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Zeinab Z. A. Farhan
Galal A. R. El-Sherbeny
Emadeldin A. Maher
Abdelsabour G. A. Khaled

Genetics Department
Faculty of Agriculture
Sohag University
Sohag
Egypt

Corresponding author:
Abdelsabour G. A. Khaled

Combining Ability and Gene Action Controlling Morpho-Agronomical Traits in Bread Wheat Genotypes under Non-Stressed and Drought-Stressed Conditions

Zeinab Z. A. Farhan, Galal A. R. El-Sherbeny, Emadeldin A. Maher and Abdelsabour G. A. Khaled

Abstract

The study assessed six parents of bread wheat and their 15 F_1 crosses under normal and drought stress conditions to evaluate genotypic variation. Results showed highly significant genotypic and genotype-environment (G × E) interactions across all traits, indicating substantial variability and differential responses among genotypes. Under normal conditions, Diebera and Pectora were earliest to flower, while Canada-462 and Giza-171 were earliest under drought. Canada-462, Diebera, and Sids-12 consistently exhibited superior performance for traits like plant height, spike length, and grain yield. Their crosses, particularly P1 × P2, P1 × P3, and P2 × P6, also performed best under both conditions. Drought stress caused notable reductions in all traits, especially grain yield (up to 21.07% in parents). Drought susceptibility index (DSI) identified tolerant parents (Pectora, Sahel-1, Giza-171, and Sids-12) and crosses (e.g., P4 × P6, P5 × P6). Combining ability analysis showed that both additive (GCA) and non-additive (SCA) gene actions were significant, with non-additive effects predominating in most traits. Heritability estimates were higher in broad sense than narrow sense. Overall, the results highlight promising parents and crosses for breeding drought-tolerant wheat with enhanced yield and adaptability, emphasizing the utility of both additive and dominance gene actions in selection strategies.

Key words: Bread wheat, genotypic variation, drought stress, Genetic parameters.

INTRODUCTION

Cereals including rice, wheat and maize majorly contributed to food and animal feed globally. With expected 9.7 billion global human populations by 2050, annual cereal production must be augmented so that future requirement can be met out. Bread wheat (*Triticum aestivum* L.) is the first important cereal crop for the world's population. Most of the currently cultivated wheat varieties belong to hexaploid wheat, which is known as common bread wheat. It is the important stable food (edible grain) of about two billion people (36% of the world population); provides nearly 55% of the carbohydrates and 20% of the food calories consumed globally (Breiman and Graur, 1995). Egypt's total wheat production of grain reached about 9 million tons resulted from 3.4 million faddens (2.65 ton / Fadden), while the consumption of wheat grains is about 15 million tons. Egypt has become one of the world's leading wheat importers. It imports over 12 million tons of wheat, a figure likely to increase to more than 15 million tons by 2028 (FAO 2024), this gab still there between production and consumption. In spite of grown under a wide range of climates and soils, wheat is the best adapted crop in most regions. Abiotic environmental factors are considered to be the main source 71% of yield reduction (Boyer, 1982). The limiting factor in Egypt is the availability of irrigation water. Potential expansion of wheat area is only possible in Egyptian deserts, where the soil in these areas is sandy with low water holding capacity exposing wheat plants to dry environments. It is essential to know the genetic architecture of traits related to drought tolerance and their mode of inheritance to meet the increasing consumption due to the increasing number of population (Farshadfar et al. 2011; Abd El-Mohsen et al. 2015). Hybridization is the principle breeding procedure for the development of new recombination in wheat. The main role of hybridization is to create hybrid populations with new genetic variation from which new recombination's of genes may be selected (Singh, 2000). Through recombination, combining many favorable alleles into single genotype is the main objective of plant breeders (Esch et al. 2007). For any breeding efforts involving hybridization, identification of putative parents, demonstrating variability and diversity for traits of interest is an essential pre-requisite before evaluating the genetic architecture of such traits. Diallel mating fashion widely used to obtain information on the inheritance of quantitative traits to select the best parental combination for crosses, and to determine the heterotic responses and heterotic patterns (Griffing, 1956). This fashion helps breeders to generate the superior hybrids (Yan and Kang, 2003). Combining ability and heterotic analysis is one of the powerful techniques available which help in selecting desirable parents and hybrids for their full exploitation (El-Maghraby et al. 2005, Iqbal et al. 2007).The general and specific combining ability effects and variances obtain from a set of F_1's would enable a breeder to select desirable parents and crosses for each of the quantitative components separately (Sprague and Tatum, 1942).The general combining ability (GCA) was largely due to additive gene action, while the specific combining ability (SCA) due to non-additive gene action. GCA indicates average performance of parental lines as reflected in its hybrid combination; SCA indicates average performance of a specific cross. If both GCA and SCA are non-significant for some traits, the epistasis gene effects plays role for such traits (Fehr, 1993).The objectives of present investigation were to investigate the effect of drought stress on the performance of genotypes; to evaluate the nature and magnitude of combining ability of parents and their crosses by studying the nature of gene action in all studied traits and to enhance our understanding about the genetic variability and heritability of drought tolerance in wheat.

MATERIALS AND METHODS

Genetic Materials:

The present study was carried out at the El Kawther Experimental Research Station, Faculty of Agriculture, Sohag University, Sohag, in Upper Egypt, during the two successive wheat seasons 2021/2022 and 2022/2023. Table 1 showed names and sources of six different genotypes of bread wheat that representing a wide range of variability in their morpho-agronomical traits chosen as parents in this work.

Table 1: Names and sources of the six parental genotypes used as parents.

