10	DVERD 2 / AE - SQUARROSA (214)// 2* BCN /5/ WEAVER /4/ NAC / TH.AC // 3* PVN /3/ MIRLO / BUC
Line 11	CHIBIA//PRLII/CM65531/3/ SKAUZ *2 / SRMA
Line 12	VEE/PJN//2*TUI/3/GALVEZ/WEAVER /4/ CHIBIA//PRLII/CM65531
Shandweel 1	SITE/MO/4/NAC/TH.AC//3*PVN/3/MIRLO/BUC
Line 14	VOROBAY
Line 15	CHEN / AEGILOPS SQUARROSA (TAUS) // BCN /3/ 2*KAUZ /4/ HAAMA-11
Line 16	OASIS / SKAUZ // 4* BCN /6/ GIZA 158 /5/ CFN /CNO "S" // RON /3/ BB / NOR 67 /4/ TL /3/ FN / TH //2* NAR 59
Line 17	WHEAR/VIVITSI//WHEAR
Line 18	PASTOR/SITE/MO/3/CHEN/AEGILOPS SQUARROSA (TAUS)//BCN/4/WBLL1

According to the data of the Egyptian Wheat Research Department, ARC.

TABLE 2. Mechanical and chemical soil analyses during two growing seasons.

Location	Sample depth	Soil structure	pH	EC	Anions my/L				Cations mg/L			
					CO ₃ ⁻	HCO ₃ ⁻	CL ⁻	SO ₄ ⁻	Ca ⁺⁺	Mg ⁺⁺	Na ⁺	K ⁺
2015/2016												
Normal soil	0 - 30	Clayey	8.6	2.33	-	2.5	10	43.3	10.6	6.1	12.4	0.29
	30 - 60	Clayey	8.7	2.1	-	2.25	13	48.7	6.6	4.9	8	0.33
2016/2017												
Normal soil	0 - 30	Clayey	8.1	2.01	-	3	8.1	9.11	5.6	3.91	10.3	0.31
	30 - 60	Clayey	7.9	1.5	-	2.5	4.8	7.16	3.23	2.33	8.42	0.29

TABLE 3. Monthly mean of air temperature (AT °C), relative humidity (RH %) and rainfall (mm/month) in winter seasons 2015/2016 and 2016/2016 at Sakha location.

Month	AT °C 2015/16		AT°C 2016/17		RH %		Rainfall (mm)	
	Max.	Min.	Max.	Min.	2015/16	2016/17	2015/16	2016/17
December	24.3	13.8	24.8	14.4	74.15	75.62	20.6	12.15
January	22.3	9.72	20.4	8.33	76.05	78.27	5.7	25
February	18.7	6.46	18.4	6.3	74.6	74.1	42.55	40.7
March	19	7.65	23.5	6.7	74.75	70	30.8	-
April	22.7	11.7	23.7	11.6	70.59	69.76	6.25	13.2
May	27.6	13.7	30	14.2	63.4	61.72	16.9	-
Means	30.2	18.8	31.2	19	61.7	58.33	-	-

Max= Maximum temperature, Min= Minimum temperature.

A wide border (25m) surrounded each experiment to minimize the underground water permeability. The wheat grains were planted in six rows/ plots (3.5m long and 20cm apart). Thus, the plot area was 4.2m² where the harvest area was 2.8m² included the four guarded rows. All other cultural practices were applied as recommended for wheat cultivation. The studied characteristics were: Days to heading (DH) and days to maturity (DM), grain filling period (GFP) in days and equal to the number of days from heading to maturity, grain filling rate (GFR) in g/m² per days⁻¹ and equal to GY divided by GFP, flag leaf area (FLA), chlorophyll a (Cha), chlorophyll b (Chb), proline content (P), plant height (PH, cm), number of spikes/m² (S/m²), number of kernels/ spike (K/S), 1000-kernel weight (1000 KW in g), straw yield (SY in ton fed⁻¹) and grain yield (GY, ardab fed⁻¹) (one feddan equal 0.42 hectares, harvest index HI).

Statistical analysis

Stress tolerance indices

The data were subjected to individual and combined analysis of variance of randomized complete block design over the two cultivated sites (normal and shortage irrigation) for each season (Steel et al., 1997). As a routine statistical step, Levene test was run prior to the combined analysis to confirm the homogeneity of individual error terms (Levene, 1960). Least significant difference (LSD) test was used to detect the significant differences among the proper items at probability level of 0.05. For each genotype, six stress tolerance indices were calculated based on average grain yield under normal irrigation (Y_n) and water stress conditions (Y_s) over the two seasons. The names, equations and references of

the stress tolerance indices are shown in Table 4. The genotypes which possess high values of mean productivity (MP), harmonic mean (HM), geometric mean productivity (GMP), stress tolerance index (STI), yield index (YI), and modified stress tolerance index (MSTI) are considered to be more tolerant for reduced irrigation.

Genetic parameters

Based on the combined analysis of each irrigation condition (normal irrigation N and reduce irrigation S) over the two seasons, the genotypic and phenotypic variances and their corresponding coefficient of variations (GCV and PCV) were estimated using the proper mean square expectations according to the method suggested by Johnson et al. (1955). Broad sense heritability (h_b^2) and genetic advance (GA %) in terms of percentage of mean (with 10% selection intensity) were estimated according to Allard (1999).

The genotype by yield*trait (GYT)

The values for the yield-trait combinations were obtained by multiplying the yield value with the trait value for each genotype (e.g., Y*1000 KW, Y* P, Y* PH, Y*FLA, Y* Cha, Y* Chb and Y* K/S). These were measures of how grain yield and traits content were combined in a genotype. For grain filling rate (GFR), days to maturity (DM), days to heading (DH) and straw yield (SY) which were so measured that a larger value means less desirable, the values by the yield-trait combinations were obtained by dividing the yield value for the trait value for each genotype (e.g., Y/GFR). The units for the yield-trait combinations are not important as it is the standardized data that are used in genotype evaluation.

TABLE 4. The name, equation and reference of some stress tolerance indices.

No.	Index name	Formula	Reference
	% Reduction	$(Y_n - Y_s) * 100 / Y_n$	
The high values of these indices indicated to stress tolerance			
1	Mean productivity (MP)	$(Y_n + Y_s) / 2$	(Rosielle & Hamblin, 1981)
2	Harmonic mean (HM)	$(2 * Y_n * Y_s) / (Y_n + Y_s)$	(Jafari et al., 2009)
3	Geometric mean productivity (GMP)	$(Y_n * Y_s)^{0.5}$	(Fernandez, 1992)
4	Stress tolerance index (STI)	$(Y_n * Y_s) / (\bar{Y}_n)^2$	(Fernandez, 1992)
5	Yield index (YI)	Y_s / \bar{Y}_s	(Gavuzzi et al., 1997)
6	Modified stress tolerance index (MSTI)	$(YI)^2 * STI$	(Farshadfar & Sutka, 2002)

- Y_n and Y_s indicate to average grain yield of each genotype under normal and stress conditions.

- \bar{Y}_n and \bar{Y}_s indicate to average grain yield overall genotypes under normal and stress conditions

To rank the tested wheat genotypes for water deficit tolerance, Superiority Index (weight of selection criteria) was computed for each genotype as the average over the standardized data of yield-trait combination values.

Data standardization

Data were standardized so that the mean for each trait or yield-trait combination becomes 0 and the variance becomes unit (e.g., see Table 8). The standardization was performed as:

$$P_{ij} = T_{ij} - T_j / S_j$$

where P_{ij} is the standardized value of genotype i for trait or yield-trait combination j in the standardized table, T_{ij} is the original value of genotype i for trait or yield-trait combination j in the GYT data, T_j is the mean across genotypes for trait or yield-trait combination j and S_j is the standard deviation for trait or yield-trait combination j .

