

Research Article

Genetical behavior of some quantitative characters in some bread wheat crosses under nitrogen stress

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Abstract:

In an attempt to determine the genetic behavior governing inheritance of yield and its component traits, this investigation was conducted throughout the four growing seasons 2018/19 to 2021/22 under normal and nitrogen stress conditions. The parents and their five populations (P1, P2, F1, F2 and F3) of two crosses were layout in a randomized complete block design with three replications. Scaling test illustrated the existence of non-allelic interactions (epistasis) for most studied characters in the two crosses. Results demonstrated that additive and non-additive gene effects were significant and govern the inheritance of yield and its component traits while, dominance gene effects were higher in magnitude than additive effect under normal and nitrogen stress conditions. Significant positive heterotic estimates relative to mid and better parents were obtained for most studied characters under normal and nitrogen stress conditions. Regarding potence ratio, over and partial dominance was observed for all the studied characters in both crosses at normal and nitrogen stress conditions. broad sense heritability estimates ranged from 73 % to 98 % under normal condition and from 65 % to 97 % under nitrogen stress condition. Moreover, Narrow sense heritability estimates ranged from 29 % to 96 % under normal condition and from 17 % to 89 % under nitrogen stress condition. The most accurate predictions of expected genetic advance (GA%) and narrow sense heritability (h²) revealed selection efficiency for the no. of spikes per plant, no. of kernels spike, and grain yield in these studied populations under normal and nitrogen stress conditions.

1. Introduction

Wheat is the most important cereal crop in Egypt, and worldwide. In Egypt increasing grain yield of cereal crops is considered one of the important national goals to face the growing needs of the populations. Therefore, it has become necessary to develop genotypes which are consistent by showing superior performance.

The plant breeder in their estimation of gene effects in order to formulate the most advantageous breeding procedures for improving his breeding program. Therefore, breeders need information about the nature of gene action, heterosis, inbreeding depression, heritability and predicted genetic gain from selection for yield and its component characters. Sence decision making about effective breeding system to be used in mainly dictated by type of gene action controlling the genetic variation, such information is helpful for the breeders to predict in early generations the effective breeding program. The potential of new recombination lines that could be delved of a lowing series of selfing generations. Science genetic information obtained from multi population (P₁, P₂, F₁, F₂ and F₃) are considered the one which may be give detailed genetic information of the employed genotypes.

Nitrogen (N) is an essential element for plants and is considered the most important mineral nutrient. It plays a key role in many aspects of plant metabolism as a constituent of cell components such as proteins, phytohormones, co-enzymes, chlorophyll, and nucleic acids

(Hawkesford et al., 2012). Evaluation of genotype performance under different nitrogen levels is important in plant breeding. The differential response of genotype when subjected to different nitrogen levels possesses a major problem of relating phenotypic performance to genetic constitution and makes it difficult to decide which genotype should be selected. It is important to fully understand the nature of genotype x nitrogen interaction to make testing and selection of genotype more efficient.

Heterosis is a complex genetical phenomenon, which depends on the balance of different combinations of gene effects as well as on the distribution of plus and minus alleles in the parents of mating. Generation mean analysis is a useful technique in plant breeding for estimating main gene effects (additive and dominance) and their digenic (additive x additive, additive x dominance, and dominance x dominance) interactions responsible for inheritance of quantitative traits. It helps us in understanding the performance of the parents used in crosses and potential of crosses to be used either for heterotic exploitation or pedigree selection (Sareen et al., 2018; Sharma et al., 2003).

The current study aimed to investigate the influence of low nitrogen stress compared to normal condition on the genetic behavior controlling the inheritance of yield and its components using five parameters method in two bread wheat crosses cultivated under normal and

nitrogen stress conditions; Practicing selection between and within genotypes to select the best one from either homogenous or segregated genotypes; and determining the best line, which can be used as useful genetic source in wheat breeding programs and as sustainable production.

2. Materials and Methods

The present study was carried out in Sakha Agricultural Research Station, Kafr El-Sheikh Governorate, Wheat Research Department, Agricultural Research Center (ARC) during the four growing seasons 2018/19 to 2021/22. Four bread wheat genotypes were used as parental lines. The commercial names and pedigree of these parents are presented in Table (1).