No.	Genotypes	Pedigree	Source
P1	**Canada-462**	-------	**Canada**
P2	**Diebera**	-------	**Sudan**
P3	**Pectora**	-------	**Sudan**
P4	**Sahel-1**	N.S.732/Plm/veery“S” D735-4Sd-1Sd-OSd	**Egypt**
P5	**Giza- 171**	Sakha 93/Gemmeiza9(Gz 2003-101-1Gz-4Gz-1Gz-2Gz-0Gz)	**Egypt**
P6	**Sids-12**	BUC//7C/ALD/5/MAYA74/ON//II60.147/3/BB/GLL/4/ CHAT"S"/6/MAYA/VUL//CMH74A.630/4*SX	**Egypt**

Experimental procedure:

In the winter season 2021/2022, 6 parental genotypes were planted and crossed according to half diallel mating design to produce 15 F_1 hybrids. In the winter season 2021/2022, seeds of six parents and their 15 F_1 hybrids were sown under normal and drought environmental conditions in a randomized complete block design (RCBD) with three replications. Each plot consisted of 3 rows with long 3 m and 30 cm. wide. Plants were spaced by 10 cm. within row. The soil at the experimental site was sandy to loamy sand. All recommended cultural practices were applied on the experiment, and the irrigation throughout the growing season was every 10 days under normal conditions and every 20 days drought stress. All data were recorded on ten plants per genotype chosen at random from each plot for all studied traits. Firstly, days to 50% flowering calculated as number of days from sowing date to the date at which 50% of main spike have emerged from the flag leaves. The plant height in centimeters (cm) was measured as plant length from the soil surface to the tip of the main spike in centimeters at the time of the final harvest. The spike length trait was measured as main spike length from the bottom of spike to the tip of the same spike in cm at the time of the final harvest. While, the total no. of spikes/plant were counted at the time of each picking and finally were summed up and mean value was worked out. Also, the no. of grains per spike was counted at the time picking and finally summed up. The 100-grain weight trait weighted using sensitive balance and recorded in grams (gm). Finally, the grains weight per plant were measured as weight of the grains of each individual plant in gm using sensitive balance and recorded in gm at the time of all the picking spikes were summed up and mean value was calculated.

Statistical analysis:

Analysis of variance and gene action:

Data were subjected to general analysis of variance for RCBD according to Steel and Torrie (1980). Mean squares of genotypes and replications for all studied traits were tested for significance according to the F-test. The form of analysis of variation (S.O.V) was outlined by Cochran and Cox (1957). GCA and SCA were partitioned from total genetic variance in each experiment according to Griffing (1956) model-1/method-2 (Table 2). In addition, the combined analysis over the two environments was calculated to partition the mean squares of genotypes and the interaction of genotypes with environments into sources of variations due to GCA, SCA, GCA x E, SCA x E. The genetic components could be obtained from the estimates variance of GCA (σ^2g), SCA (σ^2s), GCA x E (σ^2g x E), SCA x E (σ^2s x E) as described by Matzinger and Kempthorne (1956), and Singh (1979) as follow:

$\sigma^2A = 2\ \sigma^2g$

$\sigma^2D = \sigma^2s$

$\sigma^2AxE = 2\ \sigma^2gxE$ and $\sigma^2DxE = \sigma^2sxE$

Table 2: Mean squares of half diallel analysis for each studied environment and the combined data:

S.O.V.	D.F	S.S	M.S	E.M.S.
Environments(E)	E-1	SS_E		
Rep/E	E(r-1)	$SS_{r/1}$		
Genotypes (G)	G-1	SS_G		
GCA	P-1	SS_g	M_5	$\sigma^2_e 1+\sigma^2_{SxE}+(P+2)\sigma^2_{gxE}+E\sigma^2_S+E(P+2)\ \sigma^2_g$
SCA	P(P-1)/2	SS_S	M_4	$\sigma^2_e 1+\sigma^2_{SxE}+\ E\sigma^2_S$
G x E	(G-1)(E-1)	SS_{GxE}		
GCA x E	(P-1)(E-1)	SS_{gxE}	M_3	$\sigma^2_e 1+\sigma^2_{SxE}+(P+2)\ \sigma^2_{gx1}$
SCA x E	P(P-1)(E-1)/2	SS_{SxE}	M_2	$\sigma^2_e 1+\sigma^2_{SxE}$
Error	E(G-1)(r-1)	$SS_{G/r}$	M_1	$\sigma^2_e 1$

E and r: Number of environments and replications, respectively. G and P: Number of genotypes and parents, respectively. M1: Error mean square, M2 and M3: SCA x E and GCA x E mean square, respectively. M4 and M5: SCA and GCA mean squares, respectively.

Estimates of heritability:

Estimates of heritability in both broad and narrow sense were calculated according to the following equations, for each environment:

$h^2_{b.s.}\ \% = [(\sigma^2A+\sigma^2D) / (\sigma^2A+\sigma^2D+\sigma^2e)] \times 100$

and $h^2_{n.s}.\ \% = [(\sigma^2A) / (\sigma^2A+\sigma^2D+\sigma^2e)] \times 100$

While for the combined data, we used the following equations:

$h^2_{b.s.}\ \% = [(\sigma^2A+\sigma^2D) / (\sigma^2A+\sigma^2D+\sigma^2AxE+\sigma^2DxE+\sigma^2e)] \times 100$ and $h^2_{n.s}.\ \% = [(\sigma^2A) / (\sigma^2A+\sigma^2D+\sigma^2AxE+\sigma^2DxE+\sigma^2e)] \times 100$, where: $h^2_{b.s}.\ \%$ = heritability in broad sense and $h^2_{n.s}.\ \%$ = heritability in narrow sense; σ^2A, σ^2D and σ^2e are the additive, dominance and environmental variances, respectively.

Percentage of reduction due to drought stress (R %):

$R\%\ P = (M.P_f - M.P_s/M.P_f) \times 100$ and $R\%\ F_1 = (M.F_{1f} - M.F_{1s}/M.F_{1f}) \times 100$.

Drought susceptibility index (DSI):

Drought Susceptibility Index was computed according to Fischer and Maurer (1978) equation as follows: $DSI = [(1-Y_D/Y_W) / (1-Y_{MD}/Y_{MT})]$, where: Y_D: is the yield under drought stress, Y_W: is the yield under normal condition, Y_{MD}: is the mean yield for all genotypes under drought and Y_{MT}: is mean yield for all genotypes under normal condition. Genotypes with average susceptibility or resistance to drought have an "S" value of 1.0. Values of less than 1.0 indicate less susceptibility and greater resistance to drought. While, a value of S=0 indicates maximum possible drought resistance (no effect of drought on yield).