Construction of a GYT biplot

The GYT biplot was based on the first two principal components (PC) resulting from singular value decomposition (SVD) of the standardized data. SVD decomposes the GYT table into genotype Eigen values, yield-trait combination Eigen values, and singular values:

$$P = (d\lambda_1^{\alpha} \zeta_{i1}) (\lambda_1^{1-\alpha} \tau_1^j / d) + (d\lambda_2^{\alpha} \zeta_{i2}) (\lambda_2^{1-\alpha} \tau_{2j} / d) + \epsilon_{ij}$$

where ζ_{i1} and ζ_{i2} are the eigen values for PC1 and

PC2, respectively, for genotype i ; τ_{1j} and τ_{2j} are the eigen values for PC1 and PC2, respectively for yield-trait combination j and ϵ_{ij} is the residual from fitting the PC1 and PC2 for genotype i on trait j ; λ_1 and λ_2 are the singular values for PC1 and PC2, respectively. α is the singular value partitioning factor. When $\alpha = 1$ (i.e., SVP = 1 in terms of GGE biplot), the biplot is said to be genotype-focused, and is suitable for comparing genotypes. When $\alpha = 0$ (i.e., SVP = 2), the biplot is said to be yield-trait combination -focused, and is suitable for visualizing correlations among yield-trait combination. Genotypes by yield-trait combination relations are not affected by the choice of α . The scalar d is chosen such that the length of the longest vector among genotypes is equal to that among yield-trait combination, which is important for generating a functional biplot 3. The GYT biplot was constructed by plotting $(d\lambda_1^{\alpha} \zeta_{i1})$ against $(d\lambda_2^{\alpha} \zeta_{i2})$ for genotypes and plotting $\lambda_1^{1-\alpha} (\tau_{1j} / d_{1j}) j_1$ against $\lambda_2^{1-\alpha} (\tau_{2j} / d_{2j}) j_2$ for yield-trait combination in the same plot (Yan & Fréreau-Reid, 2018).

Results and Discussion

The results of Levene test proved homogeneity of separate error variances for all studied traits that permits to apply combined analysis.

Mean performance

Highly significant differences were found among the 18 wheat genotypes for fifteen studied traits, during the two growing seasons of

2015/2016 and 2016/2017 under both normal and water stress conditions as shown in Table 5.

Results in Table 5 show that means of all genotypes decreased significantly under the stress conditions for all characters in the two seasons, except chlorophyll b, proline, and harvest index in the two seasons and 1000-kernel weight in the first season only. The highest values were showed by genotypes No. 17, 14 for plant height under both conditions in the two seasons, while the shortest plants were observed by Line No. 10 under adequate and stress conditions.

Under the full and reduced irrigations in the two seasons, Lines No. 1 and 5 were the latest in heading and maturely, respectively while Lines No.10 and 15 were the earliest ones among the studied genotypes.

The longest grain filling period (GFP) was recorded by genotypes No. 9, 10 and 16 while Lines No. 3, 5 and 18 had the shortest GFP under the two conditions in the 1st and 2nd seasons.

The highest GFR value was observed by genotype No. 18 under the two irrigation regimes. However, Line No. 3 in the first season under normal condition; and genotype 17 recorded highest GFR under reduces irrigation condition in first season. Line 16 showed the slowest GFR under the two conditions in first season. The highest values of No. of spikes/m² (S/m²) were found in genotype 5, 18, under the two conditions, while the lowest values were obtained in Line 7 and genotype 12 under the two conditions. Genotype 9, 13, showed the highest K/S under the two conditions, while Line 10 vice versa under all conditions in first season, Line 12 in the second season under the two conditions. The highest 1000- KW resulted from genotype 15, Line 17 in under the two conditions at first season, while the lowest values belonged to Line 1 and Line 8 under the two conditions. The highest GY was obtained from genotype 18 and genotype 3, under the two conditions, while, the lowest GY belonged to genotype 12, and Line 16 under the two conditions.

Based on the results of each trait the response of genotypes at each condition was different. The studied traits of all studied genotypes have been observed to be affected by reduce irrigation stress to a considerable extent. These genotypes

produced the best values of the studied traits during the normal conditions but some genotypes could perform well under reduce irrigation stress conditions.

In addition, the values of the studied characters hold the same trend for the overall means under the two conditions in the two seasons. Moreover, the ranges between the values of all characters decreased under the reduce irrigation condition in the two seasons in most cases except chlorophyll b, proline. Reduce irrigation affects most physiological processes in wheat lead to reduce plant growth by affecting various physiological and biochemical processes, such as photosynthesis, respiration, translocation, ion uptake, carbohydrates, and nutrient metabolism and growth promoters. The highest proline content was observed in the genotypes 11, 18 binge 1.9 and 1.8, respectively in the first season and genotypes 7,5,3,2 binge (2.5, 2.2, 2.1, 2.1), respectively at second season. Bayoumi et al. (2008) reported a similar positive relationship between grain yield and proline accumulation under stress conditions in wheat. This suggests that the high proline content in the genotypes is probably a positive adaptive mechanism for overcoming the stress conditions. It is well documented that accumulated proline plays a role as a proper solute in plants, regulating and reducing water loss from the cell under water deficit conditions. Also, that high proline accumulation in the plants could provide energy for growth and survival and thereby helping the plant to tolerate stress. Using mean performance as an indicator of adaptation, the genotypes 18, 6, 17, and 4 appear to be broadly adapted and relatively drought tolerant under stress conditions because the best values for other studied traits were recorded by these genotypes. In general, these results are in harmony with those reported by Amer (2011), Hassanein et al. (2012), Saad et al. (2014), Deef et al. (2016), El-Hashash & Agwa (2018), Fouad (2018) and Juan et al. (2019).

Genetic parameters

Table 6 presented the estimates of phenotypic (PCV) and genotypic (GCV) coefficients of variation, broad sense heritability (h_b^2) and expected genetic advance as a percent of the mean (EGA %) for the studied traits under each of well and stress conditions.

TABLE 5. Mean values of earliness and yield attributes for 18 wheat genotypes evaluated under normal and stress conditions during 2015/2016 and 2016/2017 seasons.

Genotype	Days to heading						Days to maturity						Grain filling period					
	2015/2016		2016/2017		2015/2016		2016/2017		2015/2016		2016/2017		2015/2016		2016/2017			
	N	S	Mean	N	S	Mean	N	S	Mean	N	S	Mean	N	S	Mean	N	S	Mean
Line 1	102	100.7	101.3	105	103.3	104.2	151.3	147.3	149.3	153	149	151	49.3	46.7	48	48	45.7	46.8
Line 2	95.7	93.7	94.7	98	96.3	97.2	146.3	143	144.7	146.7	143.3	145	50.7	49.3	50	48.7	47	47.8
Line 3	92.7	91	91.8	95	93.7	94.3	141.3	138	139.7	143.7	138.7	141.2	48.7	47	47.8	48.7	45	46.8
Giza 171	97.7	96	96.8	98.7	97	97.8	150	147.3	148.7	152.3	148	150.2	52.3	51.3	51.8	53.7	51	52.3
Line 5	101.3	98.3	99.8	104.7	102.3	103.5	149.3	145.7	147.5	151.3	148	149.7	48	47.3	47.7	46.7	45.7	46.2
Line 6	97.7	96	96.8	98.3	97.7	98	149.3	145.3	147.3	149	147.7	148.3	51.7	49.3	50.5	50.7	50	50.3
Gemmiza 11	96	93.3	94.7	96.3	94.7	95.5	146.3	142.3	144.3	147.7	144	145.8	50.3	49	49.7	51.3	49.3	50.3
Line 8	96	94.3	95.2	96.7	95	95.8	148.7	145	146.8	149.3	147.3	148.3	52.7	50.7	51.7	52.7	52.3	52.5
Sids 12	93.3	90.7	92	93	91.3	92.2	146	145	145.5	147.3	145.7	146.5	52.7	54.3	53.5	54.3	54.3	54.3
Line 10	91.7	85.3	88.5	89.7	88	88.8	142	140.3	141.2	147	140	143.5	50.3	55	52.7	57.3	52	54.7
Line 11	96	92.7	94.3	95.3	93	94.2	145.7	143	144.3	147.3	143	145.2	49.7	50.3	50	52	50	51
Line 12	95.3	93	94.2	95	92.7	93.8	145	139	142	145	141.3	143.2	49.7	46	47.8	50	48.7	49.3
Shandweel 1	97.7	96	96.8	96.3	95.3	95.8	149.7	145	147.3	151.3	148.7	150	52	49	50.5	55	53.3	54.2
Line 14	100	96	98	105.3	102.3	103.8	149.7	143.7	146.7	150.7	146.7	148.7	49.7	47.7	48.7	45.3	44.3	44.8
Line 15	89.7	82.7	86.2	91.7	91	91.3	137.7	136.7	137.2	141.7	136.7	139.2	48	54	51	50	45.7	47.8
Line 16	93.3	91.3	92.3	92.3	90	91.2	146.3	143.7	145	147.3	141.3	144.3	53	52.3	52.7	55	51.3	53.2
Line 17	98	96.7	97.3	102	100.3	101.2	149.3	144.7	147	150.7	148	149.3	51.3	48	49.7	48.7	47.7	48.2
Line 18	98.3	97	97.7	100.3	97.7	99	147	143.3	145.2	147.3	143.7	145.5	48.7	46.3	47.5	47	46	46.5
Mean	96.2	93.6	94.9	97.4	95.6	96.5	146.7	143.2	144.9	148.3	144.5	146.4	50.5	49.6	50.1	50.8	48.9	49.8
LSD _{0.05} I	*				*		**	**	**	**	**	**	NS	NS	NS	NS	NS	*
LSD _{0.05} G	1.39				1.26		1.47	1.47	1.2	1.2	1.2	1.2	2.1	2.1	2.1	2.1	2.1	1.33
LSD _{0.05} IxG	1.97				NS		2.08	2.08	1.7	1.7	1.7	1.7	2.97	2.97	2.97	2.97	2.97	1.89

- LSD: Least significant difference, I: Irrigation, G: Genotypes, IxG: Interaction.