In the first season of 2018/19, two crosses were crossed among the parents to produce F₁ hybrid grains for the two crosses; cross 1 (Giza 171 X Misr 3) and cross 2 (Sakha 95 X Sids 14). In the second season, 2019/20, the hybrid seeds of the two crosses were sown to give the F₁ plants. These plants were selfed to produce F₂ seeds. Moreover, the same parents were crossed again to produce F₁ seeds. The new hybrid seeds and part of the seeds obtained from F₁ selfed plants (F₂ seeds) were kept in refrigerator to the final experiment. In the third season 2020/21, seeds from the parents, F₁ and F₂ were sown to produce enough F₁, F₂ and F₃ seeds.

In the fourth season 2021/22, the five population P₁, P₂, F₁, F₂ and F₃ of the two crosses were evaluated under normal nitrogen condition (with 75 kg nitrogen/ fad.) and nitrogen stress condition (with 25 kg nitrogen/ fad.) as single plants using a randomized complete block design with three replications. Each row included 25 plants spaced 20 cm apart within row and 25 cm apart between the rows. At both experiments, normal and nitrogen stress for each plot consisted of 26 rows, two rows were devoted for each parent and F₁ progenies and ten rows for each of F₂ population and F₃ families for each cross. Data were scored on 40 individual plants selected randomly from each parent and F₁ generation and 250 plants from F₂ population and 200 plants from F₃ families to measure the studied traits; plant height (cm), number of spikes/plant, number of kernels / spike, 100-kernel weight and grain yield / plant for the two crosses under normal and nitrogen stress conditions. All recommended agriculture practices, except nitrogen fertilization, for wheat production were applied at the proper time. Physical and chemical properties of the soil samples before wheat planting 2021/2022 illustrated in Table (2). Data in Table (2) illustrated the soil characterization assisted with the selection of a suitable site for the subsequent experiments performed, mainly to avoid potentially confounding soil factors (mineral toxicities and soil nutritional deficiencies) that might have impacted on the genotypic performance under the different nitrogen conditions. In general, the selected site showed a slightly alkaline pH at both depths (averaged 7.87). No salinity problems were detected and electrical conductivity levels were low (averaged, 1.25 dSm⁻¹).

Biometrical and genetical methods

T-test was used to estimate the significance of parent differences. Furthermore, various biometrical parameters, in this investigation, were only calculated in the F₂ genetic variance that was found to be significant. The Reduction Index (RI) was used to measure the reduction in grain yield under nitrogen stress condition. RI was calculated for each genotype according to the modified formula of (Fisher and Maurer, 1978): $RI = (1 - Y_{NS} / Y_{OC}) / D$, Where. RI = an index of nitrogen stress reduction, Y_{NS} = yield from nitrogen stress experiment for each genotype, Y_{OC} = yield from optimum (normal) condition experiment for each genotype and D = nitrogen stress intensity = $1 - (\text{mean of } Y_{NS} \text{ for all genotypes} / \text{mean of } Y_{OC} \text{ for all genotypes})$.

Scaling test

Concerning scaling test, the test of adequacy of scales is important because in most cases, the estimation of additive and dominance components of variances are made assuming the absence of gene interaction. The scaling test was estimated according to Mather (1949) and (Hayman and Mather, 1955).

Type of gene action

Type of gene action effects were estimated according to Hayman model in 1958 as described by (Singh and Chaudhary, 1985).

Estimates of heritability in broad and narrow sense, heterosis relative to mid and best parent, potence ratio, and inbreeding depression (%) were calculated according to (Mather and Jinks, 1982). Moreover, the expected genetic advance from selection (Δg) was computed according to (Johnson *et al.*, 1955). The t-test was used to determine the significance of these parameters where the standard error (SE) was calculated.

3. Results and discussion

Generations Mean

Data in Table (3) showed the mean performance, variance and standard error of the studied characters in the two crosses at normal and nitrogen stress conditions. The validity of parental differences and the existence of genetic variance within F₂ and F₃ populations in normal and nitrogen stress conditions were examined. Generally, the differences between each of the two parents were found to be highly significant. Concerning parents, Sakha 95 recorded the highest estimates for plant height and number of spikes / plant at normal and nitrogen stress conditions and 100-kernel weight at normal condition. Moreover, Giza 171 scored the highest estimates for number of kernels per spike and grain yield/plant at normal and nitrogen stress conditions.

Table 1: Cross name, Pedigree and Origin of the four parental bread wheat genotypes.