RESULT AND DISCUSSION

Analysis of variance:

All genotypes of bread wheat (6 parental genotypes and their 15 F_1 crosses) were evaluated to estimate the magnitude of genotypic variations among genotypes, under normal (N) and drought (D) stress conditions. The results of days to 50% flowering and plant height traits showed that the mean squares of environment were found to be highly significant. Genotypic mean squares were highly significant under all environments, indicating the presence of a large variation among genotypes. Moreover, mean square due to genotype x environment G x E was also highly significant. It could be observed that the mean squares of environments, genotypes and G x E were found to be highly significant for all yield component traits (spike length, No. of spikes, No. of grains par spike, 100 grain weight and grain weight/plant) under each environment and their combined data (Table 3). Generally, it could be noticed that the mean squares of genotypes were highly significant for most studied traits, reflecting a great variance among them. Moreover, the mean squares of the interaction of genotype-environment (G x E) were also found to be highly significant for all studied traits, suggesting a differential response of the genotypes from environment to another. Similar results obtained by Saied et al. (2017); Sundeep et al. (2018); El Ameen et al. (2020); Regmi et al. (2021) and Fareed et al. (2024).

Means Performance:

The results of days to 50% flowering trait showed that the best parents for earliness were the parental genotypes Diebera and Pectora under normal conditions. While, under drought stress conditions, the best parents for earliness were the parental genotypes Canada-462 and Giza-171. While, the F_1 hybrids P1 x P2, P1 x P3, P1 x P5, P1 x P6 and P2 x P3 were the earliest under normal conditions. While, under drought stress conditions the earlier F_1 hybrids were P3 x P5, P3 x P6, P4 x P5, P5 x P6. The results indicated that the tallest parental genotypes were Canada-462 (P1), Diebera (P2) and Sids-12 (P6) under normal, drought stress conditions and combined data, respectively. On the other hand, the shortest genotype was Giza-171 (P5) under normal, drought conditions and combined data. Regarding the plant height of hybrids exhibited that, the tallest crosses were P1 x P2, P1 x P3, P1 x P5, P1 x P6, P2 x P3, P2 x P5 and P3 x P4 under all environments (Table 4). Concerning the yield component traits, the results of spike length (cm) indicated that the longest spike length was for Diebera (P2). Meanwhile, the Canada-462 and Sids-12 had the best mean values under drought conditions. The longest spike of crosses was recorded by the crosses P1 x P2, P1 x P3, P1 x P6, and P2 x P6 under normal and drought. Also, the highest no. of spikes per plant was for Canada-462, Diebera and Sids-12 under all environments. Concerning the hybrids, P1 x P2, P1 x P3, P1 x P6 and P2 x P6 had the highest no. of spikes/plant under all environments. It is cleared that the best parental genotypes and their crosses for no. of grains per spike were Canada-462 Diebera, Sids-12, P1 x P2, P1 x P3, P1 x P6 and P2 x P6 under all environments. In the same direction, the crosses P3 x P6 and P5 x P6 had highly significant values for this trait under normal and drought conditions, respectively. Adding, the best parental genotypes for 100-grain weight were P1, P2 and P6 under all environments. Likely, the results of F_1 crosses exhibited that P1 x P2, P1 x P3, P1 x P4, P1 x P6 and P2 x P6 had highest significant mean values under normal conditions and combined data, respectively. Moreover, P5 x P6 had a highly significant value for the same trait under normal conditions and combined data, respectively (Cont. Table 4).

Finally, the results of grain weight/plant trait cleared that the best parental genotypes were the same as previous traits; Canada-462, Diebera and Sids-12 under normal, drought stress conditions and combined data, respectively. Concerning to F_1 crosses, the results showed that the cross P1 x P2, P1 x P3, P1 x P6, P2 x P4 and P2 x P6 had the highest grain weight/plant under each environment and combined data. Also, the crosses P2 x P3 and P4 x P6 recorded highly significant.

Reduction due to drought stress (R %):

The results of reduction due to drought stress conditions for all studied traits showed that the mean performances of 6 parents and their 15 crosses were variable from normal to drought stress conditions. It is cleared that the drought stress caused a reduction of about 9.04%, 7.62%,12.64%, 11.15%, 16.77%, 16.90% and 21.07% in the parental genotypes performance for days to 50% flowering, plant height, spike length, No. of spikes per plant, No. of grains per spike, 100-grain weight and grain yield/plant, respectively. In the same direction, the reduction due to drought stress conditions for hybrids were 8.64%, 15.76%,11.83%,15.68%, 19.76%, 16.67% and 17.87% for days to 50% flowering, plant height, spike length, No. of spikes per plant, No. of grains per spike, 100-grain weight and grain yield per plant, respectively (Cont. Table 4).

Drought Susceptibility Index (DSI):

The estimates of drought stress susceptibility index (DSI, Cont. Table 4) based on grain weight par plant for 6 parents and their 15 F_1 crosses were presented in. It could be observed that the parents Pectora, Sahel-1, Giza-171 and Sids-12 were relatively stress tolerant parents with the values of less than one. Moreover, the results of DSI of the F_1 hybrids clarified that the crosses P2 x P4, P2 x P5, P2 x

P6, P3 x P4, P3 x P5, P3 x P6, P4 x P5, P4 x P6 and P5 x P6 were relatively tolerant to drought stress with the values of 0.73, 0.80, 0.56, 0.91, 0.81, 0.77, 0.88, 0.58 and 0.28, respectively. These results indicated that the tolerant parents P3, P4, P5 and P6 transmitted their genes controlling drought tolerance to their hybrids. Consequently, these crosses could be considered promising populations for isolating useful segregates to be cultivated under drought stress environments. Similar results obtained by Gomaa et al. (2014); Khaled et al. 2015; Renu and Satyavir, (2016); Yuxiu et al. (2017); Stanisław et al. (2018); Elsayed (2019); El-Rawy and Hassan (2021); Sallam et al. (2024). In this work certain wheat genotypes perform better under drought conditions due to a combination of inherited traits that enhance their ability to tolerate water stress and maintain productivity. These traits include efficient water use, stress tolerance mechanisms, and the ability to maintain photosynthesis and growth under limited water availability.