- N: Indicates to normal conditions, S: Indicates to stress conditions.

- NS: Not significant, *: Significant, **: Highly significant.

TABLE 5. Cont.

Genotype	Grain filling rate						Flag leaf area						Chlorophyll a								
	2015/2016		2016/2017		2015/2016		2016/2017		2015/2016		2016/2017		2015/2016		2016/2017		2015/2016		2016/2017		
	N	S	Mean	N	S	Mean	N	S	Mean	N	S	Mean	N	S	Mean	N	S	Mean	N	S	Mean
Line 1	83.0	70.5	76.8	83.5	75.9	79.7	45.8	29.9	37.9	56.0	38.5	47.2	3.0	2.7	2.8	3.3	2.8	3.0	3.0	3.0	3.0
Line 2	77.4	64.8	71.1	89.6	74.9	82.2	42.4	40.6	41.5	54.4	42.5	48.5	3.1	2.7	2.9	3.3	3.0	3.1	3.1	3.1	3.1
Line 3	97.6	83.9	90.7	91.6	90.8	91.2	43.1	39.5	41.3	54.2	36.5	45.3	3.1	2.7	2.9	3.3	2.9	3.1	3.1	3.1	3.1
Giza 171	86.6	79.6	83.1	85.5	82.3	83.9	69.6	50.3	59.9	51.5	41.9	46.7	3.4	2.9	3.2	3.5	2.8	3.1	3.1	3.1	3.1
Line 5	92.0	87.9	89.9	94.1	81.6	87.9	44.9	30.5	37.7	51.0	41.5	46.3	3.2	2.6	2.9	3.1	2.9	3.0	3.0	3.0	3.0
Line 6	84.4	83.6	84.0	88.8	80.8	84.8	38.5	38.1	38.3	50.2	40.3	45.2	3.2	2.7	2.9	3.3	2.7	3.0	3.0	3.0	3.0
Gemmiza 11	86.9	72.8	79.8	75.9	69.5	72.7	75.6	49.4	62.5	65.5	40.6	53.0	3.1	2.7	2.9	3.2	2.9	3.1	3.1	3.1	3.1
Line 8	76.2	64.8	70.5	64.5	58.9	61.7	56.7	45.2	51.0	59.6	39.1	49.3	3.4	2.8	3.1	3.1	2.7	2.9	2.9	2.9	2.9
Sids 12	79.9	66.3	73.1	72.3	62.5	67.4	64.5	56.2	60.3	51.1	42.3	46.7	3.3	2.9	3.1	3.4	3.0	3.2	3.2	3.2	3.2
Line 10	78.3	61.9	70.1	76.7	73.9	75.3	47.6	35.1	41.3	51.3	39.6	45.4	3.3	2.8	3.1	3.3	2.9	3.1	3.1	3.1	3.1
Line 11	82.5	71.5	77.0	82.8	78.9	80.8	48.4	39.7	44.0	53.6	46.2	49.9	3.1	2.7	2.9	3.1	2.8	2.9	2.9	2.9	2.9
Line 12	70.3	64.7	67.5	64.5	55.1	59.8	45.0	27.9	36.5	54.9	38.3	46.6	3.4	2.9	3.2	3.2	2.8	3.0	3.0	3.0	3.0
Shandweel 1	89.7	78.9	84.3	85.4	77.9	81.6	47.9	23.1	35.5	55.5	41.7	48.6	3.2	3.0	3.1	3.3	2.9	3.1	3.1	3.1	3.1
Line 14	85.2	81.0	83.1	92.2	87.6	89.9	59.8	43.2	51.5	59.0	39.1	49.1	3.0	2.7	2.8	2.9	2.8	2.8	2.8	2.8	2.8
Line 15	87.8	65.9	76.9	86.4	82.5	84.5	52.7	46.5	49.6	61.6	43.6	52.6	3.2	2.8	3.0	3.1	2.9	3.0	3.0	3.0	3.0
Line 16	69.5	63.2	66.4	72.2	66.1	69.1	48.6	41.7	45.2	56.0	38.0	47.0	3.0	2.7	2.9	3.3	2.9	3.1	3.1	3.1	3.1
Line 17	88.3	85.7	87.0	97.7	91.6	94.7	60.3	40.2	50.2	56.8	37.3	47.0	3.0	2.8	2.9	3.3	2.9	3.1	3.1	3.1	3.1
Line 18	100.6	92.6	96.6	110.7	99.3	105.0	40.2	30.7	35.4	53.1	44.6	48.8	3.2	2.8	3.0	3.2	2.9	3.1	3.1	3.1	3.1
Mean	84.2	74.4	79.3	84.1	77.2	80.7	51.8	39.3	45.5	55.3	40.6	48.0	3.2	2.8	3.0	3.2	2.8	2.9	3.0	3.0	3.0
LSD _{0.05} I	**	**	**	**	**	**	*	*	*	**	**	**	**	**	**	**	**	**	**	**	**
LSD _{0.05} G	3.0	3.0	3.0	2.91	2.91	2.91	4.14	4.14	4.14	3.40	3.40	3.40	0.15	0.15	0.15	0.07	0.07	0.07	0.07	0.07	0.07
LSD _{0.05} IxG	4.22	4.22	4.22	4.12	4.12	4.12	5.86	5.86	5.86	4.81	4.81	4.81	NS	NS	NS	0.11	0.11	0.11	0.11	0.11	0.11

- LSD: Least significant difference, I: Irrigation, G: Genotypes, IxG: Interaction.

- N: Indicates to normal conditions, S: Indicates to stress conditions,

- NS: Not significant, *: Significant, **: Highly significant.

TABLE 5. Cont.