Crosses	parents	Pedigree and Selection history	Origin
1	(P1) GIZA 171	SAKHA 93/GEMMEIZA 9 (S.6-1GZ-4GZ-1GZ-2GZ-0S)	EGYPT
	(P2) MISR 3	ATTILA*2/PBW65*2/KACHU CMSS06Y00582T-099TOPM-099Y-099ZTM-099Y-099M-10WGY-0B-0EGY	CIMMYT
2	(P1) SAKHA 95	PASTOR // SITE / MO /3/ CHEN / AEGILOPS SQUARROSA (TAUS) // BCN /4/ WBLL1. CMA01Y00158S-040POY-040M -030ZTM-040SY-26M-0Y-0SY-0S.	CIMMYT
	(P2) SIDS 14	Bow''s''/Vee''s''//Bow's'/Tsi/3/BANI SUEF1 SD293-1SD-2SD-4SD-0SD	EGYPT

Table 2: Physical and chemical properties of the soil samples before wheat planting 2021/22.

Soil depth (cm)	Particle size distribution			Texture class	EC (ds/m)	OM %	CaCO ₃ %	Available N, P, K (mgkg ⁻¹ soil)		
	Sand %	Silt %	Clay %					N	P	K
0	26.65	23.42	50.75	clayey	1.56	1.62	3.81	28.60	6.30	292.7
30	28.27	25.86	46.65	clayey	0.94	1.20	3.68	13.50	4.65	245.3
Soil depth (cm)	Anions (meqL ⁻¹)				Cations (meqL ⁻¹)				pH	
	CO ₃ ²⁻	HCO ₃ ⁻	CL ⁻	SO ₄ ²⁻	Ca ⁺⁺	Mg ⁺⁺	Na ⁺	K ⁺		
0	-	3.13	12.50	9.93	5.03	5.55	15.15	0.18	7.82	
30	-	2.82	11.04	3.66	1.97	1.83	13.66	0.06	7.92	

Table (3): Mean (\bar{X}), variance (S^2) and standard error ($S_{\bar{X}}$) of P₁, P₂, F₁, F₂ and F₃ populations for the studied characters of the five crosses under normal (N) and nitrogen stress (S) conditions.

Characters	Crosses	Statistical Parameter	P1		P2		F1		F2		F3	
			N	S	N	S	N	S	N	S	N	S
Plant Height	1	\bar{X}	107.05	98.90	99.95	85.80	110.70	101.90	108.95	96.51	104.76	90.95
		S^2	6.92	5.94	14.72	4.27	14.16	7.89	79.40	73.74	72.71	52.29
		$S_{\bar{X}}$	0.42	0.39	0.61	0.33	0.60	0.44	0.56	0.54	0.60	0.65
	2	\bar{X}	118.65	99.05	104.90	96.23	105.25	99.40	99.16	94.94	103.53	94.03
		S^2	9.72	12.87	7.27	9.77	7.27	8.91	105.31	100.94	121.41	96.31
		$S_{\bar{X}}$	0.49	0.57	0.43	0.49	0.43	0.47	0.65	0.64	0.78	0.69
No of Spikes per plant	1	\bar{X}	20.96	14.88	25.32	19.29	30.35	19.00	22.57	18.00	21.33	17.78
		S^2	3.26	2.94	3.10	3.69	3.93	1.64	161.45	85.20	131.70	73.44
		$S_{\bar{X}}$	0.29	0.27	0.28	0.30	0.31	0.20	0.80	0.58	0.81	0.61
	2	\bar{X}	28.65	22.85	19.90	15.96	25.05	16.50	20.77	17.18	19.52	16.42
		S^2	2.90	1.87	9.32	1.19	4.05	2.41	141.04	47.24	120.04	49.93
		$S_{\bar{X}}$	0.27	0.22	0.48	0.17	0.32	0.25	0.75	0.43	0.77	0.50
No of Kernels per Spike	1	\bar{X}	83.85	70.58	79.65	64.75	85.08	74.20	72.03	64.52	74.04	67.60
		S^2	52.39	23.38	21.46	46.35	76.89	26.22	272.12	282.94	249.11	266.17
		$S_{\bar{X}}$	1.14	0.76	0.73	1.08	1.39	0.81	1.04	1.06	1.12	1.15
	2	\bar{X}	72.63	59.68	64.60	54.90	64.88	53.50	63.02	58.02	62.27	56.26
		S^2	16.80	33.66	23.73	26.66	35.91	36.36	189.63	239.90	248.22	269.64
		$S_{\bar{X}}$	0.65	0.92	0.77	0.82	0.95	0.95	0.87	0.98	1.11	1.16
100-Kernels Weight	1	\bar{X}	6.73	6.41	6.56	6.26	7.29	6.60	6.48	6.08	6.51	6.40
		S^2	0.26	0.26	0.36	0.20	0.24	0.17	1.07	0.88	0.89	0.45
		$S_{\bar{X}}$	0.08	0.08	0.10	0.07	0.08	0.06	0.07	0.06	0.07	0.05
	2	\bar{X}	7.07	6.38	6.52	5.73	7.23	6.03	6.62	6.12	6.91	6.15
		S^2	0.17	0.07	0.26	0.18	0.18	0.26	0.83	0.48	1.12	0.53
		$S_{\bar{X}}$	0.07	0.04	0.08	0.07	0.07	0.08	0.06	0.04	0.07	0.05
Grain Yield	1	\bar{X}	61.58	34.40	55.98	32.13	68.30	31.58	54.60	35.21	54.38	30.61
		S^2	4.80	22.61	6.92	6.83	8.68	4.39	402.81	139.96	395.72	128.65
		$S_{\bar{X}}$	0.35	0.75	0.42	0.41	0.47	0.33	1.27	0.75	1.41	0.80
	2	\bar{X}	50.12	29.88	41.00	24.38	49.90	22.83	47.94	23.50	48.25	20.62
		S^2	3.73	5.57	5.54	4.98	11.22	2.60	338.14	109.29	290.42	62.07
		$S_{\bar{X}}$	0.31	0.37	0.37	0.35	0.53	0.25	1.16	0.50	1.21	0.74