Combining abilities effects:

The results in Table 5 of general combining ability effects indicated that the parental genotype P3 exhibited significant negative gi toward earliness under normal, drought stress conditions and combined data, respectively. Also, P1 and P2 had significant negative g_i toward earliness under normal conditions. Adding, P5 genotype had highly significant negative g_i toward earliness under drought conditions and combined data. Regarding for yield component traits, the results of spike length trait showed that the parents Canada-462 Diebera and Sids-12 were the excellent general combiners under all environments. The results of no. of spikes/ plant exhibited that the genotypes Canada-462, Diebera and Sids-12 were the best general combiners. The results of 100-grain weight trait, demonstrated that as previous; Canada-462, Diebera and Sids-12 were the best general combiners. On the contrary, the poorest general combiner parental genotypes were Pectora, Sahel-1 and Giza-171 under all environments. In the same direction, grains weight/plant exhibited that the parental genotypes P1, P2 and P6 were always the excellent general combiners. On the other hand, the rest of parental genotypes are the poorest general combiner with negative significant values (Table 5). Consequently, these promising parents could be utilized in wheat breeding program to improve studied traits under drought stress conditions. The results in Table 6 indicated that the best cross for days to 50% flowering was P4 x P5 under all environments. Additionally, P1 x P5 and P1 X P6 were the best earliest crosses under normal conditions with negative significant values. While, under drought stress conditions P3 x P5, P4 x P5 and P5 x P6 were the best earliest crosses. The highest desirable SCA effects for plant height trait toward tallness were obtained from P1 x P3, P1 x P6, P2 x P5 and P3 x P4 under. Additionally, P1 x P5 and P2 X P3 and P4 x P6 had highly significant values toward tallness under normal conditions. Concerning yield component traits, it is clarified that the excellent crosses for spike length were P1 x P3, P1 x P6, P2 x P6 and P5 x P6 under all environments. Moreover, P1 x P2 and P2 x P5 had significant values of SCA effects for the same trait under drought and normal conditions, respectively. Regarding to no. of spikes per plant, demonstrated that the desirable SCA effects was obtained from the cross P1 x P2, P1 x P3, P1 x P6 and P2 x P6 under all environments. In the same direction, the cross P4 x P5 had a significant positive SCA effect under normal conditions. The results also revealed that the crosses P1 x P2, P1 x P3, P1 x P6, P2 x P5 and P2 x P6 had desirable SCA effects for increasing no. of grains per spike. Noting that, the crosses P1x P5 and P4 x P5 had also significant values of SCA effects under drought and normal stress conditions. The excellent crosses for 100-grain weight were P1 x P2, P1 x P3, P1 x P4, P1 x P6, P2 x P6 and P5 x P6 under all environments. One of the most important results was for grain weight/plant trait, cleared that the crosses P1 x P3, P2 x P3, P2 x P6 and P4 x P6 exhibited desirable SCA effects for increasing grain weight. Moreover, the cross combinations (P1 x P6, P3 x P5 and P4 x P5) and (P1 x P2, P2 x P4 and P5 x P6) recorded significant values of SCA effects under normal and drought stress conditions. It could be observed that the promising crosses were resulted from the crossing (good x good), (good x poor) and (poor x poor) general combiners. Therefore, it is not necessary that parents having high estimates of GCA effects would also give high estimates of SCA effects in their respective crosses. In general, the promising crosses which showed desirable SCA effects gave also high estimate of useful heterosis as previously mentioned. These finding indicate that non-additive gene action played an important role in the inheritance of these traits. The same results were obtained by Gomaa et al. (2014); Kumar et al. (2015); Saied et al. (2017), Emad et al (2018); Elsayed (2019); Kajla et al. (2020**)**; Gimenez et al. (2021); Kumawat et al. (2023) and Fareed et al. (2024).

Genetic parameters:

Half diallel design is a type of mating system which assets plant breeders to estimates the values of general combining ability (GCA) and specific combining ability (SCA). These values indicate for additive and non-additive genetic variances. The genetic parameters could be divided to additive (σ^2A) and non-additive (σ^2D) genetic variances assuming that there are no epistasis. Moreover, the values of heritability in broad sense ($h^2_{b.s}$ %) measures the amount of genetic variance included additive and non-additive relative to phenotypic variance. While, the heritability in narrow sense ($h^2_{n.s}$ %) presents the amount of additive genetic variance relative to the phenotypic variance. The results of days to 50% flowering trait in Table 8, exhibited that the mean square of GCA and SCA was highly significant. Furthermore, the ratio of GCA/SCA was less than unity under all environments, indicating the presence of partial dominance. The results of the interaction with environments, demonstrated that GCAxE and SCAxE mean square was also highly significant under each environment and their combined data. In addition, the ratio of GCA x E/SCA x E mean square was less than one, indicating the greater amount of non-additive gene action determining the performance of all traits. The results of genetic parameters indicated that the magnitudes of σ^2A were smaller than those of σ^2D for this trait under all environments. Also, the magnitude of σ^2A x E was less than σ^2D x E for the same trait. The estimates of broad sense heritability were larger than those of narrow sense heritability (Table7). The mean squares of GCA and SCA for plant height were highly, confirming the important role of all types of gene action in the inheritance of this trait. The ratio of GCA/SCA was found to be more than the unity under all environments, suggesting that additive was much larger and more important than non-additive gene effects in the inheritance of plant height trait. Moreover, the mean square of the interaction for GCA x E and SCA x E was highly significant, and the ratio of GCA x E/SCA x E was less than one. Concerning plant height trait**,** the values of σ^2A were also smaller than those of σ^2D under normal and drought conditions, respectively. Adding, the magnitude of σ^2A x E (7.20) was smaller than that of σ^2D x E for trait. In addition, the estimates of $h^2_{b.s}$% were larger than those of $h^2_{n.s}$% **(**Table 7). The results showed that the mean squares of GCA and SCA were highly significant for all yield component traits under all environments, excluding the SCA for grain weight per plant under drought conditions. These results confirm the important role of all types of gene action in the inheritance of these traits. The ratios of GCA/SCA were more than unity for and no. of grains/spike and weight of grain per plant under all environments. While, the ratios of GCA/SCA were less than unity for the spike length and 100 grain weight under normal, drought stress conditions and combined data, respectively. Regarding, the mean square of the interaction of GCA x E and SCA x E, also were highly significant for all yield component traits under all environments. The ratio of GCA x E/SCA x E was less than one for studied traits, excluding weight of grains/plant. The results of gene action for yield component traits cleared that, the values of σ^2A for no. of spikes, no. of grains per spike, 100 grain weight and grain weight per plant were bigger than those of σ^2D for no. of spikes, no. of grains per spike, 100 grain weight and grain weight per plant under normal, drought stress conditions and combined data, respectively. Adding, the magnitude of σ^2A x E was smaller than that of σ^2D x E for all component traits, excluding spike length and no.

of spikes per plant. In addition, the estimates of $h^2_{b.s}$% for all studied traits were larger than those recorded for $h^2_{n.s}$% under all environments. Generally, the mean squares due to GCA and SCA were highly significant for most traits under this work. This finding indicates that most types of gene action are involved in the inheritance of these traits. The results also showed that the interactions of GCA x E and SCA x E mean squares were highly significant for most studied traits, suggesting that the magnitudes of all types of gene action fluctuated from normal to stress conditions. Likely, Said et al. (2014) showed importance of dominance in the inheritance of No. of spikelets/spike and 100-seed weight in wheat crosses. Also, El-Rawy and Youssef (2014) found that the additive and dominance effects were significant in 1000-Kernel weight while dominance was more important. These results of our study were in agreement with the results previously obtained by Gomaa, et al. (2014); Kumar *et al.* (2015); Samir and Ismail (2015); Saied et al. (2017); Elmassry *et al.* (2020); Feltaous (2020); Yadav *et al.*(2022); Kaur (2023) and kaur and kumar (2024).