Genotype	Chlorophyll <i>b</i>						Proline content						Plant height								
	2015/2016		2016/2017		2015/2016		2016/2017		2015/2016		2016/2017		2015/2016		2016/2017		2015/2016		2016/2017		
	N	S	Mean	N	S	Mean	N	S	Mean	N	S	Mean	N	S	Mean	N	S	Mean	N	S	Mean
Line 1	1.4	1.8	1.6	2.0	1.9	1.9	1.4	1.6	1.5	1.6	2.0	1.8	1.8	115.0	106.7	110.8	115.0	105.0	110.0	110.0	
Line 2	1.4	1.7	1.5	1.8	1.8	1.8	1.4	1.5	1.4	1.5	2.1	1.8	1.8	115.0	106.7	110.8	113.3	105.0	109.2	109.2	
Line 3	1.8	1.5	1.6	1.7	1.8	1.8	1.5	1.6	1.6	1.4	2.1	1.7	1.7	111.7	100.0	105.8	111.7	103.3	107.5	107.5	
Giza 171	1.9	1.7	1.8	1.7	1.8	1.8	1.3	1.4	1.3	1.5	2.0	1.7	1.7	125.0	111.7	118.3	123.3	115.0	119.2	119.2	
Line 5	1.6	1.5	1.5	1.9	1.9	1.9	1.2	1.4	1.3	1.4	2.2	1.8	1.8	115.0	110.0	112.5	118.3	106.7	112.5	112.5	
Line 6	1.8	1.8	1.8	1.9	1.9	1.9	1.2	1.4	1.3	1.5	2.0	1.7	1.7	115.0	106.7	110.8	115.0	105.0	110.0	110.0	
Gemmiza 11	1.8	2.0	1.9	1.9	2.2	2.1	1.4	1.6	1.5	1.5	2.5	2.0	2.0	116.7	113.3	115.0	120.0	111.7	115.8	115.8	
Line 8	1.7	1.8	1.7	1.9	1.9	1.9	1.3	1.5	1.4	1.4	2.0	1.7	1.7	110.0	98.3	104.2	111.7	101.7	106.7	106.7	
Sids 12	1.9	1.9	1.9	1.9	1.9	1.9	1.2	1.4	1.3	1.5	1.6	1.6	1.6	108.3	103.3	105.8	108.3	101.7	105.0	105.0	
Line 10	1.7	1.9	1.8	1.8	1.8	1.8	1.3	1.6	1.5	1.4	1.5	1.5	1.5	105.0	98.3	101.7	105.0	95.0	100.0	100.0	
Line 11	1.7	1.7	1.7	1.9	1.8	1.8	1.3	1.9	1.6	1.4	1.4	1.4	1.4	106.7	101.7	104.2	106.7	96.7	101.7	101.7	
Line 12	1.5	1.8	1.7	1.8	1.9	1.9	1.4	1.7	1.6	1.4	1.5	1.5	1.5	116.7	108.3	112.5	115.0	105.0	110.0	110.0	
Shandweel 1	1.4	2.0	1.7	1.8	1.8	1.8	1.3	1.6	1.4	1.4	1.4	1.4	1.4	120.0	110.0	115.0	120.0	110.0	115.0	115.0	
Line 14	1.3	1.9	1.6	1.8	2.0	1.9	1.4	1.6	1.5	1.3	1.5	1.4	1.4	131.7	126.7	129.2	128.3	121.7	125.0	125.0	
Line 15	1.4	1.9	1.7	2.0	2.0	2.0	1.2	1.5	1.3	1.5	1.6	1.6	1.6	115.0	111.7	113.3	116.7	108.3	112.5	112.5	
Line 16	2.7	1.4	2.0	1.8	1.7	1.8	1.4	1.5	1.4	1.5	1.4	1.4	1.4	120.0	113.3	116.7	118.3	110.0	114.2	114.2	
Line 17	2.0	1.3	1.6	1.8	2.1	1.9	1.2	1.5	1.3	1.4	1.7	1.6	1.6	138.3	128.3	133.3	133.3	121.7	127.5	127.5	
Line 18	2.4	1.7	2.1	1.8	1.8	1.8	1.2	1.8	1.5	1.4	1.5	1.4	1.4	118.3	115.0	116.7	123.3	115.0	119.2	119.2	
Mean	1.7	1.7	1.7	1.8	1.9	1.9	1.3	1.6	1.4	1.4	1.8	1.6	1.6	116.9	109.4	113.1	116.9	107.7	112.3	112.3	
LSD _{0.05} I	NS	NS	NS	NS	NS	NS	NS	**	**	**	**	**	**	**	**	**	**	**	**	**	**
LSD _{0.05} G	0.16	0.16	0.16	0.07	0.07	0.07	0.10	0.10	0.10	0.07	0.07	0.07	0.07	3.03	3.03	3.03	3.03	2.73	2.73	2.73	2.73
LSD _{0.05} IxG	0.23	0.23	0.23	0.10	0.10	0.10	0.14	0.14	0.14	0.09	0.09	0.09	0.09	4.29	4.29	4.29	4.29	3.86	3.86	3.86	3.86

- LSD: Least significant difference, I: Irrigation, G: Genotypes, IxG: Interaction.
 - N: Indicates to normal conditions, S: Indicates to stress conditions.
 - NS: Not significant, *: Significant, **: Highly significant.

TABLE 5. Cont.

Genotype	Number of spike/m ²												Straw yield					
	2015 / 2016			2016 / 2017			2015 / 2016			2016 / 2017			2015 / 2016			2016 / 2017		
	N	S	Mean	N	S	Mean	N	S	Mean	N	S	Mean	N	S	Mean	N	S	Mean
Line 1	418.7	331.3	375.0	383.3	341.0	362.2	27.3	22.0	24.6	26.7	23.1	24.9	6.66	5.33	5.99	6.61	4.87	5.74
Line 2	396.0	301.3	348.7	307.5	288.3	297.9	26.1	21.3	23.7	29.1	23.5	26.3	6.25	5.06	5.65	5.73	4.52	5.12
Line 3	358.7	346.7	352.7	376.0	361.7	368.8	31.7	26.3	29.0	29.8	27.3	28.5	6.04	5.19	5.61	6.08	5.25	5.66
Giza 171	354.0	288.0	321.0	292.7	282.5	287.6	30.2	27.2	28.7	30.6	28.0	29.3	6.80	5.21	6.01	6.48	5.29	5.89
Line 5	480.0	408.0	444.0	417.5	372.5	395.0	29.4	27.7	28.6	29.3	24.8	27.1	6.50	5.05	5.78	6.44	5.55	6.00
Line 6	337.3	330.7	334.0	375.8	351.8	363.8	29.1	27.5	28.3	30.0	27.0	28.5	6.48	5.21	5.84	5.87	4.90	5.38
Gemmiza 11	300.0	262.7	281.3	297.7	274.2	285.9	29.2	23.8	26.5	26.0	22.9	24.4	6.44	5.55	6.00	6.27	5.13	5.70
Line 8	320.0	280.0	300.0	323.3	309.2	316.3	26.8	21.9	24.3	22.7	20.6	21.6	6.49	5.30	5.89	6.36	5.32	5.84
SIDS 12	290.7	204.0	247.3	359.2	341.7	350.4	28.0	24.0	26.0	26.2	22.7	24.4	6.04	5.46	5.75	6.32	5.47	5.90
Line 10	368.0	332.0	350.0	337.5	324.2	330.8	26.3	22.7	24.5	29.3	25.6	27.5	5.76	5.32	5.54	6.23	5.02	5.63
Line 11	412.0	364.0	388.0	413.5	369.0	391.3	27.3	24.0	25.7	28.7	26.3	27.5	5.59	5.44	5.52	5.83	5.25	5.54
Line 12	309.3	280.0	294.7	321.7	245.0	283.3	23.3	19.9	21.6	21.5	17.9	19.7	6.69	5.74	6.22	6.55	5.26	5.90
Shandweel 1	376.0	334.7	355.3	335.0	314.2	324.6	31.1	25.8	28.4	31.3	27.7	29.5	7.49	5.88	6.69	7.05	5.80	6.43
Line 14	340.0	305.3	322.7	366.7	305.8	336.3	28.2	25.7	27.0	27.9	25.9	26.9	7.36	6.11	6.74	7.38	6.29	6.83
Line 15	388.0	329.3	358.7	419.2	369.2	394.2	28.1	23.7	25.9	28.8	25.1	26.9	5.55	4.75	5.15	6.50	5.33	5.92
Line 16	382.7	337.3	360.0	388.3	340.0	364.2	24.6	22.0	23.3	26.5	22.6	24.5	6.27	5.04	5.66	6.89	5.38	6.14
Line 17	386.0	309.3	347.7	377.5	313.3	345.4	30.2	27.4	28.8	31.7	29.1	30.4	8.22	6.32	7.27	8.25	6.29	7.27
Line 18	418.7	341.3	380.0	351.8	330.0	340.9	32.6	28.6	30.6	34.7	30.4	32.6	6.36	5.60	5.98	6.77	5.81	6.29
Mean	368.7	315.9	342.3	358.0	324.1	341.0	28.3	24.5	26.4	28.4	25.0	26.7	6.50	5.42	5.96	6.53	5.37	5.95
LSD _{0.05} I	NS	NS	NS	*	*	**	**	**	**	**	**	**	**	**	**	**	**	**
LSD _{0.05} G	50.0	50.0	42.25	42.25	1.30	1.30	1.30	1.30	1.30	0.97	0.97	0.97	0.97	0.26	0.26	0.26	0.26	0.26
LSD _{0.05} IxG	NS	NS	NS	NS	1.84	1.84	1.84	1.84	1.84	1.37	1.37	1.37	1.37	0.37	0.37	0.37	0.37	0.36

- LSD: Least significant difference, I: Irrigation, G: Genotypes, IxG: Interaction.

- N: Indicates to normal conditions, S: Indicates to stress conditions,

- NS: Not significant, *: Significant, **: Highly significant.

TABLE 5. Cont.