Cross 1 (Giza 171 x Misr 3) and Cross 2 (Sakha 95 x Sids 14).

and 100-kernel weight at nitrogen stress condition. Meanwhile, the opposite trend was showed by Sids 14 for 100-kernel weight and grain yield/plant at normal and nitrogen stress conditions and number of spikes per plant at normal condition, Misr 3 for plant height at normal and nitrogen stress conditions and Giza 171 for number of spikes per plant at nitrogen stress condition. Regarding F_1 ; F_2 and F_3 data revealed that, the first cross (Giza 171 X Misr 3) was the superior one at normal and nitrogen stress conditions for all the studied characters. except for 100-kernel weight in F_2 and plant height at nitrogen stress and 100-kernel weight at normal condition in F_3 families.

Generally, it's worthy to note that the means of both crosses and generations within crosses decreased significantly under the nitrogen stress condition for all studied characters in compared to normal condition.

Reduction index (RI) for grain yield of the five populations in the two crosses is illustrated in Table (4) The (RI) was used as a parameter to provide a measure of nitrogen stress tolerance based on minimization of yield losses under nitrogen stress compared to relatively optimum condition. Low Reduction index ($RI < 1$) was recorded for P_1 , P_2 , F_2 and F_3 populations in the first cross (Giza 171 X Misr 3), also P_1 and P_2 in the second cross (Sakha 95 X Sids 14), indicating that these genotypes had tolerance to nitrogen stress condition.

Scaling test

The purpose of scaling tests C and D Table (5) was to determine how additive-dominance model is adequate for studying types of gene action in the inheritance of different traits. When the scale test is adequate the values of C and D should be zero within the limits of their respective standard errors. The significance of any one of these scales indicates the presence of non-allelic interaction. The mean performance and variance of mean of five populations (P_1 , P_2 , F_1 , F_2 and F_3) were used to calculate the two scaling tests. C and D values which showed significant or highly significant for most traits in the two crosses at normal and nitrogen stress conditions, suggesting that additive-dominance model is inadequate for these traits and indicating the role of non-allelic interaction in governing these traits more particularly dominance \times dominance type of non-allelic interaction (epistasis). These results are in harmony with those obtained by (Abd-Allah and Amin, 2013; El-Hawary et al., 2022; Gebrel et al., 2020; Mohamed et al., 2021; Sharshar et al., 2020; Shehab-Eldeen et al., 2020; Zaazaa, 2017)

Nature of gene action and types of epistasis:

Gene action refers to the behavior or mode of expression of genes in a genetic population. Knowledge of nature of gene action helps to select parents for the hybridization programs also, in the choice of appropriate breeding procedure for the genetic improvement of various quantitative traits. Hence, insight into the nature of gene action involved in the expression of various quantitative traits is essential to plant breeders for starting a judicious breeding program (Singh and Naraynan, 2000). Types of gene effects for the studied characters in the two crosses

at normal and nitrogen stress conditions are shown in Table (6), The mean effect of parameter (m) that reflects the contribution due to the over-all mean plays the locus effect and interactions of the fixed loci was found to be highly significant for all characters in all crosses at normal and nitrogen stress conditions. Initially, it is clear that all the studied traits were quantitatively inherited.