Table 3: Analysis of variances and mean squares of the six parents and their F_1 hybrids for seven traits under normal, (N) drought (D) conditions and combined data (C).

S.V	d.f		Mean squares								
			Days to 50% flowering			**Plant height**			**Spike Length**		
	S	C	N	D	C	N	D	C	N	D	C
Environment (E)	--	1	----	----	2,104.96**	----	----	4,956.94**	----	----	64.39**
Replication (R)	2	--	16.78	11.48	----	3.90	4.27	----	0.46	0.10	----
Rep. /Env.	--	4	----	----	14.123	----	----	4.09	----		0.28
Genotypes (G)	20	20	26.06**	58.82**	37.87**	146.95**	368.34**	383.90**	7.86**	5.52**	12.84**
G x E	--	20	----	----	47.01**	----	----	131.39**	----	----	0.54**
Error	40	80	1.54	0.96	1.25	1.01	4.55	2.78	0.13	0.12	0.12

S.V	d.f		**No. of Spikes per plant**			**No. of Grains per Spike**		
	S	C	N	D	C	N	D	C
Environment (E)	--	1	----	----	109.20**	----	----	3,001.79**
Replication(R)	2	--	0.07	0.06	----	0.07	0.82	----
Rep. /Env.	--	4	----	----	0.07	----	----	1.95
Genotypes (G)	20	20	20.07**	31.82**	50.44**	20.07**	402.67**	842.14**
G x E	--	20	----	----	1.45**	----	----	15.67**
Error	40	80	0.19	0.08	0.13	0.19	0.35	0.56

S.V	d.f		**100 Grain Weight**			**Grain Weight per Plant**		
	S	C	N	D	C	N	D	C
Environment (E)	--	1	----	----	76.22**	----	----	361.76**
Replication (R)	2	--	0.14	0.03	----	2.44	7.69	----
Rep. /Env.	--	4	----	----	0.08	----	----	5.06
Genotypes (G)	20	20	54.04**	46.83**	99.66**	54.81**	31.65**	81.86**
G x E	--	20	----	----	1.21**	----	----	4.60**
Error	40	80	0.16	0.12	0.14	0.25	0.19	0.22

*, ** Significant at 5% and 1% levels of probability, respectively.

Table 4: Mean performance of the 6 parents and their 15 F_1 hybrids for all studied traits under normal, (N) drought (D), conditions and combined data (C).

Genotypes	**Days to 50% flowering**			**Plant height**			**Spike Length**		
	N	D	C	N	D	C	N	D	C
Canada-462(P1)	91.67	79.33**	85.5**	98.03**	91.7**	94.87**	12.2*	11.1**	11.65**
Diebera(P2)	88.33**	85	86.67	94.6**	87.5*	91.05**	12.77**	10.13	11.45**
Pectora(P3)	89*	86.33	87.67	88.55	81.4	84.98	11.07	9.73	10.4
Sahel-1(P4)	94.33	84	89.17	87.5	82.85	85.18	10.53	9.63	10.08
Giza–171(P5)	95.67	79.33**	87.5	81.57	69.1	75.33	9.93	8.9	9.42
Sids-12 (P6)	90.33	85.67	88	94.9**	91.07**	92.98**	12.3*	10.63*	11.47**
P Mean	91.56	83.28	87.42	90.86	83.94	87.40	11.47	10.02	10.75
Reduction %	**9.04%**			**7.62%**			**12.64%**		
P1 x P2	91**	87.67	89.33	99.4**	92.05**	95.73**	13.8**	12.1**	12.95**
P1 x P3	91.67**	87.67	89.67	101.93**	98.13**	100.03**	14.67**	13.16**	13.91**
P1 x P4	98	91	94.5	90.6	77.75	84.18	12.2	10.1	11.15
P1 x P5	91.67*	87	89.33	101.9**	84.8**	93.35**	11.8	9.9	10.85
P1 x P6	89.67**	87	88.33*	103.8**	97.25**	100.53**	15**	13.53**	14.27**
P2 x P3	91**	87	89	98.5**	57.9	78.2	11.67	10.2	10.93
P2 x P4	95	89.67	92.33	87.9	67.65	77.78	10.93	9.77	10.35
P2 x P5	97	91.67	94.33	95.6*	84.7**	90.15**	12.37	10.07	11.22
P2 x P6	94.33	87.67	91	95.2	76.85	86.03	14.83**	13.03**	13.93**
P3 x P4	93.33	88.33	90.83	98.25**	91.45**	94.85**	9.97	9.67	9.82
P3 x P5	97	75.67**	86.33**	84.6	72.4	78.5	10	9.3	9.65
P3 x P6	98	79.33**	88.67*	95.5	67.5	81.5	10.9	10.03	10.47
P4 x P5	94	80.33**	87.17	81.8	73.45	77.63	9.87	8.7	9.28
P4 x P6	96	89	92.5	92.05	68.25**	80.15	10.77	10.1	10.43
P5 x P6	93.67	80.33**	87	80.9	75.9	78.4	12.55	10.3	11.43
F1's Mean	94.09	85.96	90.02	93.86	79.07	86.47	12.09	10.66	11.38
Reduction %	**8.64%**			**15.76%**			**11.83%**		
L.S.D 5%	2.05	1.62	1.28	1.66	3.52	1.92	0.59	0.57	0.40
L.S.D 1%	2.74	2.16	1.70	2.22	4.71	2.54	0.80	0.76	0.53

*, ** Significant at 5% and 1% levels of probability, respectively.