Genotype	Harvest index %						1000-kernel weight						Kernels per spike					
	2015/2016		2016/2017		2015/2016		2016/2017		2015/2016		2016/2017		2015/2016		2016/2017			
	N	S	Mean	N	S	Mean	N	S	Mean	N	S	Mean	N	S	Mean	N	S	Mean
Line 1	38.1	38.2	38.1	37.8	41.5	39.6	36.4	38.0	37.2	35.0	42.3	38.6	67.2	56.3	61.8	56.6	48.7	52.6
Line 2	38.6	38.7	38.6	43.2	43.8	43.5	40.5	41.7	41.1	41.3	38.7	40.0	58.1	53.8	56.0	55.8	45.5	50.7
Line 3	44.1	43.2	43.6	42.4	43.8	43.1	40.0	39.2	39.6	38.3	42.1	40.2	64.7	55.6	60.2	63.5	61.3	62.4
Giza 171	40.0	44.0	42.0	41.5	44.2	42.8	48.6	52.1	50.4	46.6	47.9	47.2	76.3	64.8	70.5	63.0	60.1	61.6
Line 5	40.4	45.2	42.8	40.6	40.2	40.4	40.9	42.9	41.9	40.3	41.1	40.7	55.7	58.3	57.0	52.8	52.1	52.5
Line 6	40.2	44.2	42.2	43.4	45.2	44.3	42.1	43.7	42.9	41.2	39.9	40.5	59.7	56.9	58.3	61.0	58.5	59.7
Gemmiza 11	40.5	39.1	39.8	38.3	40.1	39.2	47.7	51.3	49.5	41.9	41.8	41.8	58.3	49.2	53.8	57.0	52.4	54.7
Line 8	38.3	38.3	38.3	34.8	36.7	35.8	41.3	42.7	42.0	36.3	33.0	34.6	57.4	52.9	55.1	57.7	50.0	53.9
Sids 12	41.0	39.7	40.4	38.3	38.3	38.3	43.5	48.1	45.8	37.3	34.2	35.7	76.8	68.7	72.8	66.3	58.3	62.3
Line 10	40.6	39.0	39.8	41.4	43.4	42.4	44.3	48.1	46.2	45.8	48.6	47.2	55.4	53.6	54.5	51.1	48.7	49.9
Line 11	42.4	39.8	41.1	42.5	42.9	42.7	39.3	41.9	40.6	40.5	40.4	40.4	65.9	59.3	62.6	62.5	57.8	60.2
Line 12	34.3	34.2	34.2	33.0	33.8	33.4	45.3	46.9	46.1	37.5	36.2	36.8	61.1	54.7	57.9	47.9	44.2	46.1
Shandweel 1	38.4	39.7	39.0	40.0	41.7	40.9	39.5	42.3	40.9	39.2	36.4	37.8	68.5	64.7	66.6	66.7	58.0	62.3
Line 14	36.5	38.7	37.6	36.1	38.2	37.2	42.2	45.1	43.7	40.0	40.6	40.3	62.9	59.5	61.2	65.1	56.3	60.7
Line 15	43.1	42.9	43.0	39.9	41.4	40.7	49.3	47.9	48.6	47.9	38.7	43.3	68.1	58.3	63.2	52.7	48.9	50.8
Line 16	37.0	39.6	38.3	36.6	38.7	37.6	40.7	45.4	43.0	46.1	45.5	45.8	63.9	56.2	60.0	49.2	48.8	49.0
Line 17	35.5	39.4	37.5	36.6	41.0	38.8	47.3	48.7	48.0	46.3	44.7	45.5	59.7	61.1	60.4	59.8	51.3	55.6
Line 18	43.5	43.4	43.5	43.5	44.0	43.7	46.9	50.1	48.5	47.0	47.3	47.1	60.3	55.0	57.7	54.3	50.0	52.1
Mean	39.6	40.4	40.0	39.4	41.1	40.2	43.1	45.3	44.2	41.6	41.1	41.3	63.3	57.7	60.5	57.9	52.8	55.4
LSD _{0.05} I	*			**	**		**	**	**	NS	NS	NS	**	**	**	**	**	**
LSD _{0.05} G	1.35			1.02		1.02		2.42		1.07		1.07		3.84		3.25		3.25
LSD _{0.05} IxG	1.91			1.45		1.45		NS		1.51		1.51		5.42		4.59		4.59

- LSD: Least significant difference, I: Irrigation, G: Genotypes, IxG: Interaction.

- N: Indicates to normal conditions, S: Indicates to stress conditions,

- NS: Not significant, *: Significant, **: Highly significant.

TABLE 6. Genetic parameters of grain yield and its attributes computed from 18 wheat genotypes evaluated under normal and stress conditions across the two seasons.

Traits	Genetic parameters									
	Grand mean		GCV (%)		PCV (%)		hb ² (%)		EGA (10 %)	
	Normal	Stress	Normal	Stress	Normal	Stress	Normal	Stress	Normal	Stress
DH	96.83	94.62	4.05	4.67	4.25	4.82	0.91	0.94	6.80	7.94
DM	147.49	143.87	2.22	2.31	2.33	2.48	0.91	0.87	3.71	3.80
GFP	50.66	49.25	4.83	5.69	5.66	6.55	0.73	0.75	7.25	8.68
GFR	84.19	75.82	11.75	14.02	12.20	14.35	0.93	0.95	19.91	24.11
FLA	53.52	39.98	14.28	15.46	16.34	16.54	0.76	0.87	21.96	25.43
Chl. a	3.20	2.81	3.63	3.63	5.40	4.21	0.45	0.74	4.29	5.49
Chl. b	1.79	1.81	13.98	9.14	15.49	10.49	0.82	0.76	22.22	14.00
Proline	1.37	1.67	7.48	16.39	9.12	16.96	0.67	0.93	10.80	27.87
PH	116.85	108.56	6.50	7.06	6.79	7.47	0.92	0.89	10.95	11.75
NS/m ²	363.44	320.09	10.70	10.18	14.50	16.10	0.54	0.40	13.90	11.33
HI	39.50	40.72	7.19	6.97	7.76	7.32	0.86	0.91	11.72	11.68
1000 GW	42.34	43.20	8.79	10.75	10.12	11.54	0.75	0.87	13.43	17.62
NG/S	60.64	55.27	10.44	9.50	11.67	10.92	0.80	0.76	16.45	14.55
SY	6.52	9.11	9.41	7.30	10.11	8.07	0.87	0.82	15.42	11.63
GY	28.34	24.78	9.56	11.26	10.24	11.90	0.87	0.89	15.71	18.74

The phenotypic (PCV) and genotypic (GCV) coefficient of variation (Table 6) were closest to each other in some studied characters namely DH, DM, GFP, GFR, P, PH and HI indicating that the variations among tested genotypes were mostly returned to genetic makeup rather than environmental effect of the two conditions. On the other hand, the values of (PCV) were slightly higher than their corresponding values of (GCV) for FLA, Cha, Chb, NS/m², NG/S, 1000GW, SY and GY indicating the role of environmental effects in the expression of the characters.

The highest estimates of phenotypic (PCV) and genotypic (GCV) coefficients of variation were obtained by FLA (14.28 and 16.34) and (15.46 and 16.54), under normal and reduce irrigation, respectively. Under stress conditions, the characteristics of P, NS/m², 1000 GW, and GY recorded also high estimates phenotypic (PCV) and genotypic (GCV) coefficients of variation being 16.39 and 16.96, 10.18 and 16.10, 10.75 and 11.54 and 11.26 and 11.90, respectively, reflecting a wide pattern of genotypic variation among tested genotypes considering the previous characters. In accordance, the selection among the tested genotypes would be effective to improve

these traits. Meanwhile, moderate values of (PCV and GCV) were only observed under reduce irrigation with PH (7.06 and 7.47) and GFP (5.69 and 6.55), in the two seasons, respectively. On the other hand, DH, DM, and Cha recorded low estimates of PCV and GCV in the two levels. Similar results were reported by Abd El-Mohsen et al. (2015).

It is important to emphasize that, without considering genetic advance (GA), the heritability values (h²) would not be practically valuable in the selection depending on phenotypic appearance. Johnson et al. (1955) confirmed that heritability estimates in conjunction with genetic advance would give more reliable index of selection value.

In the present study, the broad sense heritability values (h_b²) ranged from 45 for Cha to 93 for GFR under normal condition while it ranged from 40 for NS/m² to 95 for GFR under reduce irrigation condition. The values of genetic advance (GA), based on 10 % selection intensity, ranged from 3.71 for DM to 22.22 for Chb under normal irrigation whereas it ranged from 3.80 for DM to 27.87 for P under reduce irrigation condition.

Maximum values of broad sense heritability (h_b^2) coupled with their corresponding genetic advance (GA) values at 10 % selection intensity were obtained by GFR (93 and 19.91) and chb (82 and 22.22) in the adequate hydration condition, respectively. Regarding the shortage irrigation condition, the GFR (95 and 24.11), FLA (87 and 25.43) and P (93 and 27.87) recorded the highest values of h_b^2 and GA, respectively.