Concerning additive gene effects (d^*), highly significant additive gene effects were found for all characters in the two crosses at normal and nitrogen stress conditions. except for 100 kernel weight for the first cross (Giza 171 X Misr 3) at normal and nitrogen stress conditions, indicating that the additive gene effects played a major role in the inheritance of these traits and the potential for obtaining further improvements of these characters.

With respect to dominance gene effects (h), highly significant or significant dominance gene effects were attained for all characters in both crosses at normal and nitrogen stress conditions. except for the following cases: no. of kernels spike for the two crosses at normal and nitrogen stress conditions, no. of spikes per plant for the two crosses at nitrogen stress condition, 100 kernels weight for the second cross (Sakha 95 X Sids 14) at normal and nitrogen stress conditions and grain yield for the second cross at normal condition, revealing the importance of dominance gene effects in the inheritance of these traits.

Regarding additive \times additive (i) epistatic effect, highly significant additive \times additive gene effects were found for all characters in all crosses at normal and nitrogen stress conditions. except for the following cases: 100 kernel weight and grain yield for the two crosses at both condition, no. of kernels spike for the first cross (Giza 171 X Misr 3) at both condition and no. of spikes per plant for the first cross (Giza 171 X Misr 3) at normal condition

In relation to dominance \times dominance (L) epistatic effect, highly significant or significant dominance \times dominance type of gene action was scored for most characters in the two crosses at normal and nitrogen stress conditions, except for, no. of spikes per plant for the two crosses at both conditions, no. of kernels per spike and grain yield for the second cross (Sakha 95 X Sids 14) at normal condition and 100 kernels weight for the same cross at nitrogen stress condition. Generally, it may be deduced that, additive and non-additive gene effects were significant and govern the inheritance of yield and its component traits, while the non-additive gene effects were higher in magnitude than additive gene effects, indicating that selection index and phenotypic trait selection based on the accumulation of additive effects were successful in improving of the characters under investigation. However, to maximize selection advance, procedures known to be effective in shifting gene frequency *viz.*, recurrent selection when both additive and non-additive genetic variations are involved would be preferred.

Table (4): Reduction index (RI) for grain yield of five populations in the two studied crosses.

R.I.	Cross	P ₁	P ₂	F ₁	F ₂	F ₃
	1	0.99	0.96	1.21	0.80	0.98
	2	0.83	0.83	1.11	1.04	1.17

Table (5): Scaling test for the studied characters of the two crosses under normal (N) and nitrogen stress (S) conditions.

cross	scaling test	Plant height		No of Spike per plant		No of kernels per spike		100-kernels weight		Grain yield/plant	
		N	S	N	S	N	S	N	S	N	S
		1	C	7.41**	-2.45	-16.71**	-0.17	-45.54**	-25.63**	-1.94**	-1.53**
D	-5.88*		-13.94**	-6.12	0.95	-11.42*	6.03	-0.23	0.76**	-9.24	-14.51**
2	C	-37.43**	-14.3**	-15.58**	-3.07	-14.9**	10.52*	-1.58**	0.31	0.84	-5.92**
	D	-7.76*	-9.06**	-12.01**	-7.5**	-14.19**	-5.6	0.82*	0.24	6	-18.76**

Cross 1 (Giza 171 x Misr 3) and Cross 2 (Sakha 95 x Sids 14). (*) and (**) significant at 0.05 and 0.01

Table (6): Gene action for the studied characters of the two crosses under normal (N) and nitrogen stress (S) conditions.

Character	Cross	m		d*		h		L		i	
		N	S	N	S	N	S	N	S	N	S
Plant Height	1	108.95**	96.51**	3.55**	6.55**	12.36**	18.44**	-17.72**	-15.32**	12.26**	21.99**
	2	99.16**	94.94**	6.88**	1.41**	-7.59**	5.42*	39.55**	6.98	12.69**	6.48**
No. of Spikes per Plant	1	22.57**	18**	-2.18**	-2.2**	8.5**	1.25	14.12	1.49	-3.07	-5.07**
	2	20.77**	17.18**	4.38**	3.45**	6.18*	1.58	4.76	-5.9	14.16**	11.38**
No of Kernels Spike	1	72.03**	64.52**	2.1**	2.91**	3.35	-1.75	45.5**	42.21**	4.22	-2.46
	2	63.02**	58.02**	4.01**	2.39**	3.24	1.7	0.94	-21.5*	15**	10.26**
100-Kenels Weight	1	6.48**	6.08**	0.08	0.08	0.48*	-0.5**	2.27**	3.04**	0.001	-0.6**
	2	6.62**	6.12**	0.28**	0.33**	-0.37	-0.13	3.19**	-0.09	-0.25	0.54**
Grain Yield	1	54.6**	35.21**	2.8**	1.14**	9.73*	9.84**	35.33**	-34.23**	5.81	13.81**
	2	47.94**	23.5**	4.56**	2.75**	0.48	7.22**	6.88	-17.12**	5.26	17.02**