Con. Table (4):

Genotypes	**No. of Spikes per plant**			**No. of Grains per Spike**		
	N	D	C	N	D	C
Canada-462 (P1)	15.4**	14.57**	14.98**	56.93**	45.63**	51.28**
Diebera (P2)	15.67**	13.8**	14.73**	57.73**	50.67**	54.2**
Pectora (P3)	12.17	10.1	11.13	44.43	36.2	40.32
Sahel-1 (P4)	11.03	10.13	10.58	42.2	32.93	37.57
Giza – 171 (P5)	10.17	8.3	9.23	31.37	26.4	28.88
Sids-12 (P6)	15.73**	14.3**	15.02**	61.13**	52.73**	56.93**
P Mean	13.36	11.87	12.61	48.97	40.76	44.86
Reduction %	**11.15%**			**16.77%**		
P1 x P2	17.17**	15.97**	16.57**	69.63**	56.8**	63.22**
P1 x P3	16.67**	15.93**	16.3**	70.77**	58.23**	64.5**
P1 x P4	10.53	7.67	9.1	51.1	36.77	43.93
P1 x P5	10.93	7.13	9.03	46.57	40.27	43.42
P1 x P6	16.83**	16.03**	16.43**	69.4**	56.57**	62.98**
P2 x P3	12.17	9.73	10.95	51.93	43.17*	47.55
P2 x P4	12	9.1	10.55	41.93	34.97	38.45
P2 x P5	11.07	9.6	10.33	55.8**	40.2	48
P2 x P6	16.83**	16**	16.42**	71.07**	62.97**	67.02**
P3 x P4	10.23	8.93	9.58	38.43	25.93	32.18
P3 x P5	10.03	6.9	8.47	33.47	23.9	28.68
P3 x P6	12.67	10.6	11.63	55.03**	42.7	48.87**
P4 x P5	10.5	6.73	8.62	35.27	24.37	29.82
P4 x P6	13.03	10.97	12**	50.43	40.83	45.63
P5 x P6	11.57	10.8	11.18	47	44.4**	45.7
F1's Mean	12.82	10.81	11.81	52.52	42.14	47.33
Reduction %	**15.68%**			**19.76%**		
L.S.D 5%	0.72	0.47	0.13	1.45	0.98	0.86
L.S.D 1%	0.96	0.62	0.17	1.94	1.31	1.14

*, ** Significant at 5% and 1% levels of probability, respectively.

Con. Table (4):

Genotypes	**100 Grain Weight**			**Grain Weight per Plant**			DSI
	N	D	C	N	D	C	
Canada-462 (P1)	10.4**	9.4**	9.9**	21.77**	14.97**	18.37**	1.31
Diebera (P2)	10.17**	8.93**	9.55**	22.97**	17.17**	20.07**	1.06
Pectora (P3)	5.03	4.33	4.68	11.4	9.9	10.65	0.55
Sahel-1 (P4)	6.8	4.53	5.67	14.87	11.37	13.12	0.99
Giza – 171 (P5)	4.3	3.13	3.72	9.27	8.5	8.88	0.35
Sids-12 (P6)	11.23**	9.5**	10.37**	19.67**	16.97**	18.32**	0.58
P Mean	7.99	6.64	7.32	16.66	13.15	14.90	---
Reduction %	**16.90%**			**21.07%**			
P1 x P2	14.33**	12.83**	13.58**	24.2**	19.1**	21.65**	1.09
P1 x P3	16.9**	15.3**	16.1**	22.7**	16.07*	19.38**	1.51
P1 x P4	11.03**	9.67**	10.35**	19.03	15.2	17.12	1.04
P1 x P5	8.07	4.5	6.28	17.37	12.37	14.87	1.48
P1 x P6	17.27**	13.73**	15.5**	23**	18.17**	20.58**	1.08
P2 x P3	7.63	6.5	7.07	20.17**	15.97	18.07**	1.07
P2 x P4	5.27	4.37	4.82	20.27**	17.4**	18.83**	0.73
P2 x P5	6.17	5.13	5.65	17.47	14.77	16.12	0.80
P2 x P6	17.07**	16**	16.53**	23.17**	20.67**	21.92**	0.56
P3 x P4	4.97	4.23	4.6	14.2	11.7	12.95	0.91
P3 x P5	5.5	4.63	5.07	12.67	10.67	11.67	0.81
P3 x P6	7.87	6.67	7.27	17.87	15.2	16.53	0.77
P4 x P5	4.3	3.57	3.93	13.37	11.1	12.23	0.88
P4 x P6	9.83	7.77	8.8	19.1	16.97**	18.03**	0.58
P5 x P6	11.37**	8.1	9.73**	15.77	14.9	15.33	0.28
F1's Mean	9.84	8.20	9.02	18.69	15.35	17.02	---
Reduction %	**16.67%**			**17.87%**			---
L.S.D 5%	0.66	0.57	0.43	0.83	0.72	0.54	---
L.S.D 1%	0.88	0.76	0.57	1.10	0.96	0.71	---

*, ** Significant at 5% and 1% levels of probability, respectively.

Table 5: General combining ability GCA effects of parental genotypes for all studied traits under normal (N), drought (D) conditions and combined (C) data.

Parental Genotypes	**Days to 50% flowering**			**Plant height**			**Spike Length**		
	N	**D**	**C**	**N**	**D**	**C**	**N**	**D**	**C**
Canada-462(P1)	-1.10**	0.31	-0.39**	5.33**	8.77**	7.05**	1.06**	0.95**	1.01**
Diebera (P2)	-0.99**	2.13**	0.57**	1.85**	-1.13*	0.36*	0.72**	0.26**	0.49**
Pectora (P3)	-0.58*	-0.65*	-0.61**	0.61*	-1.63**	-0.51*	-0.50**	-0.19*	-0.35**
Sahel-1 (P4)	1.44**	1.27**	1.36**	-3.18**	-2.37**	-2.77**	-1.07**	-0.72**	-0.90**
Giza- 171 (P5)	1.36**	-2.81**	-0.73**	-5.39**	-4.22**	-4.80	-0.87**	-0.91**	-0.89**
Sids-12 (P6)	-0.14	-0.25	-0.19	0.78**	0.58	0.68**	0.66**	0.61**	0.64**
SE(gi)	**0.23**	0.18	**0.10**	**0.19**	**0.40**	**0.16**	**0.07**	**0.06**	**0.03**