This result indicated that the selection in early generations would be effective to develop these traits. However, PH, HI, 1000 GW, NGS⁻¹, SY and GY recorded high heritability values accompanied with moderate genetic advance value under normal and shortage irrigation conditions. DH, DM and GFP exhibited high values of broad sense heritability (h_b^2) but coupled with low genetic advance values under the irrigation regimes. From the above results, it is obvious the limited scope for improvement of these traits among the tested genotypes. The current conclusions are supported by Mohammadi (2016), Arya et al. (2017), Iqbal et al. (2017), Abdel Aziz & Abd El-Rasool (2018), El-Hashash & Agwa (2018) and Fouad (2018), who confirmed that plant breeders can safely make their selection when they take in consideration high values of h_b^2 and GA %.

Stress tolerance indices

Results in Table 7 presented the mean grain yields of genotypes under adequate hydration (Y_n) and stress condition (Y_s) as well as the estimates of six stress tolerance indices and their respective ranks. The grain yield varied from 22.40 and 18.90 for line No.12 to 33.65 and 29.50ardab/fed corresponding to G18, under normal and stress conditions, respectively with an average of 27.97ardab/fed. There were clear differences among tested genotypes in respect to grain yield/fed under normal and shortage irrigation which reflects magnitude of genetic diversity among them that enabled us to select drought tolerant genotypes.

Grain yields of tested genotypes under both normal and reduce irrigations were formulated to calculate different sensitivity and tolerance indices (Table 7). Genotypes with high values of mean productivity (MP), harmonic mean (HM), geometric mean productivity (GMP), stress tolerance index (STI), yield index (YI), and modified stress tolerance index (MSTI) could be selected as tolerant genotypes to reduce

irrigation stress.

Based on the highest values of the used indices as indicator of stress tolerant, genotypes No. 3, 4, 5, 6, 13, 14, 17 and 18 were the most tolerant genotypes under reduce irrigation stress. Accordingly, these genotypes were preferred to cultivate under the reduce irrigation condition, so they considered a promising genotypes in wheat breeding programs. On the other hand, the rest items were identified as susceptible genotypes, because of their low values of stress tolerance indices.

The similarity among the indices in ranking genotypes for stress tolerance may be attributed to that these indices are functions of each other's as above shown in Table 4. Therefore, these indices are equivalent for ranking genotypes for stress tolerance and they could be interchangeably used as a substitute for each other. A similar trend of results was found by Saad et al. (2014), Ali & El-Sadek (2016), Mohammadi (2016), Arya et al. (2017), Abdel Aziz & Abd El-Rasool (2018), El-Hashash & Agwa (2018), Fouad (2018) and Patel (2019).

*Genotype by yield*trait (GYT) biplot*

Yan and Frégeau-Reid 2018 reported that the genotype by yield*trait (GY*T) biplot graphic a comprehensive and effective tool used to ranks the genotypes based on their levels in combining yield with various target traits and at the same time shows the force and weaknesses of the genotypes.

The newness of this approach is the pattern alteration that the superiority of a genotype should not only be measured by its levels in individual traits but more importantly by its levels in combining yield with other target traits.

Polygon graph "which-won-where" is a useful tool for visualizing the trait profiles of the genotypes. The irregular polygon was formed by connecting the genotypes with the longest vectors in all directions. For each polygon side, a line was drawn to start from the biplot origin to be perpendicular to the polygon side dividing the yield-trait combinations into some sectors; corresponding to each sector there was a polygon vertex (elite genotype). The geometry of the biplot determines that the genotype placed on a vertex has the largest values for the yield-trait combinations placed within the identical sector. Also, the graph

identifies genotypes that are particularly good in certain part or side and therefore can be nominee for selection and hybridization in wheat breeding program (Yan & Frégeau-Reid, 2018). Although, yield is the only trait that can determine the usefulness of a genotype by itself while other traits (agronomic traits, quality traits, or stress resistances) are valuable to producers only when they are combined with sufficiently good yield levels. For example, wheat genotype with high proline level would be a highly valuable breeding parent to resistances drought stress. However, if its yield is lower than the best cultivars, then it will not be an elite cultivar. Similarly, a genotype had an extremely good a biotic resistance but gave very low yield would have no place in growers' fields.

Results of GY*T biplot analysis of grain yield-trait combinations of 18 bread wheat genotypes evaluated under normal and reduce (stress) irrigations across the two growing seasons are summarized and presented in Fig. 1, 2 and Table 8.

Polygon "which-won-where" (Fig. 1) presents the relationship among the aimed wheat genotypes using the grain yield-trait combinations under normal irrigation condition across the two growing seasons. The GY*T biplot of the mean performance of grain yield and its components data explained 82.57% of the total variation of the standardized data. The first and two principal components (PC1 and PC2) explained 72.73% and 9.83%, respectively. Yan & Kang (2003) mentioned that the first two PC's should reflect more than 60% of the total variation in order to achieve the goodness of fit for biplot model. It is obvious that genotype No.18 had the largest values for grain yield combining with number of spikes/m², chlorophyll a, chlorophyll b, proline, plant height, 1000 grain weight and number of kernels per spike meaning that it is a superior genotype for high grain yield and its attributes. With respect to the superiority index (Table 8), genotype No. 18 ranked as the first one among the tested genotypes which confirmed the previous results obtained by GY*T biplot graph. As well as, genotypes No. 3, 6, 13 and 15 located in the same sector and so, it reflected similar behavior toward the combining grain yield with the same aforementioned traits. According to superiority index, the abovementioned genotypes were ranked as 5, 7, 4 and 6, respectively. It is noted

that the points of these genotypes and combining grain yield-traits placed into one sector and the angles among them were acute reflecting the linear relationships among them.

Genotypes No.4 and 17 were among the best genotypes in combining grain yield with flag leaf area. Using superiority index (Table 8), the two genotypes No. 4 and 17 occupied the ranks No. 3 and 2, respectively. Also it is apparent from Fig. 1 that genotypes 4 and 17 had a contrasting trait profile to that of genotypes No. 18, 3, 6, 15 and 13, although all cultivars had good levels of yield. On the other hand, the genotypes 12, 5, 7, 16, 10, 1, 2, 8, 9 and 14 recorded the lowest values of combining grain yield-traits because obtuse angles were found between these genotypes and all characters, indicating their poor performance toward these combining grain yield-traits.

Finally, the four lines 12, 7, 8 and 5 were located far from most studied combining grain yield-traits (obtuse angles) indicating their poor performance toward these traits.

On the other hand, polygon "which-won-where" (Fig. 2) presents the relationship among the aimed wheat genotypes using the grain yield-trait combinations under reduce irrigation condition across the two growing seasons. GY*T biplot graph explained 84.39% of the total variation of the standardized data. The first and second principal components (PC1 and PC2) explained 77.79% and 6.60%, respectively. Genotypes were distributed into five sectors (Figure 2), the highest grain yield-trait combinations belonged to G18, which was the best one in agronomic performance and content of chlorophyll a, chlorophyll b, proline besides G17 and G6. Accordingly, the high proline content in these genotypes is probably a positive adaptive mechanism for overcoming the stress conditions. It is well documented that accumulated proline plays a role as a compatible solute in plants, regulating and reducing water loss from the cell under water deficit conditions (Verbruggen & Hermans, 2008; Mafakheri et al., 2010; Moayedi et al., 2011). According to superiority index (Table 8), the abovementioned genotypes were ranked as 1, 3 and 4, respectively. It is worthy that the grain yield-trait combinations value of G18, G6 and G17 were high under both normal and reduce irrigations conditions. This shows that these genotypes well adapted to both environments. According to Bijanzadeh & Emam

(2010) and Mafakheri et al. (2010) chlorophyll is one of the major chloroplast components for photosynthesis and flag leaf chlorophyll content

is an indicator of the photosynthetic activity and its stability for the conjugation of assimilate biosynthesis.

TABLE 7. Estimates of tolerance Indices and their respective ranks of 18 bread wheat genotypes based on grain yield under normal and stress conditions across the two seasons of 2015/2016 and 2016/2017.