Cross 1 (Giza 171 x Misr 3) and Cross 2 (Sakha 95 x Sids 14). (*) and (**) significant at 0.05 and 0.01

Respecting types of gene action and epistasis for yield and its component characters in the present investigation, the results and conclusions are in harmony with those obtained (Abd-Allah and Amin, 2013; El-Hawary et al., 2022; Gebrel et al., 2020; Mohamed et al., 2021; Sharshar et al., 2020; Shehab-Eldeen et al., 2020; Zaazaa, 2017).

Heterosis, inbreeding depression and potence ratio

Heterosis or hybrid vigor, refers to the superiority of the F_1 hybrid over its parent. Heterosis can result from partial, complete dominance, over dominance, epistasis, and a combination of these factors. High positive significant values of heterosis would be interest for all investigated traits. Heterosis percentage relative to mid parent (MP) and better parents or heterobeltiosis (BP), inbreeding depression and potence ratio for the studied characters in the two crosses under normal and nitrogen stress conditions are illustrated in Table (7). At the level of heterosis over mid parents, highly significant positive heterotic effects were recorded for all traits in the two crosses at normal and nitrogen stress conditions, except for plant height and no. of kernels spike in the second cross (Sakha 95 X Sids 14) at normal and nitrogen stress conditions, no. of spikes per plant and 100 kernel weight in the second cross at nitrogen stress condition and grain yield in the two crosses at nitrogen stress condition.

Concerning heterosis over better parent, significant positive heterotic effects were observed for, plant height for the first cross (Giza 171 X Misr 3) at normal and nitrogen stress conditions, no. of spikes per plant and grain yield for the first cross (Giza 171 X Misr 3) at normal condition, 100 kernel weight for the first cross (Giza 171 X Misr 3) at normal and nitrogen stress conditions and for the second cross (Sakha 95 X Sids 14) at normal condition and no. of kernels spike for the first cross (Giza 171 X Misr 3) at nitrogen stress condition, while the rest of cases were either non-significant or significant in negative direction.

Referring to inbreeding depression, results revealed that under normal condition highly significant positive estimates were obtained for all traits, except for plant height in the first cross (Giza 171 X Misr 3). Moreover, under nitrogen stress condition, highly significant positive estimates were recorded for plant height in the two crosses and for no. of spikes per plant, no. of kernels spike and 100 kernel weight in the first cross (Giza 171 X Misr 3). On the other side, negative significant values were obtained for no. of spikes per plant, no. of kernels per spike and 100 kernel weight in the second cross (Sakha 95 X Sids 14) and for Grain yield in the two crosses under nitrogen stress condition.

Regarding potence ratio, results revealed that over dominance controlling the inheritance of all the studied characters in the two crosses at normal and nitrogen stress conditions where the values exceeded unity, except for no. of spikes per plant, no. of kernels per spike, 100 kernel weight and GYP in the second cross (Sakha 95 X Sids 14) under normal condition. Furthermore, no. of spikes per plant in the two crosses and 100 kernels weight in the

second cross (Sakha 95 X Sids 14) under nitrogen stress condition where partial dominance was existed. These results confirmed by those obtained by (Abd-Allah and Amin, 2013; El-Hawary et al., 2022; Gebrel et al., 2020; Mohamed et al., 2021; Sharshar et al., 2020; Shehab-Eldeen et al., 2020; Zaazaa, 2017).

Heritability and Genetic advance

The heritability for different traits is helpful to the plant breeders to estimate the response to selection in segregation generations. The heritability was categorized into three groups: high ($\geq 60\%$), moderate (30-60 %) and low (0 – 30) according to (Robinson et al., 1949). The exhibited narrow sense heritability values were lower than broad sense heritability ones, then variances between H and h^2 demonstrate the contribution of dominance effect in the genetic components of the studied traits as shown in Table (8). The heritability values in broad sense were high and detected and ranged from 65 % to 98 % for all traits in the two crosses at normal and nitrogen stress conditions.