Parental Genotypes	**No. of Spikes per plant**			**No. of Grains per Spike**		
	N	**D**	**C**	**N**	**D**	**C**
Canada-462(P1)	1.52**	1.76**	1.64**	7.60**	1.76**	6.78**
Diebera (P2)	1.22**	1.28**	1.25**	5.66**	1.28**	5.78**
Pectora (P3)	-0.59**	-0.68**	-0.64**	-2.76**	-0.68**	-3.00**
Sahel-1 (P4)	-1.55**	-1.76**	-1.66**	-7.37**	-1.76**	-7.65**
Giza- 171 (P5)	-2.05**	-2.50**	-2.27**	-9.96**	-2.50**	-9.12**
Sids-12 (P6)	1.45**	1.90**	1.68**	6.83**	1.90**	7.21**
SE(gi)	**0.08**	**0.05**	**0.04**	**0.16**	**0.05**	**0.07**

Parental Genotypes	**100 Grain Weight**			**Grain Weight per Plant**		
	N	**D**	**C**	**N**	**D**	**C**
Canada-462(P1)	2.90**	2.57**	2.74**	2.88**	0.98**	1.93**
Diebera (P2)	0.70**	1.05**	0.88**	3.06**	2.40**	2.73**
Pectora (P3)	-1.53**	-1.03**	-1.28**	-2.04**	-1.70**	-1.87**
Sahel-1 (P4)	-2.02**	-1.95**	-1.99**	-1.38**	-0.99**	-1.19**
Giza-171 (P5)	-2.65**	-2.76**	-2.70**	-3.95**	-2.78**	-3.36**
Sids-12 (P6)	2.59**	2.12**	2.36**	1.43**	2.10**	1.77**
SE(gi)	**0.07**	**0.07**	**0.04**	**0.09**	**0.08**	**0.04**

Table 6: Specific combining ability GSA effects for all studied traits, under normal, (N) drought (D), conditions and combined data (C).

Crosses	**Days to 50% flowering**			**Plant height**			**Spike Length**		
	N	**D**	**C**	**N**	**D**	**C**	**N**	**D**	**C**
P1 x P2	-0.09	-0.10	-0.10	-0.78**	3.95**	1.58*	0.11	0.41*	0.26
P1 x P3	-0.18	2.67**	1.25**	2.99**	10.53**	6.76**	2.20**	1.92**	2.06**
P1 x P4	4.30**	4.25**	4.28**	-4.56**	-9.11**	-6.83**	0.30	-0.61**	-0.16
P1 x P5	-2.11**	4.33**	1.11**	8.95**	-0.21	4.37**	-0.31	-0.62**	-0.46**
P1 x P6	-2.61**	1.77	-0.42	4.68**	7.44**	6.06**	1.37**	1.49**	1.43**
P2 x P3	-0.78	0.35	-0.21	3.04**	-19.80**	-8.38**	-0.46*	-0.35	-0.40**
P2 x P4	1.20	0.94	1.07*	-3.77**	-9.31**	-6.54**	-0.63**	-0.25	-0.44**
P2 x P5	3.28**	7.19**	5.24**	6.14**	9.59**	7.87**	0.60**	0.24	0.42**
P2 x P6	2.12**	0.46	1.29**	-0.43	-3.06**	-1.74*	1.54**	1.68**	1.61**
P3 x P4	-0.88	2.71**	0.91*	7.82**	14.99**	11.40**	-0.37	0.10	-0.13
P3 x P5	2.87**	-6.04**	-1.59**	-3.62**	-2.21	-2.92**	-0.54**	-0.08	-0.31*
P3 x P6	5.37**	-4.94**	0.21	1.11*	-11.91**	-5.40**	-1.17**	-0.87**	-1.02**
P4 x P5	-2.15**	-3.29**	-2.72**	-2.64**	-0.42	-1.53*	-0.11	-0.15	-0.13
P4 x P6	1.35*	2.81**	2.08**	1.45**	-10.42**	-4.49**	-0.73**	-0.27	-0.50**
P5 x P6	-1.07	-1.77**	-1.42**	-7.49**	-0.92	-4.21**	0.85**	0.12	0.48**
SE(gi)	**0.62**	**0.49**	**0.40**	**0.52**	**1.09**	**0.60**	**0.18**	**0.18**	**0.13**

*, ** Significant at 5% and 1% levels of probability, respectively.

Con. Table (6):

Crosses	**No. of Spikes per plant**			**No. of Grains per Spike**		
	N	**D**	**C**	**N**	**D**	**C**
P1 x P2	1.46**	1.82**	1.64**	4.87**	3.19**	4.03**
P1 x P3	2.77**	3.74**	3.26**	14.42**	13.76**	14.09**
P1 x P4	-2.40**	-3.44**	-2.92**	-0.63	-3.00**	-1.82**
P1 x P5	-1.51**	-3.24**	-2.37**	-2.57**	0.85*	-0.86**
P1 x P6	0.90**	1.26**	1.08**	3.46**	1.27**	2.37**
P2 x P3	-1.44**	-1.97**	-1.71**	-2.48**	-1.25**	-1.86**
P2 x P4	-0.64*	-1.53**	-1.08**	-7.86**	-4.75**	-6.30**
P2 x P5	-1.08**	-0.29	-0.68**	8.60**	0.84*	4.72**
P2 x P6	1.19**	1.71**	1.45**	7.07**	7.73**	7.40**
P3 x P4	-0.60*	0.27	-0.16	-2.95**	-4.64**	-3.79**
P3 x P5	-0.30	-1.03**	-0.67**	-5.32**	-6.33**	-5.82**
P3 x P6	-1.17**	-1.73**	-1.45**	-0.55	-3.40**	-1.97**
P4 x P5	1.13**	-0.11	0.51**	1.10*	-1.16**	-0.03
P4 x P6	0.17	-0.28	-0.06	-0.53	-0.57	-0.55
P5 x P6	-0.81**	0.29	-0.26	-1.37*	3.35**	0.99**
SE(gi)	**0.22**	**0.14**	**0.13**	**0.45**	**0.30**	**0.27**
Crosses	**100 Grain Weight**			**Grain Weight / Plant**		
	N	**D**	**C**	**N**	**D**	**C**
P1 x P2	1.42**	1.46**	1.44**	0.15	1.01**	0.58**
P1 x P3	6.22**	6.01**	6.11**	3.75**	2.08**	2.91**
P1 x P4	0.84**	1.29**	1.07**	-0.58*	0.50*	-0.04
P1 x P5	-1.50**	-3.06**	-2.28**	0.32	-0.55*	-0.11
P1 x P6	2.47**	1.29**	1.88**	0.57*	0.37	0.47*
P2 x P3	-0.85**	-1.27**	-1.06**	1.05**	0.55*	0.80**
P2 x P4	-2.73**	-2.49**	-2.61**	0.49	1.27**	0.88**
P2 x P5	-1.20**	-0.91**	-1.06**	0.25	0.43	0.34
P2 x P6	4.47**	5.07**	4.77**	0.57*	1.45**	1.01**
P3 x P4	-0.79**	-0.53**	-0.66**	-0.48	-0.32	-0.40*
P3 x P5	0.37	0.67**	0.52**	0.55*	0.43	0.49*
P3 x P6	-2.50**	-2.18**	-2.34**	0.37	0.09	0.23
P4 x P5	-0.34	0.52**	0.09	0.59*	0.15	0.37*
P4 x P6	-0.04	-0.16	-0.10	0.94**	1.14**	1.04**
P5 x P6	2.12**	0.98**	1.55**	0.17	0.86**	0.52**
SE(gi)	**0.20**	**0.18**	**0.13**	**0.25**	**0.22**	**0.17**