Genotype	Grain yield (Y)		Tolerance indices					
	Y normal	Y stress	MP	H M	GMP	STI	YI	MSTI
Calculated values								
Line 1	27.00	22.55	24.78	24.58	24.67	0.76	0.91	0.63
Line 2	27.60	22.40	25.00	24.73	24.86	0.77	0.90	0.63
Line 3	30.75	26.80	28.78	28.64	28.71	1.03	1.08	1.20
Giza 171	30.40	27.60	29.00	28.93	28.97	1.04	1.11	1.30
Line 5	29.35	26.25	27.80	27.71	27.76	0.96	1.06	1.08
Line 6	29.55	27.25	28.40	28.35	28.38	1.00	1.10	1.21
Gemmiza 11	27.60	23.35	25.48	25.30	25.39	0.80	0.94	0.71
Line 8	24.75	21.25	23.00	22.87	22.93	0.65	0.86	0.48
Sids 12	27.10	23.35	25.23	25.09	25.16	0.79	0.94	0.70
Line 10	27.80	24.15	25.98	25.85	25.91	0.84	0.97	0.79
Line 11	28.00	25.15	26.58	26.50	26.54	0.88	1.02	0.90
Line 12	22.40	18.90	20.65	20.50	20.58	0.53	0.76	0.31
Shandweel 1	31.20	26.75	28.98	28.80	28.89	1.04	1.08	1.21
Line 14	28.05	25.80	26.93	26.88	26.90	0.90	1.04	0.98
Line 15	28.45	24.40	26.43	26.27	26.35	0.86	0.98	0.84
Line 16	25.55	22.30	23.93	23.81	23.87	0.71	0.90	0.57
Line 17	30.95	28.25	29.60	29.54	29.57	1.09	1.14	1.41
Line 18	33.65	29.50	31.58	31.44	31.51	1.24	1.19	1.75
Corresponding ranks								
Line 1	15	14	15	15	15	15	14	15
Line 2	12	15	14	14	14	14	15	14
Line 3	4	5	5	5	5	5	5	6
Giza 171	5	3	3	3	3	3	3	3
Line 5	7	7	7	7	7	7	7	7
Line 6	6	4	6	6	6	6	4	4
Gemmiza 11	12	12	12	12	12	12	12	12
Line 8	17	17	17	17	17	17	17	17
Sids 12	14	12	13	13	13	13	12	13
Line 10	11	11	11	11	11	11	11	11
Line 11	10	9	9	9	9	9	9	9
Line 12	18	18	18	18	18	18	18	18
Shandweel 1	2	6	4	4	4	4	6	5
Line 14	9	8	8	8	8	8	8	8
Line 15	8	10	10	10	10	10	10	10
Line 16	16	16	16	16	16	16	16	16
Line 17	3	2	2	2	2	2	2	2
Line 18	1	1	1	1	1	1	1	1

TABLE 8. Standardized genotype by yield*trait (GYT) data and superiority index for the genotypes under normal and stress condition over the two seasons for all studied traits.

Genotype	DHY	DMY	ChaY	ChbY	FLAY	KSY	KWY	PHY	PY	Sm ² Y	Superiority index	Rank
	Normal irrigation											
1	-1.20	-0.82	-0.61	-0.65	-0.66	-0.20	-1.35	-0.48	0.60	0.31	-0.51	15
2	-0.29	-0.21	-0.18	-0.85	-0.84	-0.61	-0.42	-0.38	0.07	-0.37	-0.41	14
3	1.30	1.31	0.77	0.50	-0.10	1.00	0.00	0.25	1.54	0.58	0.72	5
4	0.64	0.51	1.55	0.50	1.55	1.61	1.39	1.04	0.87	-0.30	0.94	3
5	-0.30	0.17	0.26	-0.01	-0.50	-0.52	-0.06	0.24	0.13	1.73	0.11	8
6	0.32	0.33	0.49	0.45	-0.97	0.24	0.15	0.18	0.16	0.12	0.15	7
7	-0.22	-0.25	-0.48	0.13	2.04	-0.53	0.19	-0.12	0.23	-1.26	-0.03	9
8	-1.37	-1.48	-1.13	-0.96	-0.36	-1.22	-1.39	-1.31	-1.82	-1.44	-1.25	17
9	-0.06	-0.41	-0.03	-0.04	0.25	0.89	-0.61	-0.86	-0.49	-0.92	-0.23	11
10	0.52	0.01	0.02	-0.39	-0.66	-0.99	0.27	-0.91	-0.20	-0.32	-0.27	13
11	0.00	-0.05	-0.43	0.01	-0.41	0.31	-0.48	-0.75	-0.34	0.75	-0.14	10
12	-2.17	-2.13	-1.91	-1.89	-1.88	-2.04	-1.56	-1.64	-2.18	-1.98	-1.94	18
13	1.10	0.86	1.25	-0.12	0.48	1.58	0.15	0.97	0.98	0.47	0.77	4
14	-0.75	-0.31	-0.94	-1.00	0.71	0.29	-0.29	0.74	-0.60	-0.26	-0.24	12
15	0.78	0.64	-0.11	-0.36	0.52	-0.02	1.02	-0.06	-0.16	0.70	0.30	6
16	-0.68	-1.04	-1.12	0.91	-0.85	-1.14	-0.54	-0.63	-0.86	-0.30	-0.63	16
17	0.63	0.80	0.66	1.04	1.40	0.51	1.38	2.01	0.43	0.90	0.98	2
18	1.74	2.06	1.95	2.73	0.27	0.84	2.15	1.70	1.65	1.60	1.67	1
	Stress conditions											
1	-1.5	-1.1	-1.1	-0.7	-1.4	-0.9	-1	-0.7	-0.2	-0.27	-0.88	16
2	-1	-0.8	-0.8	-1.2	-0.4	-1.2	-1	-0.8	-0.1	-0.94	-0.82	14
3	1	1.1	0.7	-0.2	0.18	0.84	0.08	0.1	1.5	1.042	0.64	5
4	0.9	0.8	1.21	0.74	1.84	1.55	1.73	1	0.9	-0.06	1.06	2
5	0	0.4	0.3	-0.1	-0.3	0.33	0.17	0.4	1	1.579	0.37	7
6	0.7	0.7	0.51	1.15	0.5	0.86	0.35	0.4	0.9	0.908	0.70	4
7	-0.5	-0.5	-0.6	0.67	0.39	-0.8	0.06	-0.2	1.1	-1.18	-0.16	11
8	-1.4	-1.4	-1.5	-1.1	-0.6	-1.3	-1.5	-1.4	-0.7	-1.18	-1.21	17
9	-0.2	-0.6	-0.2	-0.1	1.04	0.48	-0.6	-0.7	-1.1	-1.1	-0.32	13
10	0.6	0	0	0.06	-0.6	-0.6	0.53	-0.9	-0.8	-0.03	-0.16	12
11	0.3	0.2	-0	-0.1	0.59	0.43	-0.2	-0.5	0.1	0.86	0.17	10
12	-2.1	-2	-1.9	-1.8	-2.4	-2	-1.6	-1.6	-1.9	-2.08	-1.95	18
13	0.6	0.5	1.08	1.04	-0.8	1.17	-0.1	0.6	-0.1	0.486	0.45	6
14	-0.1	0.3	0.13	0.98	0.48	0.53	0.18	1.2	-0.2	-0.05	0.35	8
15	0.7	0.3	0.09	0.58	0.72	-0.3	-0.1	-0	-0.7	0.387	0.17	9
16	-0.6	-0.8	-0.9	-1.9	-0.7	-0.9	-0.3	-0.5	-1.6	-0.28	-0.85	15
17	0.9	1.1	1.29	0.61	0.68	0.94	1.38	2	0.6	0.571	1.01	3
18	1.5	1.8	1.69	1.38	0.79	0.77	2.04	1.6	1.2	1.338	1.42	1

The traits codes are: DHY: Days to heading, DMY: Days to maturity, ChaY: Chlorophyll a, ChbY: Chlorophyll b, FLAY: Flag leaf area, KSY: Kernels per spike, KWY: 1000-kernel weight, PHY: Plant height, PY: Proline content and Sm²Y: Number per spikes/m².