Heritability values in narrow sense were moderate to high and ranged from 38% to 89 % for all traits except for 100-kernel weight in the two crosses under normal and nitrogen stress conditions. heritability in narrow sense results were confirmed with those obtained by (Abd-Allah and Amin, 2013; El-Hawary et al., 2022; Gebrel et al., 2020; Mohamed et al., 2021; Sharshar et al., 2020; Shehab-Eldeen et al., 2020)

Revealing that additive variance played a predominant role in the inheritance of most studied traits. Therefore, selection plants for these traits could be implemented in the early generation.

The expected genetic advance from selection as percent of F_2 mean ($\Delta g\%$) scored high estimates (more than 20%) for no. of spikes per plant, no. of kernels per spike and grain yield in the two crosses at normal and nitrogen stress conditions and moderate estimates (10 - 20 %) for plant height in the two crosses at both conditions and 100 kernel weight in the first cross (Giza 171 X Misr 3) at normal and the second cross (Sakha 95 X Sids 14) at nitrogen stress. consequently, revealing the effectiveness of selection for these traits in early generations. While, low expected genetic advance percent estimates (less than 10 %) were detected for 100 kernels weight in the first cross (Giza 171 X Misr 3) at nitrogen stress and the second cross (Sakha 95 X Sids 14) at normal condition. These results agree with those obtained by (Abd-Allah and Amin, 2013; El-Hawary et al., 2022; Gebrel et al., 2020; Mohamed et al., 2021; Sharshar et al., 2020; Shehab-Eldeen et al., 2020; Zaazaa, 2017). Meanwhile, Ditić et al. (1970) noted that high genetic gain is often is not connected with high heritability, but high genetic advance should be correlated with high heritability to allow efficient selection. Therefore, it could be noted that such crosses are important to wheat breeding program for genetic yield advancement.

Table (7): Heterosis relative to mid (MP) and better (BP) parent, inbreeding depression (ID %) and potence ratio for the studied characters of the two crosses under normal (N) and nitrogen stress (S) conditions.

Character	Cross	Heterosis % over M.P.		Heterosis % over B.P.		Potence ratio		Inbreeding depression	
		N	S	N	S	N	S	N	S
Plant Height	1	6.96**	10.34**	10.76**	3.03**	2.03	1.46	1.58	5.29**
	2	-5.84**	1.81	0.33	0.35	-1	1.25	5.79**	4.48**
No. of Spikes per Plant	1	31.16**	11.22**	19.87**	-1.48	-3.3	-0.9	25.64**	5.26**
	2	3.19**	-14.97**	-12.57**	-27.79**	0.18	-0.8	17.09**	-4.15**
No of Kernels Spike	1	4.07**	9.66**	1.46	5.14**	1.58	2.24	15.34**	13.04**
	2	-5.45**	-6.61**	-10.67**	-10.35**	-0.9	-1.6	2.86*	-8.46**
100-Kenels Weight	1	9.69**	4.1**	8.31**	2.83**	7.62	3.33	11.06**	7.75**
	2	6.4**	-0.39	2.24*	-5.46**	1.57	-0.1	8.46**	-1.48**
Grain Yield	1	16.2**	-5.07**	10.91**	-8.21**	3.4	-1.5	20.05**	-11.51**
	2	9.53**	-15.85**	-0.44	-23.6**	0.95	-1.6	3.93**	-2.94**

Cross 1 (Giza 171 x Misr 3) and Cross 2 (Sakha 95 x Sids 14). (*) and (**) significant at 0.05 and 0.01 levels of probability, respectively

Table (8). Estimate of heritability in broad and narrow sense and expected genetic advance from selection (Δg) for the studied characters of the two crosses under normal (N) and nitrogen stress (S) conditions.

Traits	Cross	Heritability				Expected Genetic advance			
		H		h ²		g Δ		%g Δ	
		N	S	N	S	N	S	N	S
Plant Height	1	0.85	0.92	0.74	0.72	13.53	12.76	12.42	13.22
	2	0.92	0.90	0.72	0.83	15.21	17.27	15.34	18.19
No. of Spikes per Plant	1	0.98	0.97	0.73	0.78	19.19	14.90	85.02	82.77
	2	0.96	0.96	0.76	0.89	18.67	12.53	89.88	72.93
No of Kernels per Spike	1	0.82	0.89	0.70	0.81	23.88	28.00	33.15	43.39
	2	0.87	0.87	0.45	0.70	12.87	22.35	20.42	38.52
100-Kernel Weight	1	0.73	0.76	0.50	0.17	1.07	0.32	16.51	5.31
	2	0.75	0.65	0.29	0.53	0.54	0.76	8.14	12.39
Grain Yield	1	0.98	0.92	0.86	0.81	39.68	19.78	72.66	56.18
	2	0.98	0.96	0.79	0.38	29.99	8.27	62.55	35.18

Cross 1 (Giza 171 x Misr 3) and Cross 2 (Sakha 95 x Sids 14).