*, ** Significant at 5% and 1% levels of probability, respectively.

Table 7: Genetic components for all studied traits under normal (N), drought (D) conditions as well as their combined data (C).

Genetic Components	Days to 50% flowering			Plant height			Spike Length		
	N	D	C	N	D	C	N	D	C
σ^2 GCA	0.28	0.65	0.21	11.02	7.44	12.83	0.69	0.42	0.53
σ^2 SCA	7.60	17.87	0.83	26.60	106.38	16.42	1.19	0.95	0.99
σ^2 GCA / σ^2 SCA	0.04	0.04	0.25	0.41	0.07	0.78	0.58	0.45	0.53
σ^2 GCA x E	----	----	1.30	----	----	3.60	----	----	0.03
σ^2 SCA x E	----	----	12.53	----	----	50.07	----	----	0.08
σ^2 GCA x E/ σ^2 SCA x E	----	----	0.10	----	----	0.07	----	----	0.38
σ^2 A	0.57	1.30	0.42	22.05	14.88	25.67	1.38	0.85	1.06
σ^2 D	7.60	17.87	0.83	26.60	106.38	16.42	1.19	0.95	0.99
σ^2 A/ σ^2 D	0.08	0.07	0.51	0.83	0.14	1.56	1.16	0.90	1.07
σ^2 A x E	----	----	2.60	----	----	7.20	----	----	0.06
σ^2 D x E	----	----	12.53	----	----	50.07	----	----	0.08
σ^2 A x E/ σ^2 D x E	----	----	0.21	----	----	0.14	----	----	0.75
Narrow h^2 % n.s	5.66	6.48	11.84	44.40	11.83	57.21	51.16	44.26	48.65
Broad h^2 % b.s	84.62	95.36	54.46	97.96	96.39	93.80	95.25	93.95	94.36

Genetic Components	No. of Spikes			No. of Grains on Spike		
	N	D	C	N	D	C
σ^2 GCA	2.31	3.08	2.71	54.10	49.64	51.85
σ^2 SCA	2.01	4.41	2.75	43.26	34.82	34.05
σ^2 GCA / σ^2 SCA	1.15	0.70	0.98	1.25	1.43	1.52
σ^2 GCA x E	----	----	0.41	----	----	0.44
σ^2 SCA x E	----	----	0.46	----	----	5.00
σ^2 GCA x E/ σ^2 SCA x E	----	----	0.89	----	----	0.09
σ^2 A	4.62	6.17	5.41	108.19	99.29	103.70
σ^2 D	2.01	4.41	2.75	43.26	34.82	34.05
σ^2 A/ σ^2 D	2.30	1.40	1.97	2.50	2.85	3.05
σ^2 A x E	----	----	0.82	----	----	0.88
σ^2 D x E	----	----	0.46	----	----	5.00
σ^2 A x E/ σ^2 D x E	----	----	1.78	----	----	0.18
Narrow h^2 % n.s	67.82	57.87	65.25	71.08	73.84	74.98
Broad h^2 % b.s	97.33	99.27	98.43	99.50	99.74	99.60

Genetic Components	No. of Spikes			No. of Grains on Spike		
	N	D	C	N	D	C
σ^2 GCA	2.31	3.08	2.71	54.10	49.64	51.85
σ^2 SCA	2.01	4.41	2.75	43.26	34.82	34.05
σ^2 GCA / σ^2 SCA	1.15	0.70	0.98	1.25	1.43	1.52
σ^2 GCA x E	----	----	0.41	----	----	0.44
σ^2 SCA x E	----	----	0.46	----	----	5.00
σ^2 GCA x E/ σ^2 SCA x E	----	----	0.89	----	----	0.09
σ^2 A	4.62	6.17	5.41	108.19	99.29	103.70
σ^2 D	2.01	4.41	2.75	43.26	34.82	34.05
σ^2 A/ σ^2 D	2.30	1.40	1.97	2.50	2.85	3.05
σ^2 A x E	----	----	0.82	----	----	0.88
σ^2 D x E	----	----	0.46	----	----	5.00
σ^2 A x E/ σ^2 D x E	----	----	1.78	----	----	0.18
Narrow h^2 % n.s	67.82	57.87	65.25	71.08	73.84	74.98
Broad h^2 % b.s	97.33	99.27	98.43	99.50	99.74	99.60

CONCLUSION

Six parental genotypes and 15 F1 wheat hybrids were evaluated under normal and drought conditions for yield and growth traits. Significant genetic variation and genotype × environment interaction were observed for all traits studied. Best parents and hybrids for early flowering, plant height, and yield traits varied across environments. Drought stress caused notable reductions in trait performance, especially grain yield and grain number. Several hybrids (e.g., P2×P6, P4×P6, P5×P6) showed strong drought tolerance based on DSI values. Additive and non-additive gene actions were important, with non-additive effects dominating most traits. Promising crosses with high combining ability are recommended for breeding drought-tolerant wheat.

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