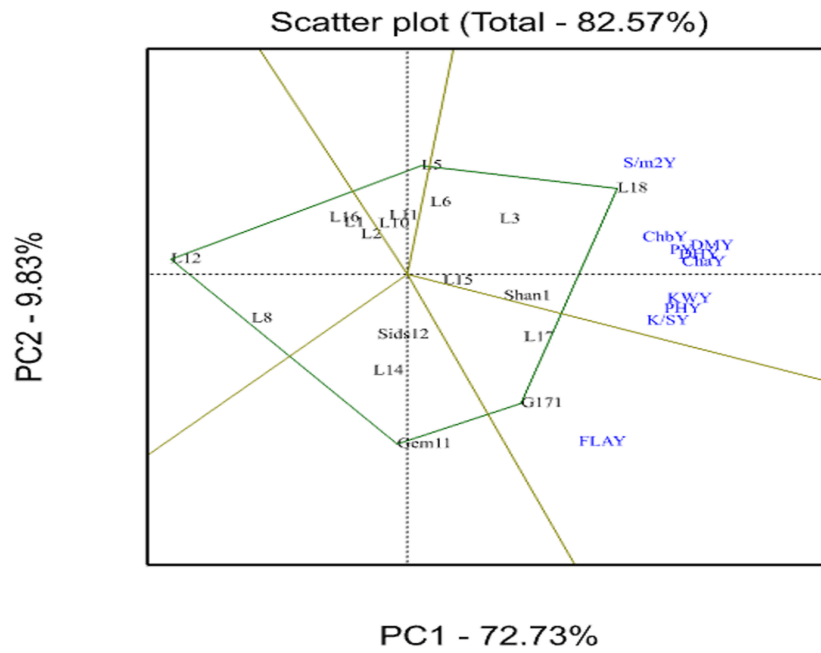


Fig. 1. The "which-won-where" view of the genotype by yield*trait (GYT) biplot to highlight genotypes with outstanding profiles [The traits codes are DHY: Days to heading, DMY: Days to maturity, FLAY: Flag leaf area, ChbY: Chlorophyll b, ChaY: Chlorophyll a, PY: Proline content, PHY: Plant height, Sm²Y: Number of spikes/m², KWY: 1000-kernel weight and GY: Grain yield].

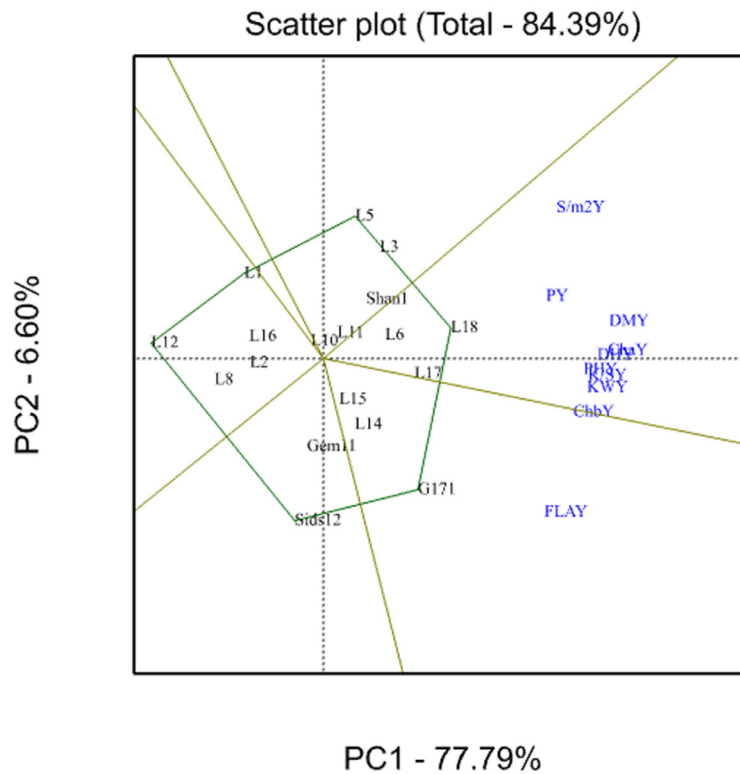


Fig. 2. The "which-won-where" view of the genotype by yield*trait (GYT) biplot to highlight genotypes with outstanding profiles. [The traits codes are DHY: Days to heading, DMY: Days to maturity, FLAY: Flag leaf area, ChbY: Chlorophyll b, ChaY: Chlorophyll a, PY: Proline content, PHY: Plant height, Sm²Y: Number of spikes/m², KWY: 1000-kernel weight and GY: Grain yield].

However, the vertex genotype No. 4 (G4) had good behaviour for grain yield-trait combination with flag leaf area besides genotypes No. 15 and 14. Concerning superiority index (Table 8), the abovementioned genotypes were ranked as 2, 8, and 9, respectively. However, Genotypes No. 5, 3, and 13 appeared to be more affected by irrigation regimes. Furthermore, genotypes 10 and 11 located closer to the center of the axis had values similar to the grand mean of the most studied traits (Fig. 2).

On the other hand, genotypes No. 12, 8, 2, 16, 1, 7 and 9 were the inferior for all measured grain yield-trait combination indicating that they are more sensitive genotypes to shortage irrigation and environmental changes (Fig. 2). Moreno-Ramos et al. (2010) reported that plant breeding has indirectly increased water use efficiency in wheat because yield has increased without additional water use and that it is possible to produce adequate grain yield under water restriction. The current results are in harmony with those obtained by Karaman (2018) and Juan et al. (2019). The aim of different breeding programs, including wheat, is to apply selection tests to improve quantity, quality and stability of yield under reduction irrigation and furthermore to develop new drought-adapted genotypes. In fact, the GY*T biplot (Fig. 1, 2) is a simple graphical presentation of the standardized GY*T data. Moreover, the GY*T biplot already allow the choices of superior wheat cultivars for grain yield and its components simultaneously. Undoubtedly, GY*T biplot graph is preferred because of it easy to interpret and more informative to identify more accurate selection criteria using grain yield and its attributes.

Conclusion

In light of the limited water resources in Egypt, it is important to select yielder genotypes that are more tolerant to water stress conditions. In the current investigation, it is obvious that all genotypes significantly decreased under the stress conditions for all characters in the two seasons, except chlorophyll b, proline and harvest index in the two seasons and 1000-kernel weight in the 1st season. The greatest grain yield was obtained by genotype 18 under the adequate and stress irrigation in the two seasons. Genotypes No. 18, 17, 4, and 13 were the best tolerant items under water stress condition and considered as promising genotype in wheat breeding programs according

to a genotype by yield*trait (GYT) biplot graph. The proposed biplot graph (GY*T) proved to be more accurate tool for selection criteria using grain yield and its attributes because it is easy to apply and understand and is more informative.

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الطريقة المعدلة لتحليل المحاور الثنائية للتراكيب الوراثية والصفات كمعيار انتخابي في القمح تحت ظروف الإجهاد المائي

السيد علي محمد عبد الحميد⁽¹⁾، مؤمن عبد الوهاب عجلان⁽¹⁾، إيمان محمود احمد حسين⁽²⁾
⁽¹⁾قسم بحوث القمح- معهد بحوث المحاصيل الحقلية- مركز البحوث الزراعية- الجيزة- مصر، ⁽²⁾المعمل المركزي لبحوث التصميم والتحليل الإحصائي- مركز البحوث الزراعية- الجيزة- مصر.

أدى الإستغلال المفرط لمورد المياه في مصر خلال السنوات الأخيرة إلى زيادة العجز في هذا المورد الهام مما أدى إلى تقليل القدرة على تحقيق أهداف التنمية الاقتصادية. أجريت هذه الدراسة في محطة البحوث الزراعية بسخا - كفر الشيخ - مصر في موسمي 2016/2015 و2017/2016 لتقييم 18 تركيب وراثي من قمح الخبز تحت الظروف العادية وظروف الإجهاد المائي حيث تم زراعة التجربة في تصميم القطاعات الكاملة العشوائية في ثلاث مكررات. أشارت النتائج إلى أن أعلى القيم من درجة التوريث مصحوبة بأعلى قيم للتحسن الوراثي المتوقع بكفاءة اختيار بنسبة 10% قد تم الحصول عليها لصفات معدل ملء الحبوب (93% و 19.91%) والكوروفيل ب (82% و 22.22%) في الحالة الطبيعية للري، على التوالي. بينما في حالة الإجهاد المائي، سجل محصول الحبوب (89% و 18.74%)، و صفة وزن الـ 1000 حبة (87% و 17.62%) والبرولين (93% و 27.87) أعلى قيم من درجة التوريث والتحسين الوراثي، على التوالي. الأصناف 18، 17، 4، 13 هي أفضل الأصناف تحملاً في ظل ظروف الإجهاد المائي. من ناحية أخرى، الأصناف 12، 8، 16 كانت الأكثر حساسية لظروف الإجهاد المائي. طريقة المحاور الثنائية (GYT) Biplot تعتبر طريقة ناجحة ومفضلة. ومما لا شك فيه أنه يفضل استخدام الرسوم البيانية لأنه من السهل تفسيرها ومن خلالها يمكن إظهار مزيد من المعلومات.