4. Conclusions

It could be recommended to use the cross Giza 171 X Misr 3 in breeding programs and advanced studies to improve yield and its component characters under nitrogen stress condition.

5. References

- Abd-Allah, Soheir M.H and I.A. Amin (2013). Genotypic differences for heat tolerance traits in bread wheat using five parameters genetic model. *Alex. J. Agric. Res.*, 58 (2): 83 - 96.
- Ditix P.K.; P. O. Sexena and L. K. Bhatia (1970). Estimation of genotype variability of some quantitative characters in groundnut. *Indian. Agric. Sci.*, 40: 197-201
- El-Hawary, M. N. A.; M. M. M. Gab Alla; O. E. Abd El Badeea and Mona I. E. Elsayed (2022). Improvement grain yield and yellow rust resistance in four bread wheat crosses. *J. of Plant Production, Mansoura Univ.*, 13 (10): 799 -806.
- Fischer, R. A. and R. Maurer (1978). Drought resistance in spring wheat cultivars. I. Grain yield responses. *Aust. J. Agric. Res.* 29: 897- 912.
- Gebrel, E. M. A. ; M. N. A. El-Hawary and M. Y. El-Masry (2020). Genetic behavior of some agronomic traits in three bread wheat crosses using five population model. *J. of Plant Production, Mansoura Univ.*, 11 (5): 413 – 418.
- Hawkesford, M.; W. Horst; T. Kichey; H. Lambers; J. Schjoerring; I.S. Møller and White, P. (2012). Functions of macronutrients marschner's mineral nutrition of higher plants (Chapter 6). *Marschners Mineral Nutr. High. Plants*, 3rd ed., pp. 135 -189.
- Hayman, B. I. and K. Mather (1955). The description of genetic interaction in continuous variation. *Biometrics*, 11: 69-82.
- Hayman, B.I. (1958). The separation of epistatic from additive and dominance variation in generation means. *Heredity*, 12:37-40
- Johnson, H.W.; H. F. Robinson and R. E. Comstock (1955). Estimation of genetic and environmental variability in soybeans. *Agron. J.*, 47: 314-318.
- Mather, K. (1949). *Biometrical Genetics*. Dover Publications, Inc., London.
- Mather, K., and J. L. Jinks. (1982). *Biometrical Genetics* 3rd ed. Chapman and Hall., London.
- Mohamed M. M.; A. M. E. Mohamed and R. M. E. Sherif (2021). Genetic studies on yield and some related characters in two bread wheat crosses using five population model. *Scientific Journal of Agricultural Sciences* 3 (1): 101-110.
- Robinson, H.F.; R.E. Comstock and P.H. Harve (1949). Estimates of heritability and the degree of dominance in corn. *Agron. J.*, 41 (8): 352-359.
- Sareen, S.; N. Bhusal; G. Singh; B.S. Tyagi; V. Tiwari; G.P. Singh and A.K. Sarial (2018). Genetics of grain yield and its components in wheat under heat stress. *Cereal Research Communications* 46(3): 448–459
- Sharma S. N.; R. S. Sain and R. K. Sharma (2003). Genetics of spike length in durum wheat. *Euphytica* 13: 155–161.
- Sharshar, A.M.; M.S. Genedy and Zeinab, E. Ghareeb (2020). Effect of sowing dates on genetic behavior for some bread wheat genotypes using five parameters model. *Annals of Agric. Sci., Moshtohor*, 58(4): 931 – 940.
- Shehab-Eldeen, M.T; M. A. H Darwish and Zeinab, E. Ghareeb (2020). Gene effect estimation for yield–characters and inheritance of yellow rust resistance among generations in three bread wheat crosses. *IJI-SET - International Journal of Innovative Science, Engineering & Technology*, Vol. 7 Issue 12, December
- Singh, L.P. and S.S. Narayanan (2000). *Biometrical Techniques in plant Breeding*. Klyani Publishers, New, Delhi, 2nd ed.
- Singh, R. k. and B. D. Chaudhry (1985). *Biometrical Methods in Quantitative Genetic Analysis*. Kalyani publishers, New Delhi, Ludhiana, India.
- Zaazaa, E. I. (2017). Genetic analysis of yield and its components in some bread wheat crosses (*Triticum aestivum L.*) using five parameters model. *J. Plant Production, Mansoura Univ.*, 8(11): 1215 – 1220.